

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:32 ; Search time 149.949 Seconds  
(without alignments)  
328.182 Million cell updates/sec

Title: US-10-632-706-86

Perfect score: 590  
Sequence: 1 DIETOSPAIMSPGKVT.....QSNEDPYTGGSDQGNKR 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: Geneseq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003s:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	590	100.0	112	ADR38684 Mouse lig
2	510.5	86.5	107	ADR38683 Mouse lig
3	461.5	78.2	108	AAR79884 Anti-EGFR
4	460.5	78.1	108	AAY97236 Variable
5	460.5	78.1	108	AAB82710 VEGF anta
6	460.5	78.1	108	AAB825956 Mouse ant
7	460.5	78.1	108	AAB74413 Antigen-b
8	460.5	78.1	108	ABJ26725 VEGF bind
9	460.5	78.1	108	ADK18202 Mouse VEG
10	460.5	78.1	240	AAB25960 KDR bindi
11	460.5	78.1	240	AAB74419 Antigen-b
12	460.5	78.1	240	ABJ26731 VEGF bind
13	460.5	78.1	240	ADK18221 Mouse kin
14	460.5	78.1	330	AAH70842 SNV-env 1
15	456.5	77.4	106	AAH13144 Humanised
16	456.5	77.4	106	AAU74418 Antigen-b
17	456.5	77.4	106	ABJ26730 VEGF bind
18	456.5	77.4	106	ADK18217 Mouse VEG
19	456.5	77.4	109	ABU63531 Anti-cucu
20	456.5	77.4	125	AAB82702 VEGF anta
21	456.5	77.4	125	AAH13146 Chimeric
22	456.5	77.4	125	AAH25966 Mouse ant
23	456.5	77.4	238	AAH25961 KDR bindi
24	456.5	77.4	238	AAH25963 KDR bindi

25	456.5	77.4	238	5	AAU74420	AAU74420 Antigen-b
26	456.5	77.4	238	6	ABJ26732	ABJ26732 VEGF bind
27	456.5	77.4	238	8	ADK18222	ADK18222 Mouse kin
28	453.5	76.9	125	5	AAH28917	AAH28917 C-PI31 V
29	449.5	76.2	108	2	AAW41388	AAW41388 Anti-CRA
30	449.5	76.2	235	2	AAW41392	AAW41392 Chimeric
31	449.5	76.2	266	8	ADH77307	ADH77307 Yeast k11
32	448.5	76.0	108	2	AAH21294	AAH21294 Murine VL
33	448.5	76.0	108	2	AAH21294	AAH21294 Anti-p53
34	448.5	76.0	258	4	AAH82898	AAH82898 Anti-p53
35	447.5	75.8	107	4	AAH83159	AAH83159 Mouse gan
36	447.5	75.8	107	9	ADZ52586	ADZ52586 Mouse ant
37	447.5	75.8	108	2	AAH21290	AAH21290 Murine VL
38	447.5	75.8	129	2	AAH53329	AAH53329 KM-796 an
39	447.5	75.8	129	2	AAH28385	AAH28385 Anti-CW2
40	447.5	75.8	129	2	AAH28357	AAH28357 Antibody
41	445.5	75.5	110	2	AAH21305	AAH21305 Murine VL
42	443.5	75.2	106	8	ADH15137	ADH15137 Mouse ant
43	443.5	75.2	236	2	AAH34096	AAH34096 Partial a
44	439.5	74.5	105	2	AAH03182	AAH03182 Guy's 13
45	439.5	74.5	109	5	AAH81278	AAH81278 Murine tr

## ALIGNMENTS

RESULT 1  
ADR38684  
ID ADR38684 standard; peptide; 112 AA.

AC ADR38684;

DT 02-DEC-2004 (first entry)

DE Mouse light chain variable region scFv seqid 86.

KM antibacterial; antibody; botulinum neurotoxin type A; BONT/A;

KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;

KM light chain variable region; single chain antibody; scFv.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PP 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

PA (REGC ) UNITV CALIFORNIA.

PI Marks JD, Amersdorfer P;

PS WPI, 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,

PT useful for diagnosing botulism or for treating pathologies associated

PT with botulinum neurotoxin poisoning.

PS Example 1; SEQ ID NO 86; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds

CC to an epitope specifically bound by an antibody expressed by a specific

CC clone where (I) binds to and neutralises botulinum neurotoxin type A

CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope

CC specifically bound by an antibody expressed by a clone chosen from clone

CC S25, C39, C39, 1C6, 3D12, B4, 1F3, huc25, A1, Ar2, WRI (V), WRI (V), 3-1,

CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum

CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)

CC comprising BONT/A neutralising epitope having an epitope that is

CC		specifically bound by an antibody expressed by clones as mentioned in (I)
CC		, producing (I), and a composition (II) comprising several anti-
CC		botulinum neurotoxin antibodies, where each antibody is specific for a
CC		different epitope of a botulinum neurotoxin and the combination of
CC		antibodies shows greater toxin neutralisation than the single antibodies
CC		in surplus. The following are disclosed: a pharmaceutical composition
CC		comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC		BONT/A antibody and for neutralising a botulinum neurotoxin which
CC		involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC		specific for a different epitope of the botulinum neurotoxin and the
CC		combination of antibodies shows greater toxin neutralisation than the
CC		single antibodies in surplus. (I) is useful for diagnosing the botulinum
CC		or for treating pathologies associated with botulinum neurotoxin
CC		poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
CC		enables rapid detection or diagnosis of botulinum. This is the amino acid
CC		sequence of a mouse light chain variable fragment anti-botulinum toxin
CC		sCfV.
XX		
SQ	Sequence 112 AA;	
Qy	Query Match	100.0%; Score 530; DB 8; Length 112;
Db	Best Local Similarity	100.0%; Pred. No. 1.6e-38;
	Matches 112; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Qy	1 DIETOSPALMSASPKKVTTCRASVSVDYSGHSPMFOOKPPTSLMTYSTNSLAS	60
Db	1 DIETOSPALMSASPKKVTTCRASVSVDYSGHSPMFOOKPPTSLMTYSTNSLAS	60
Qy	61 GVDPARFSGSGSGLTYSRLTSRMEADDAATYYCOQSNEDPYTFGSDGDQGNKR	112
Db	61 GVDPARFSGSGSGLTYSRLTSRMEADDAATYYCOQSNEDPYTFGSDGDQGNKR	112
RESULT 2		
ID	ADR38683	
XX	ADR38683 standard; peptide; 107 AA.	
XX	ADR38683;	
DT	02-DEC-2004 (first entry)	
DE	Mouse light chain variable region scfv seqid 85.	
KX	antibacterial; antibody; botulinum neurotoxin type A; BONT/A;	
KW	BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;	
KW	toxin neutralisation; botulinum neurotoxin poisoning; mouse;	
KX	light chain variable region; single chain antibody; scFv.	
OS	Mus sp.	
XX		
XX	US2004175385-A1.	
PN		
PD	09-SEP-2004.	
PF	01-AUG-2003; 2003US-00632706.	
PR	31-AUG-1998; 98US-00144886.	
PR	01-AUG-2002; 2002US-0400721P.	
PA	(REGC ) UNIV CALIFORNIA.	
PJ	Marks JD, Amerdorfer P;	
DR	WPI; 2004-652009/63.	
XX		
PT	New isolated antibody that neutralizes botulinum neurotoxin type A,	
PT	useful for diagnosing botulinum or for treating pathologies associated	
PS	with botulinum neurotoxin poisoning.	
PS	Example 1; SEQ ID NO 85; 110pp; English.	
CC	The invention describes an isolated antibody (I) that specifically binds	
CC	to an epitope specifically bound by an antibody expressed by a specific	

Query Match	86.5%	Score 510.5	DB 8	Length 107
Best Local Similarity	91.0%	Pred. No. 2.4e-32		
Matches 101	Conservative 1	Mismatches 4	Indels 5	Gaps 1
Qy	1	DIETOSPALMSAPGGRKNTTTCRASSYDSYGHSPFMQOQRPQTSPKLMTYSTNLAS	60	
Db	1	DIETOSPALMSAPGGRKNTTTCRASSSV-----SYGMRQOQRPQTSPKLMTYSTNLAS	55	
Oy	61	GVPARFGSGSGTSYSLTISRMEADATATYYCOOSNEDPYTFGSGDQAGNK	111	
Db	56	GVPARFGSGSGTSYSLTISRMEADATATYYCOOSNEDPYTFGSGDQAGNK	106	
RESULT 3				
AA79884				
ID	AA79884	standard; protein; 108 AA.		
XX	AA79884;			
XX	02-JUL-1996	(first entry)		
DT	XX	Anti-SGFR antibody light chain variable region (clone L2 8C).		
DE	XX	Single chain antibody; antibody; epidermal growth factor receptor; EGFR;		
XX	KW	tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;		
KV	KW	phage antibody library.		
XX	XX	Mus musculus.		
DS	XX			
XX	XX	Location/Qualifiers		
FT	FT	1..23		
FT	FT	/label= Framework region 1.		
FT	FT	24..33		
FT	FT	/label= CDRL1.		
FT	FT	34..48		
FT	FT	/label= Framework region 2.		
FT	FT	49..55		
FT	FT	/label= CDR2.		
FT	FT	56..87		
FT	FT	/label= Framework region 3.		
FT	FT	88..96		
FT	FT	/label= CDR3.		
FT	FT	97..108		
FT	FT	/label= Framework region 4.		
XX	XX			
FN	FN	W09525167-A1		



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XX PD 21-SEP-1995.
XX PF 16-MAR-1995; 95WO-EP000978.
XX PR 17-MAR-1994; 94EP-00104160.
XX PR 02-DEC-1994; 94EP-00118970.
XX PA (MERE ) MERCK PATENT GMBH.
XX PI Kettleborough AC, Bendig MW, Ansell KH, Guessow D, Adan J;
XX PI Mitjans F, Rosell E, Blasco F, Piulats J;
XX DR WPI, 1995-336972/43.
XX PT Anti-EGFR antibodies and single chain Fv antibody fragments - obtained
XX PT from phage-antibody libraries, useful for diagnosis and therapy of
XX PT tumours.
XX PS Disclosure; Fig 1A; 93pp; English.
XX CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies and
XX CC antibodies constructed from anti-EGFR antibody fragments can be used for
XX CC diagnosis of tumours and assessment of tumour growth in vitro and in
XX CC vivo. They may also be used in a pharmaceutical composition for the
XX CC therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and
XX CC fragments are derived from mice but are humanised so as to cause minimum
XX CC reaction against them. They are produced using the phage antibody library
XX SQ Sequence 108 AA;

Query Match 78.2%; Score 461.5; DB 2; Length 108;
Best Local Similarity 82.1%; Pred. No. 1.6e-28;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIELTQSPAIMSASGKRYTTTCRASBSVDYSGHSPMQFOOKPGTSPKLTWYTSNLA 60
DB 1 DIELTQSPAIMSASGKRYTTTCRASBSVDYSGHSPMQFOOKPGTSPKLTWYTSNLA 55
QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFGSGDQGNKR 112
DB 56 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFGSGDQGNKR 107

RESULT 4
AAB97236
ID AAB97236 standard; protein; 108 AA.
XX AC AAB97236;
XX DT 19-DEC-2000 (first entry)
XX DE Variable light chain fragment of anti-SI(KDR) antibody.
XX KW Immunoglobulin; antibody; complementary determining region; CDR; VEGF;
XX KW vascular endothelial growth factor; KDR;
XX KW kinase insert domain containing receptor; multivalent; monovalent;
XX KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
XX KW glioblastoma multiforme; hemangioblastoma; AIDS;
XX KW central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
XX KW acquired immune deficiency syndrome; AIDS; human.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200044777-A1.
XX PD 03-AUG-2000.
XX PF 28-JAN-2000; 2000WO-US002180.
XX PR 29-JAN-1999; 99US-00240736.
XX PR 29-JAN-1999; 99US-0117726P.

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XX PA (IMCL-) IMCLONE SYSTEMS INC.
XX PI Zhu Z, Witte L;
XX DR WPI, 2000-505966/45.
XX DR N-PSDB; AAA53768.
XX PT Novel immunoglobulin molecules binding kinase insert domain-containing
XX PT receptor with the same affinity as vascular endothelial growth factor,
XX PS used to reduce tumor growth.
XX PS Claim 4; Page 51; 55pp; English.
XX CC New immunoglobulin molecules are described that bind kinase insert domain
XX CC -containing receptor (KDR) with a comparable affinity to human vascular
XX CC endothelial growth factor (VEGF). The antibodies neutralise KDR
XX CC activation. The immunoglobulin may be a multivalent single chain
XX CC antibody, a monovalent single chain antibody, a diabody, a triabody, a
XX CC humanised antibody or a chimerised antibody. The immunoglobulin molecules
XX CC bind specifically to an extracellular domain of the KDR receptor with the
XX CC same affinity as VEGF. Overexpression of VEGF has been implicated in a
XX CC number of human tumour cell lines including glioblastoma multiforme,
XX CC hemangioblastoma, central nervous system neoplasms and AIDS associated
XX CC Kaposi's sarcoma. The antibodies therefore have applications in treating
XX CC these conditions. This sequence encodes a preferred heavy chain
XX CC complementary determining region of the immunoglobulins of the invention
XX SQ Sequence 108 AA;

Query Match 78.1%; Score 460.5; DB 3; Length 108;
Best Local Similarity 82.1%; Pred. No. 1.9e-28;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIELTQSPAIMSASGKRYTTTCRASBSVDYSGHSPMQFOOKPGTSPKLTWYTSNLA 60
DB 1 DIELTQSPAIMSASGKRYTTTCRASBSVDYSGHSPMQFOOKPGTSPKLTWYTSNLA 55
QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFGSGDQGNKR 112
DB 56 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFGSGDQGNKR 107

RESULT 5
AAB82710
ID AAB82710 standard; protein; 108 AA.
XX AC AAB82710;
XX DT 11-SEP-2003 (revised)
XX DT 15-OCT-2001 (first entry)
XX DE VEGF antagonist antibody IMC-1C11 light chain variable region.
XX KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
XX KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
XX KW tumour; breast carcinoma; collagen-vascular disease; autoimmune disease;
XX KW colon carcinoma; ovarian carcinoma; neuroblastoma;
XX KW glioblastoma multiforme; melanoma; therapy; light chain.
XX OS Mus sp.
XX OS Homo sapiens.
XX OS Chimeric.
XX FH Key
XX FT 24. 33 Location/Qualifiers
XX FT /label= CDR-L1
XX FT /note= "complementarity determining region 1"
XX FT 49. 55
XX FT /label= CDR-L2
XX FT /note= "complementarity determining region 2"
XX FT 88. 96
XX FT Region

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FT	/label= CDR-L3
XT	/note= "complementarity determining region 3"
FN	WO200154723-A1.
PD	02-AUG-2001.
XX	
PF	29-JAN-2001; 2001WO-US002839.
XX	
PR	28-JAN-2000; 2000US-0178791P.
PR	31-MAR-2000; 2000US-00539692.
XX	
PA	(SUNN-) SUNNIBROOK HEALTH SCI CENT.
PA	(IMCL-) IMCLONE SYSTEMS INC.
XX	
PI	Kerbel R,
DR	WPI; 2001-514531/56.
DR	N-PSDB; AAH26406.
XX	
PT	Treating or controlling an angiogenic dependent condition (e.g. a
PT	neoplasm, collagen-vascular or auto-immune disease) in mammal by
PT	administering a combination of an anti-angiogenic molecule and a
PT	chemotherapeutic agent.
XX	
PS	Disclosure; Page 38-39; 42pp; English.
XX	
CC	The present sequence is that of the light chain variable region of IMC-
CC	1C11, a mouse-human chimeric antibody that has vascular endothelial
CC	growth factor (VEGF) antagonist activity. The antibody, or a fragment of
CC	it, can be used as an anti-angiogenic molecule, together with a
CC	chemotherapeutic acid, for the treatment of an angiogenic dependent
CC	condition in a mammal, especially a human. The invention relates
CC	generally to a method of treating or controlling an angiogenic dependent
CC	condition by administering an anti-angiogenic molecule and a
CC	chemotherapeutic agent, to produce a regression or arrest of the
CC	condition while minimizing or preventing significant toxicity of the
CC	chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks
CC	the action of a vascular endothelium survival factor such as VEGF or its
CC	receptor, and is especially IMC-1C11. Conditions that can be treated
CC	include a neoplasm, a collagen-vascular disease or an autoimmune disease,
CC	especially a solid tumour, including breast carcinoma, lung carcinoma,
CC	prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian
CC	carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma,
CC	glioblastoma multiforme or melanoma (all claimed). (Updated on 11-SEP-
CC	2003 to standardise OS field)
XX	
8Q	Sequence 108 AA;
XX	
Query Match	78.1%; Score 460.5; DB 4; Length 108;
Best Local Similarity	82.1%; Pred. No. 1.9e-28;
Matches	92; Conservative 4; Mismatches 11; Indels 5; Gaps 1
QY	1 DIELTQSPAINASGEGEYKTTTCRASEYSDYSGHSPQMFOQKPTGTPKLTMTYTSNLAS 60
DB	1 DIELTQSPAINASGEGEYKTTTCRASSSV-----SYMHFQKPPPTSPKLTMTYTSNLAS 55
QY	61 GVPARFSPGSGSTSYLTITSRMEADATYYCGQSNEDPDYTGSGDDQGNKR 112
DB	56 GVPARFSPGSGSTSYLTITSRMEADATYYCQKRSYPTFGSGTKLEIKR 107
RESULT 6	
AAE25956	AAE25956 standard; protein; 108 AA.
XX	
AC	AAE25956;
XX	
DT	15-NOV-2002 (first entry)
XX	
DE	Mouse anti-KDR p1C11 scFv antibody VL region #1.
XX	
XX	Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;

KM	foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;
KM	VEGF; tumour growth; light chain variable region; VL; angiogenesis;
KM	p1c11; scFv antibody.
XX	
XX	Mus musculus.
XX	
XX	US2002064528-A1.
XX	
XX	30-MAY-2002.
XX	
XX	12-OCT-2001; 2001US-00976787.
XX	
XX	28-JAN-2000; 2000US-00493539.
PR	
PA	(ZHUZ/) ZHU Z.
PA	(WITTE/) WITTE L.
XX	
PI	Zhu Z, Witte L;
DR	WPI; 2002-589175/63.
DR	N-PSDB; AAD42821.
PT	Novel immunoglobulin molecule for reducing tumor growth, binds to kinase
PT	insert domain-containing receptor with an affinity comparable to human
PT	vascular endothelial growth factor, and neutralizes activation of KDR.
XX	
XX	Claim 4; Page 11; 34pp; English.
XX	
CC	The present invention relates to novel immunoglobulin molecules that bind
CC	to kinase insert domain-containing receptor (KDR) (a human homologue of
CC	mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable
CC	to human vascular endothelial growth factor (VEGF) and that neutralises
CC	activation of KDR. Sequences of the invention are useful for neutralising
CC	the activation of KDR, for reducing tumour growth and for inhibiting
CC	angiogenesis. The present sequence is mouse anti-KDR p1c11 scFv antibody
XX	light chain variable region (VL)
XX	
XX	Sequence 108 AA;
XX	
XX	Query Match 78.1%; Score 460.5; DB 5; Length 108;
XX	Best Local Similarity 82.1%; Pred. No. 1,9e-28;
XX	Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
QY	1 DIELTQSPALMSASPGKRVTTTCRASSVDSTGHSFMQWFOQKGTSPKMTIYSTNLAS 60
DB	1 DIELTQSPALMSASPGKRVTTTCRASSSV-----SYNHWFOQKGTSPKMTIYSTNLAS 55
QY	61 GVPARFSGSGGCTSYSLTIRMEADATYYTQOSNEDPTFFSGDDAQNKR 112
DB	56 GVPARFSGSGGCTSYSLTIRMEADATYYTQQRSSSYPTFFSGGTLEIKR 107
XX	
XX	RESULT 7
XX	AAU74413
XX	ID AAU74413 standard; peptide; 108 AA.
XX	
XX	AAU74413;
XX	
XX	26-MAR-2002 (first entry)
XX	
DE	Antigen-binding protein light chain variable domain (VH) #1.
XX	
XX	Antigen-binding protein; antibody light chain variable domain;
KM	cytotoxic; angiogenesis inhibitor; tumour; leukaemia; antibody;
KM	vascular endothelial growth factor receptor; VEGF;
KM	cell proliferation inhibitor.
XX	
OS	Mus sp.
XX	
XX	MO200190192-A2.
XX	
XX	29-NOV-2001.
XX	

PF 24-MAY-2001; 2001WO-US016924.  
 XX  
 PR 24-MAY-2000; 2000US-0206749P.  
 XX  
 PA (IMCL-) IMCLONE SYSTEMS INC.  
 XX  
 PI Zhu Z;  
 XX  
 DR WPI; 2002-106189/14.  
 DR N-PSDB; AAS20284.  
 PT New bispecific immunoglobulin-like antigen-binding protein for reducing  
 PT tumor growth and for inhibiting angiogenesis, comprises a complex of two  
 PT polypeptides and two second polypeptides.  
 XX  
 PS Claim 57; Page 57; 64pp; English.  
 XX  
 CC The invention describes an antigen-binding protein (1) comprising a  
 CC complex of two polypeptides (p1) and two second polypeptides (p2) which  
 CC are stably associated in an immunoglobulin like complex. p1 has an  
 CC antigen-binding site located to the N terminus of immunoglobulin (1g)  
 CC light chain constant domain (CL domain), and p2 has an antigen-binding  
 CC site located to the N terminus of the CH1 domain. (1) is useful for:  
 CC neutralising the activation of a vascular endothelial growth factor  
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
 CC reducing endothelial cell proliferation; inhibiting VEGF induced  
 CC migration of human leukaemia cells; blocking interaction of a protein and  
 CC its ligand; promoting interactions between immune cells and target cells;  
 CC and in vivo and in vitro for investigative, diagnostic or treatment  
 CC methods. The design of (1) provides for efficient production so that  
 CC substantially all of the antigen-binding proteins produced are assembled  
 CC in the desired configuration. (1) is bivalent and bispecific, homogeneous  
 CC and in tetrameric form. The heavy chain constant domains which constitute  
 CC the FC region (e.g., CH2 and CH3 for an Igg molecule) of a natural  
 CC antibody and which provide other antibody functions can be present. There  
 CC is no requirement for processing in vitro to obtain the complete product.  
 CC This sequence represents a light chain variable domain (VH) incorporated  
 CC into Fv, an engineered protein containing a heavy chain variable domain  
 CC and a light chain variable domain in one polypeptide chain, described in  
 CC the method of the invention  
 XX  
 SQ Sequence 108 AA;  
 Query Match 78.1%; Score 460.5; DB 5; Length 108;  
 Best Local Similarity 82.1%; Pred. No. 1.9e-28;  
 Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;  
 QY 1 DIELTQSPAINASPGKVTTCRASVSVDYGHGFQWFOOKPRTSPKMTYISTSNLAS 60  
 DB 1 DIELTQSPAINASPGKVTTCRASVSVDYGHGFQWFOOKPRTSPKMTYISTSNLAS 55  
 QY 61 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYFGSGDQGNKR 112  
 DB 56 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYFGSGDQGNKR 107  
 RESULT 8  
 ABJ26725  
 ID ABJ26725 standard; protein, 108 AA.  
 XX  
 AC ABJ26725;  
 XX  
 DT 01-MAY-2003 (first entry)  
 XX  
 DE VEGF binding related protein SEQ ID No 8.  
 XX  
 KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
 KW leukaemia cell; vascular endothelial growth factor; tumour;  
 XX bispecific antigen-binding protein; mouse; murine.  
 OS Mus sp.  
 XX  
 PN WO2003002144-A1.

XX  
 PD 09-JAN-2003.  
 XX  
 PF 26-JUN-2002; 2002WO-US020332.  
 XX  
 PR 26-JUN-2001; 2001US-0301299P.  
 XX  
 PA (IMCL-) IMCLONE SYSTEMS INC.  
 XX  
 PI Zhu Z;  
 XX  
 DR WPI; 2003-201468/19.  
 DR N-PSDB; ABT23303.  
 PT New bispecific antibodies having antigen-binding sites specific for a  
 PT first vascular endothelial growth factor (VEGF) receptor and for a second  
 PT VEGF receptor, useful for inhibiting migration of leukemia cells, or for  
 PT treating tumors.  
 XX  
 PS Claim 7; Page 49-50; 98pp; English.  
 XX  
 CC The invention relates to a novel antibody having a first antigen binding  
 CC site specific for a first vascular endothelial growth factor (VEGF)  
 CC receptor and a second antigen-binding site specific for a second VEGF  
 CC receptor. The bispecific antigen-binding proteins block activation of the  
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
 CC cellular functions such as mitogenesis of vascular endothelial cells and  
 CC migration of leukaemia cells. The antibodies are useful for treating  
 CC tumours and for in vivo or in vitro for investigative and diagnostic  
 CC methods. This sequence represents a mouse protein relating to the  
 CC bispecific antibodies that bind to the VEGF receptors of the invention  
 XX  
 SQ Sequence 108 AA;  
 Query Match 79.1%; Score 460.5; DB 6; Length 108;  
 Best Local Similarity 82.1%; Pred. No. 1.9e-28;  
 Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;  
 QY 1 DIELTQSPAINASPGKVTTCRASVSVDYGHGFQWFOOKPRTSPKMTYISTSNLAS 60  
 DB 1 DIELTQSPAINASPGKVTTCRASVSVDYGHGFQWFOOKPRTSPKMTYISTSNLAS 55  
 QY 61 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYFGSGDQGNKR 112  
 DB 56 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYFGSGDQGNKR 107  
 RESULT 9  
 ADK18202  
 ID ADK18202 standard; peptide, 108 AA.  
 XX  
 AC ADK18202;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Mouse VEGF receptor light chain variable domain peptide, SEQ ID No 8.  
 XX  
 KW antibody; antigen binding site; vascular endothelial growth factor;  
 KW VEGF receptor; immunoglobulin; tumour; angiogenesis; cytosstatic;  
 KW immunostimulant; vaccine; complementarity determining region; variable;  
 XX light; mouse; murine.  
 OS Mus sp.  
 XX  
 PN WO2004003211-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 24-DEC-2002; 2002WO-US041372.  
 XX  
 PR 26-JUN-2002; 2002WO-US020332.  
 XX  
 PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z;  
 XX DR WPI, 2004-083065/08.  
 XX PT New antibody having a first and second binding sites specific for a first  
 XX PT and second vascular endothelial growth factor (VEGF) receptor, useful for  
 XX PT reducing tumor growth in a mammal and for inhibiting angiogenesis.  
 PS Claim 7, SEQ ID NO 8, 99pp; English.  
 CC The invention relates to a novel antibody having a first antigen binding  
 CC site specific for a first vascular endothelial growth factor (VEGF)  
 CC receptor and a second antigen specific for a second VEGF receptor. The  
 CC invention further relates to: an antibody that specifically binds to an  
 CC extracellular domain of a first VEGF receptor and an extracellular domain  
 CC of a second VEGF receptor, where binding of the antibody to the first and  
 CC second VEGF receptor neutralizes activation of that VEGF receptor; a  
 CC method for making the antibody by co-expressing in a host cell a  
 CC recombinant DNA construct encoding a first polypeptide having the first  
 CC immunoglobulin heavy chain domain located to the N-terminus of the second  
 CC immunoglobulin light chain variable domain; a recombinant DNA construct  
 CC encoding a second polypeptide having the second immunoglobulin heavy  
 CC chain variable domain located to the N-terminus of the first  
 CC immunoglobulin light chain variable domain, for time and in a manner  
 CC sufficient to allow expression of the polypeptides and formation of the  
 CC antibody; a method for neutralizing activation of a first VEGF receptor  
 CC and the second VEGF receptor in a cell by treating a cell with the  
 CC antibody cited above; a method for reducing tumor growth in a mammal by  
 CC treating the mammal with the antibody cited above; and a method for  
 CC inhibiting angiogenesis in a mammal by treating the mammal with the  
 CC antibody cited above. The antibody has cytostatic and immunostimulant  
 CC activities. The VEGF receptor antigen can be used to create a vaccine.  
 CC The antibody is useful for reducing tumor growth in a mammal and for  
 CC inhibiting angiogenesis. This sequence represents a VEGF receptor  
 CC variable light chain peptide of the invention.  
 XX  
 SQ Sequence 108 AA;  
 Query Match 78.1%; Score 460.5; DB 8; Length 108;  
 Best Local Similarity 82.1%; Pred. No. 1.9e-28;  
 Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;  
 QY 1 DIETOSPALMSAPGEKVTTCRASGVDSYGHSPFMQFOQKPGTSPKLMYSTSLAS 60  
 DB 1 DIETOSPALMSAPGEKVTTCRASGVDSYGHSPFMQFOQKPGTSPKLMYSTSLAS 55  
 QY 61 GVPARFSGSGSGTSYSLTISRMEADATYYCOQSNEDPYTFSGDQAGNKR 112  
 DB 56 GVPARFSGSGSGTSYSLTISRMEADATYYCOQRSSTPFTFSGTKLEIKR 107  
 RESULT 10  
 AAE25960  
 ID AAE25960 standard; protein; 240 AA.  
 AC AAE25960;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE KDR binding immunoglobulin related mouse protein #1.  
 XX  
 XX Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;  
 XX foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;  
 XX VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;  
 XX pIC11; scFv antibody.  
 XX Mus sp.  
 XX OS  
 XX US2002064528-A1.  
 XX PN  
 XX PD 30-MAY-2002.  
 XX

PF 12-OCT-2001; 2001US-00976787.  
 XX  
 XX 28-JAN-2000; 2000US-00493539.  
 XX  
 XX (ZHUZ/) ZHU Z.  
 XX PA (WITTE/) WITTE L.  
 XX PI Zhu Z, Witte L,  
 XX WPI, 2002-569175/63.  
 DR N-PSDB; AAD42824.  
 XX  
 XX Novel immunoglobulin molecule for reducing tumor growth, binds to kinase  
 XX insert domain-containing receptor with an affinity comparable to human  
 XX PT vascular endothelial growth factor, and neutralizes activation of KDR.  
 XX  
 XX PS Disclosure, Page 16-17, 34pp; English.  
 XX  
 CC The present invention relates to novel immunoglobulin molecules that bind  
 CC to kinase insert domain-containing receptor (KDR) (a human homologue of  
 CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable  
 CC to human vascular endothelial growth factor (VEGF) and that neutralises  
 CC activation of KDR. Sequences of the invention are useful for neutralising  
 CC the activation of KDR, for reducing tumour growth and for inhibiting  
 CC angiogenesis. The present sequence is KDR binding immunoglobulin related  
 CC mouse protein  
 XX  
 SQ Sequence 240 AA;  
 Query Match 78.1%; Score 460.5; DB 5; Length 240;  
 Best Local Similarity 82.1%; Pred. No. 4.2e-28;  
 Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;  
 QY 1 DIETOSPALMSAPGEKVTTCRASGVDSYGHSPFMQFOQKPGTSPKLMYSTSLAS 60  
 DB 133 DIETOSPALMSAPGEKVTTCRASGVDSYGHSPFMQFOQKPGTSPKLMYSTSLAS 167  
 QY 61 GVPARFSGSGSGTSYSLTISRMEADATYYCOQSNEDPYTFSGDQAGNKR 112  
 DB 188 GVPARFSGSGSGTSYSLTISRMEADATYYCOQRSSTPFTFSGTKLEIKR 239  
 RESULT 11  
 AAU74419  
 ID AAU74419 standard; protein; 240 AA.  
 AC AAU74419;  
 XX  
 XX 26-MAR-2002 (first entry)  
 DT  
 XX  
 DE Antigen-binding protein, single chain variable fragment version #1.  
 XX  
 XX Antigen-binding protein, single chain variable fragment; scFv; antigen;  
 XX cytoelastic; angiogenesis inhibitor; tumour; leukaemia; antibody;  
 XX KM vascular endothelial growth factor receptor; VEGF;  
 XX cell proliferation inhibitor.  
 XX  
 XX Mus sp.  
 XX OS Synthetic.  
 XX  
 XX Key  
 XX Location/Qualifiers  
 XX 1..117  
 XX /label= VH  
 XX /note= "heavy chain variable domain. Specifically claimed  
 XX in claim 57"  
 XX 118..132  
 XX /label= Linker  
 XX /note= "15 amino acid linker joins the VH and VL regions  
 XX of the single chain variable protein. Encoded by  
 XX AAS20285"  
 XX 133..240  
 XX /label= VL  
 XX /note= "light chain variable domain. Specifically claimed  
 XX Region  
 XX

## in claim 57"

FT XX Mus sp.  
 FN WO200190192-A2.  
 PD 29-NOV-2001.  
 XX 24-MAY-2001; 2001WO-US016924.  
 XX 24-MAY-2000; 2000US-0206749P.  
 XX (IMCL-) IMCLONE SYSTEMS INC.  
 PA Zhu Z;  
 PI  
 XX WPI; 2002-106189/14.  
 DR  
 XX New bispecific immunoglobulin-like antigen-binding protein for reducing  
 PT tumor growth and for inhibiting angiogenesis, comprises a complex of two  
 PT polypeptides and two second polypeptides.  
 PS Claim 63; Page 62; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a  
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which  
 CC are stably associated in an immunoglobulin like complex. P1 has an  
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)  
 CC light chain constant domain (CL domain), and P2 has an antigen-binding  
 CC site located to the N terminus of the CH1 domain. (I) is useful for:  
 CC neutralising the activation of a vascular endothelial growth factor  
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;  
 CC reducing endothelial cell proliferation; inhibiting VEGF induced  
 CC migration of human leukemia cells; blocking interaction of a protein and  
 CC its ligand; promoting interactions between immune cells and target cells;  
 CC and in vivo and in vitro for investigative, diagnostic or treatment  
 CC methods. The design of (I) provides for efficient production so that  
 CC substantially all of the antigen-binding proteins produced are assembled  
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous  
 CC and in tetrameric form. The heavy chain constant domains which constitute  
 CC the FC region (e.g., CH2 and CH3 for an Igg molecule) of a natural  
 CC antibody and which provide other antibody functions can be present. There  
 CC is no requirement for processing in vitro to obtain the complete product.  
 CC This is the amino acid sequence of a single chain variable fragment  
 CC (scFv), an engineered protein containing a variable light and variable  
 CC heavy domain on one polypeptide, described in the method of the invention

XX Sequence 240 AA;

Query Match 78.1%; Score 460.5; DB 5; Length 240;

Best Local Similarity 82.1%; Pred. No. 4.2e-28;  
 Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIETQSPAIMASPGKVTTCRASGVDSYGHSMFOOKPGTSPKLTWYTSNLAAS 60  
 DB 133 DIETQSPAIMASPGKVTTCRASGVDSYGHSMFOOKPGTSPKLTWYTSNLAAS 187  
 QY 61 GVPAFFSGSGSTSYSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNKR 112  
 DB 188 GVPAFFSGSGSTSYSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNKR 239

RESULT 12

ABJ26731 ID ABJ26731 standard; protein; 240 AA.

XX ABJ26731;

XX 01-MAY-2003 (first entry)

DE VEGF binding related protein SEQ ID NO 27.

XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;  
 KW leukaemia cell; vascular endothelial growth factor; tumour;  
 KW bispecific antigen-binding protein; mouse; murine.

XX Mus sp.

FN WO2003002144-A1.

PD 09-JAN-2003.

XX 26-JUN-2002; 2002WO-US020332.

XX 26-JUN-2001; 2001US-0301299P.

XX (IMCL-) IMCLONE SYSTEMS INC.

PA Zhu Z;

PI WPI; 2003-201468/19.

PT New bispecific antibodies having antigen-binding sites specific for a  
 PT first vascular endothelial growth factor (VEGF) receptor and for a second  
 PT VEGF receptor, useful for inhibiting migration of leukemia cells, or for  
 PT treating tumors.

PS Disclosure; Page 55-56; 98pp; English.

XX The invention relates to a novel antibody having a first antigen binding  
 CC site specific for a first vascular endothelial growth factor (VEGF)  
 CC receptor and a second antigen-binding site specific for a second VEGF  
 CC receptor. The bispecific antigen-binding proteins block activation of the  
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced  
 CC cellular functions such as mitogenesis of vascular endothelial cells and  
 CC migration of leukemia cells. The antibodies are useful for treating  
 CC tumors and for in vivo or in vitro for investigative and diagnostic  
 CC methods. This sequence represents a mouse protein relating to the  
 CC bispecific antibodies that bind to the VEGF receptors of the invention

XX Sequence 240 AA;

Query Match 78.1%; Score 460.5; DB 6; Length 240;

Best Local Similarity 82.1%; Pred. No. 4.2e-28;  
 Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIETQSPAIMASPGKVTTCRASGVDSYGHSMFOOKPGTSPKLTWYTSNLAAS 60  
 DB 133 DIETQSPAIMASPGKVTTCRASGVDSYGHSMFOOKPGTSPKLTWYTSNLAAS 187  
 QY 61 GVPAFFSGSGSTSYSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNKR 112  
 DB 188 GVPAFFSGSGSTSYSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNKR 239

RESULT 13

ADK18221 ID ADK18221 standard; protein; 240 AA.

XX ADK18221;

XX 06-MAY-2004 (first entry)

DE Mouse kinase insert domain-containing receptor scFv protein, SEQ ID 27.

XX antibody; antigen binding site; vascular endothelial growth factor;  
 KW VEGF receptor; immunoglobulin; tumour; angiogenesis; cytostatic;  
 KW immunostimulant; vaccine; KDR; kinase insert domain-containing receptor;  
 KW scFv; mouse; murine.

XX Mus sp.

PN WO2004003211-A1.

XX 08-JAN-2004.

XX 24-DEC-2002; 2002WO-US041372.

```
PR 26-JUN-2002; 2002WO-US020332.
XX (IMCL-) IMCLONE SYSTEMS INC.
XX Znu 2;
XX WPI; 2004-083065/08.
PT New antibody having a first and second binding sites specific for a first
PT and second vascular endothelial growth factor (VEGF) receptor, useful for
PT reducing tumor growth in a mammal and for inhibiting angiogenesis.
XX
XX Disclosure; SEQ ID NO 27; 99pp; English.
XX
CC The invention relates to a novel antibody having a first antigen binding
CC site specific for a first vascular endothelial growth factor (VEGF)
CC receptor and a second antigen specific for a second VEGF receptor. The
CC invention further relates to: an antibody that specifically binds to an
CC extracellular domain of a first VEGF receptor and an extracellular domain
CC of a second VEGF receptor, where binding of the antibody to the first and
CC second VEGF receptor neutralizes activation of that VEGF receptor; a
CC method for making the antibody by co-expressing in a host cell a
CC recombinant DNA construct encoding a first polypeptide having the first
CC immunoglobulin heavy chain domain located to the N-terminus of the second
CC immunoglobulin light chain variable domain; a recombinant DNA construct
CC encoding a second polypeptide having the second immunoglobulin heavy
CC chain variable domain located to the N-terminus of the first
CC immunoglobulin light chain variable domain, for time and in a manner
CC sufficient to allow expression of the polypeptides and formation of the
CC antibody; a method for neutralizing activation of a first VEGF receptor
CC and the second VEGF receptor in a cell by treating a cell with the
CC antibody cited above; a method for reducing tumor growth in a mammal by
CC treating the mammal with the antibody cited above; and a method for
CC inhibiting angiogenesis in a mammal by treating the mammal with the
CC antibody cited above. The antibody has cytostatic and immunostimulant
CC activities. The VEGF receptor antigen can be used to create a vaccine.
CC The antibody is useful for reducing tumor growth in a mammal and for
CC inhibiting angiogenesis. This sequence represents a kinase insert domain-
CC containing receptor scfv protein of the invention.
XX
SQ Sequence 240 AA;
Query Match 78.1%; Score 460.5; DB 8; Length 240;
Best Local Similarity 82.1%; Pred. No. 4.2e-28;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
QY 1 DIETLSPALMSASPEKVTTCRASGVDSYGHSMQWFOQKRGTSPKMISTNLAS 60
DB 133 DIETLSPALMSASPEKVTTCRASGVDSYGHSMQWFOQKRGTSPKMISTNLAS 187
QY 61 GVPARFSGSGSGTSYSLTISRMEADATYYCOQSNEDPYTFGSGQOAGNKR 112
DB 188 GVPARFSGSGSGTSYSLTISRMEADATYYCOQSNEDPYTFGSGQOAGNKR 239
RESULT 14
ID AAB70842 standard; protein; 330 AA.
XX AAB70842;
XX
DT 11-SEP-2003 (revised)
DT 25-JUN-2001 (first entry).
XX
DE SNV-env leader/human 7B2-scFv fusion construct.
XX
XX T lymphocyte; antibody; single chain variable antibody; scFv; human;
XX cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
XX gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
XX acquired immune deficiency syndrome; severe combined immune deficiency;
XX T cell lymphoma; fusion construct.
XX
XX Homo sapiens.
XX
```

```
OS Spleen necrosis virus.
OS Chimeric.
XX
XX Key Location/Qualifiers
XX Protein 1..45
XX Protein /label= SNV-env_leader
XX Protein 46..330
XX Protein /label= 7B2-scFv
XX
XX DB19946142-A1.
XX
XX 29-MAR-2001.
XX
XX 27-SEP-1999; 99DE-01046142.
XX
XX 27-SEP-1999; 99DE-01046142.
XX
XX (BUND ) BUNDESREPUBLIK DRUT PAUL-EHRHICH-INST.
XX
XX Cichutek K, Engelstaedter M;
XX
XX WPI; 2001-246140/26.
XX
XX N-PSDB; AAF61511.
XX
XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy
XX of e.g. acquired immune deficiency syndrome, encodes a single-chain
XX variable antibody fragment.
XX
XX Claim 1, Fig 3; 18pp; German.
XX
XX This invention describes a novel cell-targeting vector (A) containing a
XX DNA sequence (i) encoding a single-chain variable antibody fragment
XX (scFv). The products of the invention have antiviral, cytostatic and
XX immunostimulant activity and can be used in gene therapy, immunization
XX and diagnosis particularly of T cell-associated diseases, specifically
XX acquired immune deficiency syndrome (AIDS), severe combined immune
XX deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
XX of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
XX human B cells, and 1000 fold selectivity over other human cells. A vector
XX designated 7A5 encodes a 329 amino acid single-chain variable antibody
XX fragment, fully defined in the specification. It was used to transform
XX CC17 (canine osteosarcoma cells susceptible to spleen necrosis virus
XX (SNV)) cells, C8166 (human T lymphocyte) cells, and Hepa (human cervical
XX carcinoma) cells. After 48 hours, the cells were stained with X-gal to
XX determine transfection. The viral titer (infectious units/ml) was over
XX 1 million for CC17, 1 million for C8166 but less than 100 for Hepa.
XX showing the high selectivity for human T cells. This sequence represents
XX the SNV-env leader/human 7B2-scFv fusion construct used in the
XX construction of novel cell targeting vectors described in the invention.
XX (Updated on 11-SEP-2003 to standardise O6 field)
XX
SQ Sequence 330 AA;
Query Match 78.1%; Score 460.5; DB 4; Length 330;
Best Local Similarity 82.1%; Pred. No. 5.8e-28;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
QY 1 DIETLSPALMSASPEKVTTCRASGVDSYGHSMQWFOQKRGTSPKMISTNLAS 60
DB 181 DIETLSPALMSASPEKVTTCRASGVDSYGHSMQWFOQKRGTSPKMISTNLAS 235
QY 61 GVPARFSGSGSGTSYSLTISRMEADATYYCOQSNEDPYTFGSGQOAGNKR 112
DB 236 GVPARFSGSGSGTSYSLTISRMEADATYYCOQSNEDPYTFGSGQOAGNKR 287
RESULT 15
ID AAE13144 standard; protein; 106 AA.
XX AAE13144;
XX
XX 11-SEP-2003 (revised)
XX
```

```

DT 28-JAN-2002 (first entry)
XX Humanised antibody light chain fragment.
DE
XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
XX cytosolic; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;
XX monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
XX human; chimeric.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
XX WO200174296-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US010504.
XX
XX 31-MAR-2000; 2000US-00540770.
XX
XX (IMCL-) IMCLONE SYSTEMS INC.
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Witte L, Rafii S;
XX
XX MPI; 2001-662942/76.
XX N-PSDB; AAD21670.
XX
XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
XX tumors such as leukemias or multiple myeloma comprises treatment with an
XX antagonist of a vascular endothelial growth factor receptor.
XX
XX Claim 8; Page 16; 68pp; English.
XX
XX The invention relates to a method for inhibiting the growth of non-solid
XX tumour cells that are stimulated by a ligand of vascular endothelial
XX growth factor receptor (VEGFR) in mammals particularly humans. The method
XX involves treating the mammals with humanised VEGFR monoclonal antibodies
XX (antagonists). Humanised monoclonal antibody comprises humanised mouse
XX variable region joined to human constant region, where the humanised
XX mouse variable region contains mouse complementarity determining region
XX (CDR) grafted into human variable region. The method is useful for
XX treating leukemias such as acute or chronic myelocytic leukaemia, acute
XX or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
XX multiple myelomas and lymphoid cells, particularly those related to non-
XX Hodgkin's and Hodgkin's disease. The present sequence is humanised
XX antibody light chain fragment used in the exemplification of the
XX invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 106 AA;

```

Query Match 77.4%; Score 456.5; DB 4; Length 106;  
 Best Local Similarity 85.7%; Pred. No. 3.9e-28;  
 Matches 90; Conservative 3; Mismatches 7; Indels 5; Gaps 1;

```

QY 1 DIELTSPAIMSASPEKVTTCRASESVSYGHSFMOWPOOKRGTSPKLMITSTSNLAS 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DIELTSPAIMSASPEKVTTCRASESVSYGHSFMOWPOOKRGTSPKLMITSTSNLAS 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDDPYTFGSG 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSRSSYPTEFGSG 100
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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OM protein - protein search, using sw model

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(without alignments)  
394.995 Million cell updates/sec

Title: US-10-632-706-86  
Perfect score: 590  
Sequence: 1 DIEITQSPAIMSASPGKEKVT.....QOSNEDPYTGGSDQGNKR 112

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 283416

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	429.5	72.8	107 2 PC4405	Ig kappa chain V r
2	427.5	72.5	140 2 PL0013	Ig kappa chain V r
3	424.5	71.9	106 2 B54378	Ig light chain V r
4	422.5	71.6	130 2 A34513	Ig kappa chain pre
5	419.5	71.1	107 2 A42848	Ig light chain V r
6	416.5	70.6	107 2 A30562	Ig kappa chain V r
7	411.5	69.7	107 2 B30562	Ig kappa chain V r
8	409.5	69.4	130 2 S04573	Ig kappa chain pre
9	407.5	69.1	100 2 S28590	Ig kappa chain V r
10	407.5	69.1	107 2 PD0011	Ig kappa chain V r
11	407.5	69.1	120 2 S66536	Ig light chain V r
12	406.5	68.9	130 1 JL0079	Ig kappa chain pre
13	405.5	68.7	103 2 S29591	Ig kappa chain V r
14	404.5	68.6	130 2 B32456	Ig kappa chain pre
15	404.5	68.6	235 2 S25058	Ig kappa chain V r
16	402.5	68.2	105 2 S26338	Ig kappa chain V r
17	401.5	68.1	132 2 B45049	Ig kappa chain V r
18	401.5	68.1	104 2 S05268	Ig kappa chain pre
19	401	68.0	108 2 G30560	Ig kappa chain V r
20	401	68.0	111 1 KJMS37	Ig kappa chain V r
21	400.5	67.9	107 2 PT0406	Ig kappa chain V r
22	399.5	67.7	99 2 D38601	Ig kappa chain V r
23	399.5	67.7	106 2 PS0071	Ig kappa chain V r
24	399.5	67.7	108 2 PL0278	Ig kappa chain V r
25	398.5	67.5	91 2 S17630	Ig kappa chain V r
26	397.5	67.4	91 2 S17626	Ig kappa chain V r
27	397	67.3	108 2 S38720	Ig light chain V r
28	395.5	67.0	93 2 S17641	Ig kappa chain V r
29	395.5	67.0	99 2 PH1058	Ig light chain V r

30	395.5	67.0	108 2 PL0277	Ig kappa chain V r
31	395.5	67.0	108 2 PL0276	Ig kappa chain V r
32	394.5	66.9	97 2 S26341	Ig light chain V r
33	394.5	66.9	99 2 PH1059	Ig light chain V r
34	392.5	66.5	97 2 PH1084	Ig light chain V r
35	392.5	66.5	106 2 PL0082	Ig kappa chain V r
36	392.5	66.5	113 2 S03410	Ig kappa chain pre
37	391.5	66.4	97 2 PH1085	Ig light chain V r
38	391.5	66.4	99 2 S29585	Ig kappa chain V r
39	391.5	66.4	107 2 S11118	Ig kappa chain V r
40	391	66.3	131 1 KJMSW6	Ig kappa chain pre
41	390.5	66.2	106 2 PS0070	Ig kappa chain V r
42	390	66.1	98 2 PH1061	Ig light chain V r
43	389.5	66.0	108 2 PS0069	Ig kappa chain V r
44	388.5	65.8	106 2 G27887	Ig kappa chain V r
45	388.5	65.8	123 2 S05269	Ig kappa chain pre

## ALIGNMENTS

## RESULT 1

PC4405  
Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)  
C/Dates: Mus musculus (house mouse)  
C/Date: 10-Nov-1997 #sequence\_revision 23-Jan-1998 #text\_change 09-Jul-2004  
C/Accession: PC4405  
R/Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.  
Chinese Biochem. J. 12, 648-653, 1996  
A/Title: Generation of a phage display library of the immunoglobulin repertoire from hum  
A/Reference number: PC4405  
A/Accession: PC4405  
A/Molecule type: mRNA  
A/Residues: 1-107 <DEN>  
A/Cross-references: UNIPROT:O8K1F0; UNIPARC:UP100001767B  
A/Experimental source: spleen cell  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
F16-89/Domain: immunoglobulin homology <IMM>

Query Match 72.8%, Score 429.5; DB 2; Length 107;  
Best Local Similarity 75.9%; Pred. No. 3.8e-30;  
Matches 85; Conservative 7; Mismatches 15; Indels 5; Gaps 1;

QY	1	DIEITQSPAIMSASPGKEKVTTCRASGVDSYGHSPQWFOOKRTSKYIYTSNLS	60
DB	1	DIEITQSPAIMSASPGKEKVTTCRASGVDSYGHSPQWFOOKRTSKYIYTSNLS	55
QY	61	GVPAIFSGSGSGTSTLTISRREADATYCCQSNEDPYTGGSDQGNKR	112
DB	56	GVPAIFSGSGSGTSTLTISRREADATYCCQSNEDPYTGGSDQGNKR	107

## RESULT 2

PL0013  
Ig kappa chain precursor V region (4C11) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000  
C/Accession: PL0013  
R/Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kleber-Emmons, T.; Kohler, H.  
Mol. Immunol. 25, 33-40, 1988  
A/Title: Structural basis of stimulatory anti-idiotypic antibodies.  
A/Reference number: PL0011; MUID:88142863; PMID:3125424  
A/Accession: PL0013  
A/Molecule type: mRNA  
A/Residues: 1-140 <CHS>  
A/Cross-references: UNIPARC:UP100001767A6  
A/Experimental source: cell line 4C11  
C/Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcho  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F11-22/Domain: signal sequence #status predicted <SIG>  
F123-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>  
F138-111/Domain: immunoglobulin homology <IMM>

F146-55/Region: complementarity-determining 1  
 F171-77/Region: complementarity-determining 2  
 F110-118/Region: complementarity-determining 3  
 F110-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 72.5%; Score 427.5; DB 2; Length 140;  
 Best Local Similarity 78.4%; Pred. No. 7.4e-30;  
 Matches 87; Conservative 3; Mismatches 16; Indels 5; Gaps 1;

2 IELTQSPALMSASGEGKVTTCRASBSYDYGSHFPMQFPQKPGTSPKLTWYTSNLSAG 61  
 24 IVLTSQSPALMSASGEGKVTTCRASBSYDYGSHFPMQFPQKPGTSPKLTWYTSNLSAG 78

62 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSGDQGNKR 112  
 79 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSGDQGNKR 129

RESULT 3  
 B54378  
 Ig light chain V region anti-triplex DNA - mouse (fragment)

C/Species: Mus musculus (house mouse)  
 C/Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C/Accession: B54378  
 R/Agazle, Y.M.; Lee, J.S.; Burkholder, G.D.

J. Biol. Chem. 269, 7019-7023, 1994  
 A/Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence  
 A/Reference number: A54378; MUID:94165109; PMID:7509814

A/Accession: B54378  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-106 <AGA>

A/Cross-references: UNIPARC:UPI00001767AC; GB:568985; NID:G545746; PIDN:AA030096.1; PID:  
 A/Experimental source: spleen and myeloma cell line MOPC 315.43

A/Note: sequence inconsistent with nucleotide translation  
 A/Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIPI:144175)

C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: immunoglobulin  
 F16-89/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 424.5; DB 2; Length 106;  
 Best Local Similarity 81.7%; Pred. No. 1e-29;  
 Matches 85; Conservative 3; Mismatches 11; Indels 5; Gaps 1;

2 IELTQSPALMSASGEGKVTTCRASBSYDYGSHFPMQFPQKPGTSPKLTWYTSNLSAG 61  
 2 IVLTSQSPALMSASGEGKVTTCRASBSYDYGSHFPMQFPQKPGTSPKLTWYTSNLSAG 56

62 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSG 105  
 57 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSG 100

RESULT 4  
 A332513  
 Ig kappa chain precursor V region (MRL22) - mouse

C/Species: Mus musculus (house mouse)  
 C/Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000  
 C/Accession: A332513

R/Kofler, R.; Strohal, R.; Balceras, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;  
 J. Clin. Invest. 82, 852-860, 1988

A/Title: Immunoglobulin kappa light chain variable region gene complex organization and  
 A/Reference number: A94689; MUID:88331394; PMID:3138286

A/Accession: A332513  
 A/Status: preliminary  
 A/Molecule type: DNA

A/Residues: 1-130 <KOF>  
 A/Cross-references: UNIPARC:UPI0000114D9C; GB:M20834; NID:G196943; PIDN:AAA38846.1; PID:  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin  
 F18-113/Domain: immunoglobulin homology <IMM>

Query Match 71.6%; Score 422.5; DB 2; Length 130;  
 Best Local Similarity 79.8%; Pred. No. 1.8e-29;

Matches 83; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

2 IELTQSPALMSASGEGKVTTCRASBSYDYGSHFPMQFPQKPGTSPKLTWYTSNLSAG 61  
 24 IVLTSQSPALMSASGEGKVTTCRASBSYDYGSHFPMQFPQKPGTSPKLTWYTSNLSAG 80

62 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSG 105  
 81 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSG 124

RESULT 5  
 A42848  
 Ig light chain V region - mouse (fragment)

N/Alternate names: I6 anti-tumor antibody  
 C/Species: Mus musculus (house mouse)  
 C/Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C/Accession: A42848; S31902

R/Fell, H.P.; Gayle, M.A.; Yellon, D.; Lipsch, L.; Schieven, G.L.; Marken, J.S.; Aruffo,  
 J. Biol. Chem. 267, 15552-15558, 1992

A/Title: Chimeric Ig anti-tumor antibody. Genomic construction, expression, and character  
 A/Reference number: A42848; MUID:92348410; PMID:1639794

A/Accession: A42848  
 A/Status: preliminary  
 A/Molecule type: DNA

A/Residues: 1-107 <FEL>  
 A/Cross-references: UNIPARC:UPI0000115334; EMBL:M90690

A/Note: sequence extracted from NCBI backbone (NCBIN:109958, NCBIPI:109959)  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: immunoglobulin  
 F16-89/Domain: immunoglobulin homology <IMM>

Query Match 71.1%; Score 419.5; DB 2; Length 107;  
 Best Local Similarity 74.8%; Pred. No. 2.8e-29;  
 Matches 83; Conservative 9; Mismatches 14; Indels 5; Gaps 1;

2 IELTQSPALMSASGEGKVTTCRASBSYDYGSHFPMQFPQKPGTSPKLTWYTSNLSAG 61  
 2 IVLTSQSPALMSASGEGKVTTCRASBSYDYGSHFPMQFPQKPGTSPKLTWYTSNLSAG 56

62 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSGDQGNKR 112  
 57 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSGDQGNKR 107

RESULT 6  
 A30562  
 Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse

C/Species: Mus musculus (house mouse)  
 C/Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
 C/Accession: A30562

R/Sikder, S.K.; Borden, P.; Gruneo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.  
 U. Immunol. 142, 888-893, 1989

A/Title: Amino acid substitutions in V-H CDR2 change the idio type but not the antigen-bir  
 A/Reference number: A30562; MUID:89110066; PMID:2464031

A/Accession: A30562  
 A/Status: preliminary  
 A/Molecule type: mRNA

A/Residues: 1-107 <STK>  
 A/Cross-references: UNIPARC:UPI00001767B0

C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F16-89/Domain: immunoglobulin homology <IMM>

Query Match 70.6%; Score 416.5; DB 2; Length 107;  
 Best Local Similarity 75.7%; Pred. No. 5e-29;  
 Matches 84; Conservative 5; Mismatches 17; Indels 5; Gaps 1;

2 IELTQSPALMSASGEGKVTTCRASBSYDYGSHFPMQFPQKPGTSPKLTWYTSNLSAG 61  
 2 IVLTSQSPALMSASGEGKVTTCRASBSYDYGSHFPMQFPQKPGTSPKLTWYTSNLSAG 56

62 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSGDQGNKR 112

Db 57 VPARFSGSGSGTSLTISRMKADATYYCQWNSNPTTGGTGLEIKR 107

## RESULT 7

IG kappa chain V region (27.10.2) - mouse (fragment)  
B30562  
C/Species: Mus musculus (house mouse)  
C/Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
C/Accession: B30562  
R/Sikder, S.K.; Borden, P.; Gruzo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.I.  
U. Immunol. 142, 888-893, 1989  
A/Title: Amino acid substitutions in V-H CDR2 change the idotype but not the antigen-bi  
A/Reference number: A30562; MUID:89110066; PMID:2464031  
A/Accession: B30562  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-107 <STK>  
A/Cross-references: UNIPARC:UPI00001767BA  
C/Suprafamily: immunoglobulin V region; immunoglobulin  
C/Keywords: heterotrimer; immunoglobulin  
F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 69.7%; Score 411.5; DB 2; Length 107;  
Best Local Similarity 73.9%; Pred. No. 1.3e-28;  
Matches 82; Conservative 6; Mismatches 18; Indels 5; Gaps 1;

Qy 2 IELTQSPAIMSASPEKVTTCRASGVDSYGHSPQWFOQKPTSPKLTWYTSNLSAG 61  
Db 2 IVLTSQSPAIMSASPEKVTTCRASGVDSYGHSPQWFOQKPTSPKLTWYTSNLSAG 56

Qy 62 VPARFSGSGSGTSLTISRMKADATYYCQWNSNPTTGGTGLEIKR 112  
Db 57 VPARFSGSGSGTSLTISRMKADATYYCQWNSNPTTGGTGLEIKR 107

## RESULT 8

IG kappa chain precursor V region (MRL-histone 7L) - mouse (fragment)  
S04573  
C/Species: Mus musculus (house mouse)  
C/Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 21-Jan-2000  
C/Accession: S04573  
R/Cofler, R.; Noonan, D.J.; Strichal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th  
Eur. J. Immunol. 17, 91-95, 1987  
A/Title: Molecular analysis of the murine lupus-associated anti-self response: involveme  
A/Reference number: S04573; MUID:87133856; PMID:3102255  
A/Accession: S04573  
A/Molecule type: mRNA  
A/Residues: 1-130 <KOP>  
A/Cross-references: UNIPARC:UPI0000115DFE; EMBL:X14620; NID:952031; PIDN:CAA32773.1; PID  
A/Note: The authors translated the codon AGC for residue 47 as Asn  
C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/1-22/Domain: signal sequence #status predicted <SIG>  
F/23-130/Product: Ig kappa chain V region (fragment) #status predicted <MAT>  
F/38-113/Domain: immunoglobulin homology <IMM>

Query Match 69.4%; Score 409.5; DB 2; Length 130;  
Best Local Similarity 76.9%; Pred. No. 2.4e-28;  
Matches 80; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

Qy 2 IELTQSPAIMSASPEKVTTCRASGVDSYGHSPQWFOQKPTSPKLTWYTSNLSAG 61  
Db 24 IVLTSQSPAIMSASPEKVTTCRASGVDSYGHSPQWFOQKPTSPKLTWYTSNLSAG 80

Qy 62 VPARFSGSGSGTSLTISRMKADATYYCQWNSNPTTGGTGLEIKR 105  
Db 81 VPARFSGSGSGTSLTISRMKADATYYCQWNSNPTTGGTGLEIKR 124

RESULT 9  
S29590  
IG kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C/Accession: S29590

R/Kavaler, J.  
submitted to the EMBL Data Library, April 1991

A/Reference number: S26459

A/Accession: S29590

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-100 <KNV>

A/Cross-references: UNIPARC:UPI0000115F56; EMBL:X59093; NID:952225; PIDN:CAA41819.1; PID:

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 407.5; DB 2; Length 100;  
Best Local Similarity 77.9%; Pred. No. 2.7e-28;  
Matches 81; Conservative 5; Mismatches 13; Indels 5; Gaps 1;

Qy 2 IELTQSPAIMSASPEKVTTCRASGVDSYGHSPQWFOQKPTSPKLTWYTSNLSAG 61  
Db 2 IVLTSQSPAIMSASPEKVTTCRASGVDSYGHSPQWFOQKPTSPKLTWYTSNLSAG 56

Qy 62 VPARFSGSGSGTSLTISRMKADATYYCQWNSNPTTGGTGLEIKR 105  
Db 57 VPARFSGSGSGTSLTISRMKADATYYCQWNSNPTTGGTGLEIKR 100

## RESULT 10

IG kappa chain V region (VLA10, anti-AFP) - mouse (fragment)  
PD0011  
C/Species: Mus musculus (house mouse)  
C/Date: 10-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 21-Jan-2000  
C/Accession: PD0011  
R/Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.  
Chinese Biochem. J. 12, 648-653, 1996  
A/Title: Generation of a phage display library of the immunoglobulin repertoire from hum  
A/Reference number: PC4405  
A/Accession: PD0011  
A/Contents: Spleen  
A/Molecule type: mRNA  
A/Residues: 1-107 <DEN>  
A/Cross-references: UNIPARC:UPI00001767AA  
C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 407.9; DB 2; Length 107;  
Best Local Similarity 73.2%; Pred. No. 2.9e-28;  
Matches 82; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

Qy 1 DIELTQSPAIMSASPEKVTTCRASGVDSYGHSPQWFOQKPTSPKLTWYTSNLSAG 60  
Db 1 DIELTQSPAIMSASPEKVTTCRASGVDSYGHSPQWFOQKPTSPKLTWYTSNLSAG 55

Qy 61 GVPARFSGSGSGTSLTISRMKADATYYCQWNSNPTTGGTGLEIKR 112  
Db 56 GVPARFSGSGSGTSLTISRMKADATYYCQWNSNPTTGGTGLEIKR 107

## RESULT 11

IG light chain V region - mouse (fragment)  
S66536  
C/Species: Mus musculus (house mouse)  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
C/Accession: S66536  
R/Tsotis, G.; Haase, W.; Engel, A.; Michel, H.  
Eur. J. Biochem. 231, 823-830, 1995  
A/Title: Isolation and structural characterization of trimeric cyanobacterial photosyten  
A/Reference number: S66536; MUID:95377318; PMID:7649183  
A/Accession: S66536  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-120 <TSI>

A:Cross-references: UNIPARC:UPI0000113780; EMBL:X88903; NID:g895870; PIDN:CAA61365.1; P4  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 407.5; DB 2; Length 120;  
Best Local Similarity 71.4%; Pred. No. 3.3e-28;  
Matches 80; Conservative 8; Mismatches 21; Indels 3; Gaps 1;

QY 1 IELTOSPAIMASPGKVTTCRASGVSDYSGHSFMQWFOOKPGTSPKLMYVSTNLASG 60  
Db 1 IELTOSPAIMASPGKVTTCRASGVSDYSGHSFMQWFOOKPGTSPKLMYVSTNLASG 57

QY 61 GVPAFSGSGSGTSTLTISRMEADATYCCQSNEDPYTFGSGDAQNGKR 112  
Db 58 GVPAFSGSGSGTSTLTISRMEADATYCCQSGSSIPFTFGGDTLEIKR 109

## RESULT 12

JL0079

Ig kappa chain precursor V region (anti-phenylloxazalone 6F6) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1991 #sequence\_revision 09-Aug-1996 #text\_change 16-Jul-1999

C:Accession: J0079; A49044; B49044

R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.

Mol. Immunol. 25, 859-865, 1988

A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-res

A:Reference number: J0076; MUID:89096973; PMID:3211160

A:Accession: J0079

A:Molecule type: mRNA

A:Residues: 1-130 &lt;KAA&gt;

A:Cross-references: UNIPARC:UPI000017371F; GB:M2792; NID:g197159

A:Experimental source: mRNA clones for anti-phenylloxazalone antibody 6F6

A:Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10

R:Maletic, C.; Ewen, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Ghelardi, E.

Eur. J. Immunol. 22, 1627-1634, 1992

A:Title: Non-random features of the repertoire expressed by the members of one V kappa g

A:Reference number: A49044; MUID:92289826; PMID:1601044

A:Accession: A49044

A:Molecule type: DNA

A:Residues: 1-25 &lt;MTT&gt;

A:Cross-references: UNIPARC:UPI000011760C; GB:S37663; NID:g520214; PIDN:AA622331.1; PID:

A:Experimental source: BALB/c germ-line

A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

A:Accession: B49044

A:Molecule type: DNA

A:Residues: 114-116 &lt;MTT2&gt;

A:Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AA622332.1; PID:

A:Experimental source: BALB/c germ-line

A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

A:Accession: B49044

A:Molecule type: DNA

A:Residues: 114-116 &lt;MTT2&gt;

A:Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AA622332.1; PID:

A:Experimental source: BALB/c germ-line

A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

A:Accession: B49044

A:Molecule type: DNA

A:Residues: 114-116 &lt;MTT2&gt;

A:Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AA622332.1; PID:

A:Experimental source: BALB/c germ-line

A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

A:Accession: B49044

A:Molecule type: DNA

A:Residues: 114-116 &lt;MTT2&gt;

A:Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AA622332.1; PID:

A:Experimental source: BALB/c germ-line

A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

A:Accession: B49044

A:Molecule type: DNA

A:Residues: 114-116 &lt;MTT2&gt;

A:Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AA622332.1; PID:

A:Experimental source: BALB/c germ-line

A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

A:Accession: B49044

A:Molecule type: DNA

A:Residues: 114-116 &lt;MTT2&gt;

A:Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AA622332.1; PID:

A:Experimental source: BALB/c germ-line

A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

A:Accession: B49044

A:Molecule type: DNA

A:Residues: 114-116 &lt;MTT2&gt;

A:Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AA622332.1; PID:

A:Experimental source: BALB/c germ-line

A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

A:Accession: B49044

A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific  
A;Reference number: S25057  
A;Accession: S25058  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-235 <PIS>  
A;Cross-references: UNIPARC:UPI0000116096; EMBL:X67211; NID:G54828; PIDN:CNA47650.1; PIR  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;38-111/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 404.5; DB 2; Length 235;  
Best Local Similarity 74.8%; Pred. No. 1.2e-27;  
Matches 83; Conservative 5; Mismatches 18; Indels 5; Gaps 1;

QY	2	IELTQSPAINSGPGEKVTTCRASBSVDYSGHSFMQWFOQKPGTSPKLMWYSTSNLASG	61
DB	24	IVLTQSPAINSGPGEKVTTCRASBSV-----SKMQWYQOKSGTSPKRWIYDTSKLASG	78
QY	62	VPARFSGSGSGTSTSLTISRMEABDAATYCCQSNEDPYTFGSDQAGNKR	112
DB	79	VGRFSGSGSGTSTSLTISRMEABDAATYCCQWSSNPLTFGAGTKLEIKR	129

Search completed: November 21, 2005, 12:22:12  
Job time : 28.2821 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55 ; Search time 165.744 Seconds  
(without alignments)  
476.756 Million cell updates/sec

Title: US-10-632-706-86  
Perfect score: 590  
Sequence: 1 DIETQSPAINMSASPGKVT.....QOSNEDPYTGGSDQGNKR 112

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first: 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	447.5	75.8	112 2	Q8K1F2_MOUSE
2	429.5	72.8	114 2	Q8K1F1_MOUSE
3	423.5	71.6	112 2	Q8K1F3_MOUSE
4	413	70.0	131 2	Q811C3_MOUSE
5	411.5	69.7	134 2	Q8VDD0_MOUSE
6	405.5	68.7	235 2	Q58EV6_MOUSE
7	402.5	68.2	237 2	Q58EV8_MOUSE
8	401.5	68.1	235 2	Q58EV8_MOUSE
9	401	68.0	111 1	KV3J_MOUSE
10	396	67.1	111 1	KV3J_MOUSE
11	395.5	67.0	106 2	Q9U410_MOUSE
12	394.5	66.9	107 1	KV6F_MOUSE
13	394.5	66.9	107 1	KV6G_MOUSE
14	394.5	66.9	107 1	KV6J_MOUSE
15	391	66.3	131 1	KV3I_MOUSE
16	389.5	66.0	107 1	KV6I_MOUSE
17	389.5	66.0	112 2	Q8K1F0_MOUSE
18	389	65.9	111 1	KV3K_MOUSE
19	388.5	65.8	107 1	KV6H_MOUSE
20	381	64.6	111 1	KV3L_MOUSE
21	379	64.2	111 1	KV3M_MOUSE
22	378	64.1	111 1	KV3O_MOUSE
23	377	63.9	97 2	Q9J176_MOUSE
24	375.5	63.6	108 1	KV6K_MOUSE
25	375	63.6	111 2	Q811U6_MOUSE
26	374	63.4	132 1	KV3N_MOUSE
27	372	63.1	111 1	KV3P_MOUSE
28	371	62.9	111 1	KV3Q_MOUSE
29	370.5	62.8	107 1	KV6B_MOUSE
30	369.5	62.6	107 1	KV6A_MOUSE
31	368	62.4	111 1	KV3A_MOUSE

32	367.5	62.3	107 1	KV6C_MOUSE	P01677 mus musculus
33	367	62.2	112 1	KV3G_MOUSE	P01659 mus musculus
34	366.5	62.1	107 1	KV3D_MOUSE	P01678 mus musculus
35	364.5	61.8	112 1	KV3B_MOUSE	P01655 mus musculus
36	363	61.5	111 1	KV3D_MOUSE	P03977 mus musculus
37	359	60.8	111 1	KV3C_MOUSE	P01656 mus musculus
38	359	60.8	111 2	Q920E9_MOUSE	Q920E9 mus musculus
39	353.5	59.9	110 1	KV3P_MOUSE	P01668 mus musculus
40	352.5	59.7	107 1	KV6B_MOUSE	P01678 mus musculus
41	352	59.7	111 1	KV3S_MOUSE	P01671 mus musculus
42	350	59.3	111 1	KV3R_MOUSE	P01670 mus musculus
43	350	59.3	111 1	KV3T_MOUSE	P01672 mus musculus
44	348.5	59.1	129 1	KV4A_MOUSE	P01680 mus musculus
45	348	59.0	236 2	Q6PIH7_HUMAN	Q6PIH7 homo sapien

## ALIGNMENTS

RESULT 1		ALIGNMENTS	
ID	Q8K1F2_MOUSE PRELIMINARY;	PRT;	112 AA.
AC	Q8K1F2:		
DT	01-OCT-2002 (TREMBLrel. 22, Created)		
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Anti-VIPase light chain variable region (Fragment).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN-BALB/c; TISSUE=Hypermuritized spleen;		
RA	Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;		
RX	PubMed=2499887;		
RT	"Two murine natural polyclonal reactive autoantibodies are encoded by		
RT	nonmutated germ-line genes."		
RL	Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).		
DR	EMBL; AF516283; AAM64201.1; -; Genomic_DNA.		
DR	PIR; H33932; H33932.		
DR	HSSP; P01837; 25C8.		
DR	SMR; Q8K1F2; 2-112.		
DR	Ensembl; ENSMUSG0000064150; Mus musculus.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_V.		
DR	SMART; SMO0406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
FT	NON_TER		
FT	NON_TER		
FT	SEQUENCE		
FT	112 AA; 11953 MW; 4716887PADB53ED CRC64;		
Query Match			
Beat Local Similarity 75.8%; Score 447.5; DB 2; Length 112;			
Matches 90; Conservative 4; Mismatches 13; Indels 5; Gaps 1;			
QY	1 DIETQSPAINMSASPGKVTTCRASEVDYGHSPFQWFOQKPGTSPKLTATYSTNLAS 60		
DB	1 DIVLTQSPAINMSASPGKVTTCNASSV-----SYMWFQOKPGTSPKLTATYSTNLAS 55		
QY	61 GVPAPFSGSGSTSYSLTISRWEADATPYCQSNEDPYTGGSDQGNKR 112		
DB	56 GVPAPFSGSGSTSYSLTISRWEADATPYCQNSSTPPLTGAATKLELR 107		
RESULT 2			
ID	Q8K1F1_MOUSE PRELIMINARY;	PRT;	114 AA.

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AC 08K1F1. 2002 (TREMBlrel. 22, Created)
BT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 26, Last annotation update)
DB 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Pubmed=2439887;
RA Baccala R., Quang T.V., Gilbert M., Terrynt T., Avrameas S.;
RT "Two murine natural polyclonal antiserum antibodies are encoded by
RT nonmutated germ-line genes."
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=9238144; Pubmed=1512540; DOI=10.1084/jem.176.3.761;
RA T. Aman D.M., You N.T., Hill R.J., Marlon T.N.;
RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
RT selective B cell stimulation in (NZB x NZW)F1 mice."
RL J. Exp. Med. 176:1761-1779(1992).
DR EMBL, AF516284; AA64202.1; --; Genomic_DNA.
DR PIR, A33933; A33933.
DR PIR, PH058; PH058.
DR HSP, P01837; 25C8.
DR SMR, 08K1F1; 2-114.
DR Ensemble; ENSEMBL0000059896; Mus musculus.
DR InterPro, IPR007110; Ig-like.
DR InterPro, IPR003596; Ig_V.
DR SMART, SM00406; IGV; 1.
DR PROSITE, PS50835; IG_LIKE; 1.
FT NON TER 1
FT 114
FT 114
SQ SEQUENCE 114 AA, 12163 MW, 88D9833DBF3EEFD1 CRC64;

Query Match 72.8%; Score 429.5; DB 2; Length 114;
Best Local Similarity 77.7%; Pred. No. 9, 5e-35;
Matches 87, Conservative 5, Mismatches 17, Indels 3; Gaps 1.

QY 1 DIELTOSPAIMASGEGKTTTCRASBSYDTSIGHSPFMOFOKPRGTSPLTWTYSTNLAS 60
DB 1 DIVLTQSPAIMASGEGKTTTCRASBSYDTSIGHSPFMOFOKPRGTSPLTWTYSTNLAS 57
QY 61 GVPAPFSGSGSTSYSLTISRMEADDAATYATYCOQSNEDPYTFGSDQAGNR 112
DB 58 GVPAPFSGSGSTSYSLTISRMEADDAATYATYCOQSNEDPYTFGSDQAGNR 109

RESULT 3
ID 08K1F3_MOUSE PRELIMINARY; PRT; 112 AA.
AC 08K1F3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;

```

```

RN Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RP
RX Nucleotide sequence.
RX PubMed:2499887.
RA Baccala R., Quang T.V., Gilbert M., Termyuk T., Avramas S. i
RT "Two murine natural polyreactive autoantibodies are encoded by
RL nonmutated germ-line genes."
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
RN
RN Nucleotide sequence.
RP
RX MEDLINE:22381444; PubMed:1512540; DOI=10.1084/jem.176.3.761;
RA Tilmann D.M., Jou N.T., Hill R.J., Marion T.N.;
RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
RL selective B cell stimulation in (NZB x NZW) F1 mice."
RL J. Exp. Med. 176:761-779 (1992).
DR EMBL: AF516282; AA64200.1; -; Genomic_DNA.
DR PIR: A33933; A33933.
DR PIR: PH1085; PH1085.
DR HSPSP, P01837, 25C8.
DR SMK, Q8K1F3, 2-112.
DR Ensemble; ENSMUSG0000063156; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS50835; IG_Like; 1.
FT
FT NON_TER 1 1
FT SEQ SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

Query Match 71.64; Score 422.5; DB 2; Length 112;
Best Local Similarity 75.94; Prod. No. 4.6e-34;
Matches 85; Conservative 6; Mismatches 16; Indels 5; Gaps

QY 1 DIELTOSPAIMASPGSKVTTTCRASBSYDSYGHSMQWFOOKPGTSPRLMTVSTSNLAS 60
Db 1 DIVLTGSPAIMSAPGKXTTISCSASSV-----STMYVYQOKPGSPKPMVYRTSNLAS 55

QY 61 GVPARFSGSGSGTSYSITTSRMFAEDPAITYCCQSNEDPYTGGSDQANKR 112
Db 56 GVPARFSGSGSGTSYSITTSRMFAEDPAITYCCQVHSPYTFGGFKLEIKR 107

RESULT 4
OB1IC3 MOUSE PRELIMINARY; PRT; 131 AA.
ID
AC OB1IC3;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DB Mus musculus gamma-3 kappa chain precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN
RN Nucleotide sequence.
RP
RC STRAIN=MRL/MPJ-1pr; TISSUE=Spleen;
RX MEDLINE:93156723; PubMed:8429833; DOI=10.1016/0161-5890(93)90089-T;
RA Takahashi S., Itoh U., Nose M., Ono M., Yamamoto T., Kyogoku M.;
RT "Cloning and cDNA sequence analysis of nephriticogenic monoclonal
RL antibodies derived from an MRL/lpr lupus mouse."
RL Mol. Immunol. 30:177-182 (1993).
DR EMBL; D14629; BAA03482.1; -; mRNA.
DR HSPSP, P01679; 2PBJ.
DR SMK, Q81IC3, 23-131.
DR Ensemble; ENSMUSG0000058987; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS50835; IG_Like; 1.
FT
FT SIGNAL 1 22 Potential.

```

FT CHAIN 23 >131 Immunoglobulin gamma-3 kappa chain.  
 FT NON TER 131  
 SQ SEQUENCE 131 AA; 14083 MW; 5E8365695466E9E CRC64;

Query Match 70.0%; Score 413; DB 2; Length 131;  
 Best Local Similarity 79.0%; Pred. No. 4,8e-33;  
 Matches 83; Conservative 7; Mismatches 11; Indels 4; Gaps 2;

2 IELTOSPAIMASPGKVTTCRASBSYDYSYGHSMQFOOKPGTSPKLMYSTSNLASG 61  
 24 IYLTOGPAIMASPGKVTTCRASBSYDYSYGHSMQFOOKPGTSPKLMYSTSNLASG 80

QY 62 VPARFSGSGSGTSTSLTISRMEDADATYYCOQSNEDP-YTFSGG 105  
 DB 81 VPARFSGSGSGTSTSLTISRMEDADATYYCOQYDSSPSITFGAG 125

## RESULT 5

OSVDDO MOUSE  
 ID OSVDDO MOUSE PRELIMINARY; PRT; 134 AA.

DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Anti-MOG 212 variable light chain (Fragment).

OS Name=Gm1502; Synonyms=anti-MOG kappa;  
 OC Mus musculus (Mouse);  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;

NP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;

RA Sembel P.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;

RA Chernajovsky Y.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;

RA Caton A.J.; Brownlee G.G.; Staudt L.M.; Gerhard W.;

RT Structural and functional implications of a restricted antibody response to a defined antigenic region on the influenza virus

RT hemagglutinin."

RL EMBL J. 5:1577-1587 (1986).

RL EMBL AL146331; CAC94866.1; -; mRNA.

DR PIR, G27887; G27887.

DR HSSP, F01834; IMIM.

DR SMR, Q8VDDO; 23-134.

DR Ensembl; ENSMUSG0000062047; Mus musculus.

DR MGI, MGI:2686348; Gm1502.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG\_v.

DR SMART, SM00406; IG\_v.

DR PROSITE, PS50835; IG\_LIKE; 1.

FT NON TER 134

SQ SEQUENCE 134 AA; 14525 MW; CFPD8E2236E2DCFC CRC64;

Query Match 69.7%; Score 411.5; DB 2; Length 134;  
 Best Local Similarity 73.9%; Pred. No. 7e-33;

Matches 82; Conservative 6; Mismatches 18; Indels 5; Gaps 1;

2 IELTOSPAIMASPGKVTTCRASBSYDYSYGHSMQFOOKPGTSPKLMYSTSNLASG 61  
 24 IYLTOGPAIMASPGKVTTCRASBSYDYSYGHSMQFOOKPGTSPKLMYSTSNLASG 78

QY 62 VPARFSGSGSGTSTSLTISRMEDADATYYCOQSNEDP-YTFSGG 112  
 DB 79 VPARFSGSGSGTSTSLTISRMEDADATYYCOQYDSSPSITFGAG 129

RESULT 6  
 ID OS8EV6 MOUSE PRELIMINARY; PRT; 235 AA.

DT 10-MAY-2005 (TREMBlrel. 30, Created)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
 DE Iqk-C protein.

DE Iqk-C protein.

GN Name=Iqk-C;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;

NP NUCLEOTIDE SEQUENCE.

RC STRAIN=FVB/N; TISSUE=Colon;

RC MBLINB=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Straubeberg R.L.; Feltingold E.A.; Grouse L.H.; Derge U.G.;

RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;

RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;

RA Diachenko L.; Marusik K.; Farmer A.A.; Rubin G.M.; Hong L.;

RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Schetz T.B.;

RA Brownstein M.J.; Uedlin T.B.; Toshiyuki S.; Carninci P.; Pange C.;

RA Bhat S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;

RA Roark S.A.; McGowan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulik S.W.;

RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

RA Fahey J.; Helton E.; Kettelman M.; Madan A.; Rodriguez S.; Sanchez A.;

RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

RA Butterfield Y.S.N.; Krzywinski M.I.; Skalska J.; Smallus D.E.;

RA Scherch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

NP NUCLEOTIDE SEQUENCE.

RC STRAIN=FVB/N; TISSUE=Colon;

RG NIH MGC Project;

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC091738; AAH91738.1; -; mRNA.

DR SMR; OS8EV6; 23-235.

DR GO; GO:0003823; P:antigen binding; IEA.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG\_C1.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; IG\_v.

DR Pfam; PF07654; C1-sect; I.

DR SMART, SM00409; IG; 2.

DR SMART, SM00407; IGc1; 1.

DR SMART, SM00406; IGv; 1.

DR PROSITE, PS50835; IG\_LIKE; 2.

DR PROSITE, PS00290; IG\_MHC; UNKNOWN 1.

SQ SEQUENCE 235 AA; 25719 MW; BEFE4ABD0578252 CRC64;

Query Match 68.7%; Score 405.4; DB 2; Length 235;  
 Best Local Similarity 73.9%; Pred. No. 9.4e-32;

Matches 82; Conservative 5; Mismatches 19; Indels 5; Gaps 1;

2 IELTOSPAIMASPGKVTTCRASBSYDYSYGHSMQFOOKPGTSPKLMYSTSNLASG 61  
 24 IYLTOGPAIMASPGKVTTCRASBSYDYSYGHSMQFOOKPGTSPKLMYSTSNLASG 78

QY 62 VPARFSGSGSGTSTSLTISRMEDADATYYCOQSNEDP-YTFSGG 112  
 DB 79 VPARFSGSGSGTSTSLTISRMEDADATYYCOQYDSSPSITFGAG 129



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ID KV3H MOUSE STANDARD; PRT; 111 AA.
AC P01650;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.B.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790 (1978).
RN [2]
RP PROTEIN SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKeon D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).
CC -1 - MISCELLANEOUS: The PC 3741 and TEPC 111 sequences are identical.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC PIR, A93204; KMS37.
DR HSSP; P01655; 10NZ.
DR Ensembl; ENSMUSG0000060064; Mus musculus.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 38 Complementarity-determining-1.
FT REGION 39 53 Complementarity-determining-2.
FT REGION 54 60 Complementarity-determining-3.
FT REGION 61 92 Framework-3.
FT REGION 93 101 Complementarity-determining-4.
FT REGION 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON TER 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 68.0%; Score 401; DB 1; Length 111;
Best Local Similarity 70.5%; Pred. No. 6.2e-32;
Matches 74; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

OY 1 DIETOSPAIMASPEKVTTCRASSEVDYGHSEFMQFOOKPGTSPKLTWYSTSNLAS 60
DB 1 DVLVQSPASLAVSLQGRATISCRASESDVSGNFMHWYQOKPGPPLTLTYLASNLES 60
61 GVPARFSGSGSGTSTSLTISRMKADDAATYYCCQSNEDPYTFGSG 105
61 GVPARFSGSGSGRTDFTLTIPVADDAVATYYCCQSNEDPYTFGCG 105

RESULT 10
KV3J MOUSE STANDARD; PRT; 111 AA.
AC P01652;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)

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DE Ig kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKeon D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).
RN [2]
RP PROTEIN SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.B.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790 (1978).
RN [3]
RP PROTEIN SEQUENCE (ABPC 22 and PC9241 sequences are identical.
CC -1 - MISCELLANEOUS: The ABPC22 and PC9241 sequences are identical.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC HSSP; P01655; 10NZ.
DR SMR; P01652; 1-111.
DR Ensembl; ENSMUSG0000060064; Mus musculus.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 38 Complementarity-determining-1.
FT REGION 39 53 Framework-2.
FT REGION 54 60 Complementarity-determining-2.
FT REGION 61 92 Framework-3.
FT REGION 93 101 Complementarity-determining-3.
FT REGION 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON TER 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 67.1%; Score 396; DB 1; Length 111;
Best Local Similarity 70.5%; Pred. No. 1.9e-31;
Matches 74; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

OY 1 DIETOSPAIMASPEKVTTCRASSEVDYGHSEFMQFOOKPGTSPKLTWYSTSNLAS 60
DB 1 NIVLQSPASLAVSLQGRATISCRASESDVSGNFMHWYQOKPGPPLTLTYLASNLES 60
61 GVPARFSGSGSGTSTSLTISRMKADDAATYYCCQSNEDPYTFGSG 105
61 GVPARFSGSGSGRTDFTLTIPVADDAVATYYCCQSNEDPYTFGCG 105

RESULT 11
Q9U410 MOUSE PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TRENDELREL. 13, Created)
DT 01-OCT-2003 (TRENDELREL. 25, Last sequence update)
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30
DE Immunoglobulin light chain variable region (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

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OX Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12567627;
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Yu X.C., Xiong Y., Yin C.C.,
RT Huang H.T., Guan X.H.,
RT "Cloning and sequence analysis of the light chain variable region
RT gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma
RT japonicum.";
RL Zhongguo Ji Sheng Chong Xue Yu Ji Sheng Chong Bing Za Zhi
RL 18:257-263(2000). AAF19434.1; -- Genomic_DNA.
DR EMBL; AF207620; AAF19434.1; --
DR HSSP; P01679; 2FBJ.
DR SMR; Q9U410; 4-106.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1_.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 106
FT NON_TER 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 67.0%; Score 395.5; DB 2; Length 106;
Best Local Similarity 77.5%; Pred. No. 2,1e-31;
Matched 79; Conservative 6; Mismatches 12; Indels 5; Gaps 14

OY 4 LTGSPALMASAPGKVTTCRASBSVDYSGHSFMQFOOKRGTSPKMIYSTSNLASGVP 63
Db 4 LTGSPALMASAPGKVTTCRASBSVDYSGHSFMQFOOKRGTSPKMIYSTSNLASGVP 58
59 VRFSGSGSGTSTSLTISRMEADATYYCCQSNEDPTFGSG 105
59 VRFSGSGSGTSTSLTISRMEADATYYCCQWTSTPTFGSG 100

RESULT 12
KV6F_MOUSE
ID KV6F_MOUSE STANDARD; PRT; 107 AA.
AC P04940;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NQ2-17.4.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
RL -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; K00735; AAA38680.1; -- mRNA.
DR HSSP; P01679; 2FBJ.
DR SMR; P04940; 1-107.
DR Ensemble; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1_.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Hydridoma; Immunoglobulin domain, Immunoglobulin V region.
KW

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FT	REGION	1	23		Fimework-1.	
FT	REGION	24	33		Complementarity-determining-1.	
FT	REGION	34	48		Fimework-2.	
FT	REGION	49	55		Complementarity-determining-2.	
FT	REGION	56	87		Fimework-3.	
FT	REGION	88	96		Complementarity-determining-3.	
FT	REGION	97	106		Fimework-4.	
FT	DISULFID	23	87		By similarity.	
FT	NON TER	107	107			
SQ	SEQUENCE	107 AA;	11561 MM;	6F694284ECFA68E6 CRC64;		
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Query Match						
		66.9%;	Score 394.5;	DB 1;	Length 107;	
Best Local Similarity		71.2%;	Pred. No.2.ee-31;			
Matches		79;	Conservative	9;	Mismatches 18;	Indels 5; Gaps 1;
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Dc	2	IIVLTGSAIMASAGQAVTMTCSASSSV-----SYHWYQOQSGTSFKPRMVIYDTSKLASG	56			
Oy	62	VPAFFSSGGSGTYSGLTISLMRAADATYYCCGSNEDEPYTPFGSDQGNKR	112			
Dc	57	VPAFFSSGGSGATSRLTITSMQAEDATYYCQOWSNPLTFGAQTKLELR	107			
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ID	KV6G_MOUSE	STANDARD;	PRT;	107 AA.		
AC	P04941;					
DT	13-AUG-1987	(Rel. 05, Created)				
DT	13-AUG-1987	(Rel. 05, Last sequence update)				
DT	10-MAY-2005	(Rel. 47, last annotation update)				
DS	IG kappa chain V-VI region NO2-48.2.2.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;					
OC	Muridae; Muridae; Murinae; Mus.					
OX	NCBI_Taxid=10090;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RX	MEDLINE=83271467; PubMed=6877353.					
RA	Kaarinen M., Griffiths G.M., Markham A.F., Milstein C.,					
RT	"mRNA sequences define an unusually restricted IgG response to 2-					
RT	phenylloxazalone and its early diversification."					
RL	Nature 304:320-324(1983).					
CC	-I- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.					
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration					
CC	between the Swiss Institute of Bioinformatics and the EMBL outpost -					
CC	the European Bioinformatics institute. There are no restrictions on its					
CC	use as long as its content is in no way modified and this statement is not					
CC	removed.					
CC	-----					
DR	EMBL, K00737; AAA38682.1; -, mRNA.					
DR	HSSP, Q91W12; IAY1.					
DR	SMR, P04941; 1-103.					
DR	Ensembl, ENSMUSG0000062047; Mus musculus.					
DR	InterPro, IPRO07110; IG_1like.					
DR	InterPro, IPRO03596; IG_v.					
DR	SMART, SM00406; IGV, 1.					
DR	PROSITE, PS50835; IG_LIKE; 1.					
KW	Hydriome; Immunoglobulin domain; Immunoglobulin V region.					
FT	REGION	1	23		Fimework-1.	
FT	REGION	24	33		Complementarity-determining-1.	
FT	REGION	34	48		Fimework-2.	
FT	REGION	49	55		Complementarity-determining-2.	
FT	REGION	56	87		Fimework-3.	
FT	REGION	88	96		Complementarity-determining-3.	
FT	REGION	97	106		Fimework-4.	
FT	DISULFID	23	87		By similarity.	
FT	NON TER	107	107			
SQ	SEQUENCE	107 AA;	11557 MM;	7248BDABEF354934 CRC64;		
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Query Match						
		66.9%;	Score 394.5;	DB 1;	Length 107;	
Best Local Similarity		71.2%;	Pred. No.2.ee-31;			
Matches		79;	Conservative	9;	Mismatches 18;	Indels 5; Gaps 1;



Best Local Similarity 71.2%; Pred. No. 2.6e-31;  
Matches 79; Conservative 9; Mismatches 18; Indels 5; Gaps 1;  
QY 2 IELTOSPAIMASGKGVTTTCRASGVDSYSGHSPFQMGPGTSPKMTYSTNLASG 61  
Db 2 ILTLTOSPAIMASGKGVTTTCRASGVDSYSGHSPFQMGPGTSPKMTYSTNLASG 56  
QY 62 VPAFSGSGSATSISLTITSMQADDAATYYCOQWSSNLTGTGAGTKLKR 107  
Db 57 VPAFSGSGSATSISLTITSMQADDAATYYCOQWSSNLTGTGAGTKLKR 107

RESULT 14  
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AC P04944  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DS Ig kappa chain V-VI region NQ5-78.2.6.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
NCBI\_Taxid=10090;  
[1]  
NM NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83271467; Pubmed=6877353;  
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;  
RT "mRNA sequences define an unusually restricted IgG response to 2-  
phenylloxazalone and its early diversification";  
RL Nature 304:320-324(1983).  
RL -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.  
-----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
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CC EMBL; K00744; AAA38689.1; -; mRNA.  
DR HSSP; P04944; 1-106.  
DR SMR; P04944; 1-106.  
DR Ensemble; ENSMUSG0000062047; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.  
FT REGION 1 23 Framework-1.  
FT REGION 24 33 Complementarity-determining-1.  
FT REGION 34 48 Framework-2.  
FT REGION 49 55 Complementarity-determining-2.  
FT REGION 56 87 Framework-3.  
FT REGION 88 96 Complementarity-determining-3.  
FT REGION 97 106 Framework-4.  
FT DISULFID 23 87 By similarity.  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11613 MW; A38290781F3C30D3 CRC64;

Query Match 66.9%; Score 394.5; DB 1; Length 107;  
Best Local Similarity 71.2%; Pred. No. 2.6e-31;  
Matches 79; Conservative 8; Mismatches 19; Indels 5; Gaps 1;  
QY 2 IELTOSPAIMASGKGVTTTCRASGVDSYSGHSPFQMGPGTSPKMTYSTNLASG 61  
Db 2 ILTLTOSPAIMASGKGVTTTCRASGVDSYSGHSPFQMGPGTSPKMTYSTNLASG 56  
QY 62 VPAFSGSGSATSISLTITSMQADDAATYYCOQWSSNLTGTGAGTKLKR 112  
Db 57 VPAFSGSGSATSISLTITSMQADDAATYYCOQWSSNLTGTGAGTKLKR 107

RESULT 15  
KV31\_MOUSE STANDARD; PRT; 131 AA.  
ID KV31\_MOUSE  
AC P01661  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DS Ig kappa chain V-III region MOPC 63 precursor.  
DE Ig kappa chain V-III region MOPC 63 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
NCBI\_Taxid=10090;  
[1]  
NM PROTEIN SEQUENCE OF 1-35.  
RX MEDLINE=78235887; Pubmed=98179;  
RA Burslein Y., Schechter I.;  
RT "Primary structures of N-terminal extra peptide segments linked to the  
RT variable and constant regions of immunoglobulin light chain  
RT precursors: implications on the organization and controlled expression  
RT of immunoglobulin genes";  
RL Biochemistry 17:2392-2400(1978).  
[2]  
NM PROTEIN SEQUENCE OF 21-131.  
RX MEDLINE=73140225; Pubmed=4691517;  
RA McKean D.J., Potter M., Hood L.B.;  
RT "Mouse immunoglobulin chains. Pattern of sequence variation among  
RT kappa chains with limited sequence differences";  
RL Biochemistry 12:760-771(1973).  
[3]  
NM SEQUENCE REVISION.  
RX MEDLINE=79012520; Pubmed=99744;  
RA McKean D.J., Bell M., Potter M.;  
RT "Mechanisms of antibody diversity: multiple genes encode structurally  
RT related mouse kappa variable regions";  
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
-----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
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CC PIR; B90412; KQSM6.  
DR HSSP; P01665; 1QNZ.  
DR SMR; P01661; 21-131.  
DR Ensemble; ENSMUSG0000060064; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 131 Ig kappa chain V-III region MOPC 63.  
FT REGION 22 43 Framework-1.  
FT REGION 44 58 Complementarity-determining-1.  
FT REGION 59 73 Framework-2.  
FT REGION 74 80 Complementarity-determining-2.  
FT REGION 81 112 Framework-3.  
FT REGION 113 121 Framework-4.  
FT REGION 122 131 Complementarity-determining-3.  
FT DISULFID 43 112 By similarity.  
FT NON\_TER 131 131  
SQ SEQUENCE 131 AA; 14291 MW; D212BC9F0dC880A CRC64;

Query Match 66.3%; Score 391; DB 1; Length 131;  
Best Local Similarity 69.5%; Pred. No. 7.4e-31;  
Matches 73; Conservative 14; Mismatches 18; Indels 0; Gaps 0;  
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Db 21 NIVLTOSPAIMASGKGVTTTCRASGVDSYSGHSPFQMGPGTSPKMTYSTNLASG 80



Qy 61 GVPARFSGSGSTSYSLTISRMBAADATYYCOOSNEDPYTFGSG 105  
Db 81 GVPARFSGSGSRIDFTLIDPEADDAATYYCOONNEDPMTFGSG 125

Search completed: November 21, 2005, 12:04:04  
Job time : 166.744 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:31 ; Search time 42.2564 Seconds  
(without alignments)  
219.131 Million cell updates/sec

Title: US-10-632-706-86

Perfect score: 590  
Sequence: 1 DIELTQSPALMSAPGKVT.....QSNEDPYTGGSDQAGNKR 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA\*  
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2: /cgn2\_6/ptodata/1/1aa/6-COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/H-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PCITUS-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RE-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	456.5	77.4	106	2	US-09-798-689-8		Sequence 8, Appl
2	456.5	77.4	238	2	US-09-798-689-21		Sequence 21, Appl
3	449.5	76.2	108	2	US-09-171-945-9		Sequence 9, Appl
4	449.5	76.2	108	2	US-09-910-059-9		Sequence 9, Appl
5	449.5	76.2	235	2	US-09-171-945-17		Sequence 17, Appl
6	449.5	76.2	235	2	US-09-910-059-17		Sequence 17, Appl
7	448.5	76.0	256	2	US-09-526-738A-2		Sequence 2, Appl
8	448.5	76.0	256	2	US-09-526-738A-4		Sequence 2, Appl
9	447.5	75.8	129	1	US-08-438-562-2		Sequence 4, Appl
10	447.5	75.8	129	1	US-08-438-562-2		Sequence 4, Appl
11	447.5	75.8	129	1	US-08-438-562-2		Sequence 4, Appl
12	442.5	75.0	108	2	US-09-726-219A-240		Sequence 92, Appl
13	442.5	75.0	108	2	US-09-196-522-240		Sequence 240, App
14	439.5	74.5	105	2	US-08-434-000A-12		Sequence 12, Appl
15	439.5	74.5	105	2	US-09-312-157-12		Sequence 12, Appl
16	439.5	74.5	105	2	US-09-312-157-12		Sequence 12, Appl
17	438.5	74.3	108	2	US-09-726-219A-244		Sequence 244, App
18	438.5	74.3	108	2	US-09-196-522-244		Sequence 244, App
19	438.5	74.3	270	1	US-08-652-507-2		Sequence 2, Appl
20	438.5	74.3	553	1	US-08-661-052-16		Sequence 16, Appl
21	438.5	74.3	553	1	US-09-188-082-16		Sequence 16, Appl
22	438.5	74.3	553	2	US-09-364-088-16		Sequence 16, Appl
23	438.5	74.3	553	2	US-09-102-716-16		Sequence 16, Appl
24	437.5	74.2	110	2	US-09-726-219A-237		Sequence 237, App
25	437.5	74.2	110	2	US-09-196-522-237		Sequence 237, App
26	436.5	74.0	110	2	US-09-726-219A-255		Sequence 255, App
27	436.5	74.0	110	2	US-09-196-522-255		Sequence 255, App

28	436.5	74.0	281	2	US-09-423-439-44		Sequence 44, Appl
29	436.5	74.0	666	2	US-09-423-439-51		Sequence 51, Appl
30	430.5	73.0	107	1	US-08-211-202-3		Sequence 3, Appl
31	430.5	73.0	246	1	US-08-469-486-57		Sequence 57, Appl
32	430.5	73.0	246	1	US-08-469-558-57		Sequence 57, Appl
33	429.5	72.8	106	1	US-07-634-278-1		Sequence 1, Appl
34	429.5	72.8	106	1	US-07-634-278-1		Sequence 1, Appl
35	429.5	72.8	106	1	US-08-477-728-1		Sequence 1, Appl
36	429.5	72.8	106	1	US-08-477-728-1		Sequence 1, Appl
37	429.5	72.8	106	1	US-08-474-040-1		Sequence 1, Appl
38	429.5	72.8	106	1	US-08-474-040-1		Sequence 1, Appl
39	429.5	72.8	106	1	US-08-487-200-1		Sequence 1, Appl
40	429.5	72.8	106	1	US-08-487-200-1		Sequence 1, Appl
41	429.5	72.8	106	1	US-08-488-113B-163		Sequence 163, App
42	429.5	72.8	106	1	US-08-477-484B-163		Sequence 163, App
43	429.5	72.8	106	1	US-08-107-669D-49		Sequence 49, Appl
44	429.5	72.8	106	1	US-08-472-788A-83		Sequence 83, Appl
45	429.5	72.8	106	1	US-08-477-531B-49		Sequence 49, Appl

## ALIGNMENTS

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RESULT 1
US-09-798-689-8
; Sequence 8, Application US/09798689
; Patent No. 6811779
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; Patent No. 6811779
; CURRENT APPLICATION NUMBER: US/09/798, 689
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 8
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-8

Query Match          77.4%  Score 456.5;  DB 2;  Length 106;
Best Local Similarity 85.7%  Pred. No. 1;6e-37;
Matches 90;  Conservative 3;  Mismatches 7;  Indels 5;  Gaps 1;

QY 1 DIELTQSPALMSAPGKVTTCRAESVDYTGHSFPMQFOOKPQTSKLTATYSTNLAS 60
DB 1 DIELTQSPALMSAPGKVTTCRAESSV-----SYHMFQOKPQTSKLTATYSTNLAS 55
QY 61 GVPARFSGSGSTSYLTISRMEADATYTCQGSNEDPYTGGSG 105
DB 56 GVPARFSGSGSTSYLTISRMEADATYTCQGSNEDPYTGGSG 100

RESULT 2
US-09-798-689-21
; Sequence 21, Application US/09798689
; Patent No. 6811779
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/ GENERAL INFORMATION:
/ APPLICANT: Rockwell, Patricia
/ APPLICANT: Goldstein, Neil I.
/ TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
/ FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
/ Patent No. 681179
/ CURRENT APPLICATION NUMBER: US/09/798,689
/ CURRENT FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 09/401,163
/ PRIOR FILING DATE: 1999-09-22
/ PRIOR APPLICATION NUMBER: 08/967,113
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 08/706,804
/ PRIOR FILING DATE: 1996-09-03
/ PRIOR APPLICATION NUMBER: 08/476,533
/ PRIOR FILING DATE: 1995-06-07
/ PRIOR APPLICATION NUMBER: 08/326,552
/ PRIOR FILING DATE: 1994-10-20
/ PRIOR APPLICATION NUMBER: 08/196,041
/ PRIOR FILING DATE: 1994-02-10
/ NUMBER OF SEQ ID NOS: 41
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 21
/ LENGTH: 238
/ TYPE: PRT
/ ORGANISM: Mouse
US-09-798-689-21

Query Match 77.4%; Score 456.5; DB 2; Length 238;
Best Local Similarity 85.7%; Pred. No. 4,2e-37;
Matches 90; Conservative 3; Mismatches 7; Indels 5; Gaps 1;

QY 1 DILTQSPAIMSASPEKVTTCRASBSVDSYGHSMQFOQKRGSPKMTYSTNLAS 60
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DB 133 DILTQSPAIMSASPEKVTTCRASBSVDSYGHSMQFOQKRGSPKMTYSTNLAS 187
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QY 61 GVPARFSGSGSGTSTLTISRMEADDAATYYCQOSNEDPYTFSG 105
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DB 188 GVPARFSGSGSGTSTLTISRMEADDAATYYCQORSTYPTFGSG 232
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RESULT 3
US-09-171-945-9
/ Sequence 9, Application US/09171945
/ Patent No. 6277599
/ GENERAL INFORMATION:
/ APPLICANT: Emery, Stephen
/ APPLICANT: Copley, Clive Graham
/ APPLICANT: Edge, Michael Derek
/ TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
/ TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
/ FILE REFERENCE: Monoclonal Antibody to CEA
/ CURRENT APPLICATION NUMBER: US/09/171,945
/ CURRENT FILING DATE: 1998-10-29
/ PRIOR APPLICATION NUMBER: GB9703103.3
/ PRIOR FILING DATE: 1997-02-14
/ PRIOR APPLICATION NUMBER: GB9609405.7
/ PRIOR FILING DATE: 1996-05-04
/ PRIOR APPLICATION NUMBER: PCT/GB97/01165
/ PRIOR FILING DATE: 1997-04-29
/ NUMBER OF SEQ ID NOS: 131
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 9
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-9

Query Match 76.2%; Score 449.5; DB 2; Length 108;
Best Local Similarity 80.4%; Pred. No. 8e-37;
Matches 90; Conservative 5; Mismatches 12; Indels 5; Gaps 1;
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Matches 90; Conservative 5; Mismatches 12; Indels 5; Gaps 1;

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DB 1 DILTQSPAIMSASPEKVTTCRASBSVDSYGHSMQFOQKRGSPKMTYSTNLAS 55
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QY 61 GVPARFSGSGSGTSTLTISRMEADDAATYYCQOSNEDPYTFSGDQAGNR 112
    |||||
DB 56 GVPARFSGSGSGTSTLTISRMEADDAATYYCQORSTYPTFGAGTKLELR 107
    |||||

RESULT 4
US-09-910-059-9
/ Sequence 9, Application US/09910059
/ Patent No. 6903203
/ GENERAL INFORMATION:
/ APPLICANT: Copley, Clive G
/ APPLICANT: Edge, Michael Derek
/ APPLICANT: Emery, Stephen Charles
/ TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
/ TITLE OF INVENTION: Their Therapeutic use in an Adept System
/ FILE REFERENCE: 1991-209
/ CURRENT APPLICATION NUMBER: US/09/910,059
/ CURRENT FILING DATE: 2001-07-23
/ PRIOR APPLICATION NUMBER: US 09/171,945
/ PRIOR FILING DATE: 1998-10-29
/ PRIOR APPLICATION NUMBER: PCT/GB97/01165
/ PRIOR FILING DATE: 1997-04-29
/ PRIOR APPLICATION NUMBER: GB 9703103.3
/ PRIOR FILING DATE: 1997-02-14
/ PRIOR APPLICATION NUMBER: GB9609405.7
/ PRIOR FILING DATE: 1996-05-04
/ NUMBER OF SEQ ID NOS: 131
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-910-059-9

Query Match 76.2%; Score 449.5; DB 2; Length 108;
Best Local Similarity 80.4%; Pred. No. 8e-37;
Matches 90; Conservative 5; Mismatches 12; Indels 5; Gaps 1;

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RESULT 5
US-09-171-945-17
/ Sequence 17, Application US/09171945
/ Patent No. 6277599
/ GENERAL INFORMATION:
/ APPLICANT: Emery, Stephen
/ APPLICANT: Copley, Clive Graham
/ APPLICANT: Edge, Michael Derek
/ TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
/ TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
/ FILE REFERENCE: Monoclonal Antibody to CEA
/ CURRENT APPLICATION NUMBER: US/09/171,945
/ CURRENT FILING DATE: 1998-10-29
/ PRIOR APPLICATION NUMBER: GB9703103.3
/ PRIOR FILING DATE: 1997-02-14
/ PRIOR APPLICATION NUMBER: GB9609405.7
/ PRIOR FILING DATE: 1996-05-04
/ PRIOR APPLICATION NUMBER: PCT/GB97/01165
/ PRIOR FILING DATE: 1997-04-29
/ NUMBER OF SEQ ID NOS: 131
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: CITY: ARLINGTON
: STATE: VIRGINIA
: COUNTRY: U.S.A.
: ZIP: 22201-4714
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: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/116,779B
: FILING DATE: 07-SEP-93
:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: WILSON, MARY J.
: REGISTRATION NUMBER: 32,955
: REFERENCE/DOCKET NUMBER: 249-59
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703)816-4000
: TELEFAX: (703)816-4100
: INFORMATION FOR SEQ ID NO: 2:
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: SEQUENCE CHARACTERISTICS:
: LENGTH: 129 amino acids
: TYPE: amino acid
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: NAME/KEY: sig_peptide
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: NAME/KEY: domain
: LOCATION: 24..33
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: Query Match 75.8%; Score 447.5; DB 1; Length 129;
: Best Local Similarity 81.1%; Pred. No. 1.5e-36;
: Matches 90; Conservative 3; Mismatches 13; Indels 5; Gaps 1
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: DB 24 IVLTPSPALMSASPEKVTITTCRASBSV-----SYDMWFQOKPGTSPKLMIVSTSNL 78
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: QY 62 VPAFSGSGGSTSYSLTISRMBAEBAALATYYCOQSNEDPYTSSGQQAQNR 112
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: DB 79 VPAFSGSGGSTSYSLTISRMBAEBAALATYYCOQSSSYPTFGGATKLEIKR 129
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: RESULT 10
: US-08-438-562-2
: Sequence 2, Application US/08438562
: Patent No. 5674255
: GENERAL INFORMATION:

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1  APPLICANT: NAKAMURA, KAZUYASU
2  APPLICANT: KOIKE, MASAMICHI
3  APPLICANT: SHITARA, KENYA
4  APPLICANT: HANAI, NOBUO
5  APPLICANT: KUMANA, YOSHIHISA
6  APPLICANT: HASEGAWA, MAMORU
7  TITLE OF INVENTION: HUMANIZED ANTIBODIES
8  NUMBER OF SEQUENCES: 49
9  CORRESPONDENCE ADDRESS:
10 ADDRESS: NIXON & VANDERHIVE P.C.
11 STREET: 1100 NORTH GLEBE ROAD
12 CITY: ARLINGTON
13 STATE: VIRGINIA
14 COUNTRY: U.S.A.
15 ZIP: 22201-4714
16
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: PatentIn Release #1.0, Version #1.25
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23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/08/438,562
25 FILING DATE: 10-MAY-95
26 CLASSIFICATION: 424
27
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 08/116,778
30 FILING DATE: 07-SEP-93
31
32 CLASSIFICATION: 424
33 ATTORNEY/AGENT INFORMATION:
34 NAME: WILSON, MARY J.
35 REGISTRATION NUMBER: 32,955
36 REFERENCE/DOCKET NUMBER: 249-76
37 TELECOMMUNICATION INFORMATION:
38 TELEPHONE: (703) 816-4000
39 TELEFAX: (703) 816-4100
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41 INFORMATION FOR SEQ ID NO: 2:
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43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 129 amino acids
45 TYPE: amino acid
46 TOPOLOGY: linear
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48 MOLECULE TYPE: protein
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50 FEATURE:
51 NAME/KEY: sig_peptide
52 LOCATION: 22..-1
53 IDENTIFICATION METHOD: BY SIMILARITY
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## PROTEINS IN PLANTS AND THEIR USES

NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 613 West Fifth Street  
Suite 4700

CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
Storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/312.157

FILING DATE: 14-May-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/434,000

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Guise, Jeffrey W.

REGISTRATION NUMBER: 34,613

REFERENCE/DOCKET NUMBER: 212/127

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 552-8400

TELEFAX: (619) 552-0159

TELEX: 67-351

SEQUENCE LISTING

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 105 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

DESCRIPTION: GUY's 13 Kappa

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-312-157-12

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Best Local Similarity 81.9%; Score 439.5; DB 2; Length 105;

Matches 86; Conservative 3; Mismatches 11; Indels 5; Gaps 1;

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DB 1 DIVMTQSPAIMSASGEGVTTTCRASGVDSYGHSPOMFOOKPETSPTKWTYSTNLS 55

QY 61 GVPARFSGSGSTSYSLTISRMEADATYYCOQSNEDPYTFGSG 105

DB 56 GVPARFSGSGSTSYSLTISRMEADATYYCHQRTSYPTTGGG 100

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Job time : 43.2564 secs

his rage dark (up)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using bw model

Run on: November 21, 2005, 11:50:51 / Search time 138.667 Seconds  
(without alignments)  
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Title: US-10-632-706-86

Perfect score: 590  
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

#### SUMMARIES

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8	460.5	78.1	108	5	US-10-203-398-8
9	460.5	78.1	108	5	US-10-778-910-8
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11	460.5	78.1	240	3	US-09-976-787-28
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25	460.5	77.4	238	5	US-10-482-630-28
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27	460.5	77.4	238	5	US-10-809-387-29

28	449.5	76.2	108	3	US-09-910-049-9	Sequence 9, Appl
29	449.5	76.2	235	3	US-09-910-049-17	Sequence 17, Appl
30	448.5	76.0	256	4	US-10-247-488-2	Sequence 2, Appl
31	448.5	76.0	258	4	US-10-247-488-4	Sequence 4, Appl
32	443.5	75.2	109	3	US-09-144-886-91	Sequence 91, Appl
33	442.5	75.0	108	4	US-10-803-622-240	Sequence 240, App
34	442.5	75.0	108	4	US-10-803-622-240	Sequence 240, App
35	439.5	74.5	105	3	US-09-982-107-12	Sequence 12, Appl
36	439.5	74.5	105	5	US-10-781-989-12	Sequence 12, Appl
37	439.5	74.5	109	4	US-10-312-316-50	Sequence 50, Appl
38	439.5	74.5	109	4	US-10-632-706-88	Sequence 88, Appl
39	438.5	74.3	108	4	US-10-803-622-244	Sequence 244, App
40	438.5	74.3	108	4	US-10-803-622-244	Sequence 244, App
41	438.5	74.3	110	5	US-10-688-255-4	Sequence 4, Appl
42	438.5	74.3	244	5	US-10-609-671-2	Sequence 2, Appl
43	438.5	74.3	669	3	US-09-807-721-2	Sequence 2, Appl
44	437.5	74.2	107	4	US-10-232-187-4	Sequence 4, Appl
45	437.5	74.2	110	4	US-10-803-622-237	Sequence 237, App

#### ALIGNMENTS

```
RESULT 1
US-10-632-706-86
; Sequence 86, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSOOPER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-86
Query Match 100.0%; Score 590; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIETQSPAINMSASGGEKVTTCRASEVDYGHSEFMQFOOKPQTSPLMTYTSNLAS 60
DB 1 DIETQSPAINMSASGGEKVTTCRASEVDYGHSEFMQFOOKPQTSPLMTYTSNLAS 60
QY 61 GVPAFSGSGSTSYLTISIRMEADATYYCOQSNEDPYTGGSDQGNKR 112
DB 61 GVPAFSGSGSTSYLTISIRMEADATYYCOQSNEDPYTGGSDQGNKR 112
RESULT 2
US-09-144-886-89
; Sequence 89, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
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/ CURRENT FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 98
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 89
/ LENGTH: 112
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Bont/A clone
US-09-144-886-89

Query Match          95.3%; Score 562; DB 3; Length 112;
Best Local Similarity 95.5%; Pred. No. 9,5e-42;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIELTQSPAIMSASPGKRVTTTCRASGSYDVSYGHSFMQWFOQKPGTSPKLMIVSTSNLAS 60
    |||||
Db 1 DIELTQSPAIMSASPGKRVTTTCRASGSYDVSYGHSFMQWFOQKPGTSPKLMIVSTSNLAS 60
    |||||

Qy 61 GVPARFSGSGSGTYSYSLTISRMEAEADAATYYCCQSNEDPYTFGSGDQAGNKR 112
    |||||
Db 61 GVPARFSGSGSGTYSYSLTISRMEAEADAATYYCCQSSSYPYTFGSGDQAGNKR 112
    |||||

RESULT 3
US-10-632-706-85
/ Sequence 85, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT APPLICATION NUMBER: US/10/632,706
/ CURRENT FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: Patentln version 3.2
/ SEQ ID NO 85
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody
US-10-632-706-85

Query Match          86.5%; Score 510.5; DB 4; Length 107;
Best Local Similarity 91.0%; Pred. No. 3e-37;
Matches 101; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

Qy 1 DIELTQSPAIMSASPGKRVTTTCRASGSYDVSYGHSFMQWFOQKPGTSPKLMIVSTSNLAS 60
    |||||
Db 1 DIELTQSPAIMSASPGKRVTTTCRASGSYDVSYGHSFMQWFOQKPGTSPKLMIVSTSNLAS 55
    |||||

Qy 61 GVPARFSGSGSGTYSYSLTISRMEAEADAATYYCCQSNEDPYTFGSGDQAGNKR 111
    |||||
Db 61 GVPARFSGSGSGTYSYSLTISRMEAEADAATYYCCQSNEDPYTFGSGDQAGNKR 106
    |||||

RESULT 4
US-09-144-886-88
/ Sequence 88, Application US/09144886
/ Patent No. US20020155114A1
/ GENERAL INFORMATION:
/ APPLICANT: Marks, James D
/ APPLICANT: Amersdorfer, Peter
/ TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
/ TITLE OF INVENTION: Botulinum Neurotoxins
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/ FILE REFERENCE: 2500.117USO
/ CURRENT APPLICATION NUMBER: US/09/144,886
/ CURRENT FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 98
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 88
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Bont/A clone
US-09-144-886-88

Query Match          83.8%; Score 494.5; DB 3; Length 107;
Best Local Similarity 87.4%; Pred. No. 7.6e-36;
Matches 97; Conservative 2; Mismatches 7; Indels 5; Gaps 1;

Qy 1 DIELTQSPAIMSASPGKRVTTTCRASGSYDVSYGHSFMQWFOQKPGTSPKLMIVSTSNLAS 60
    |||||
Db 1 DIELTQSPAIMSASPGKRVTTTCRASGSYDVSYGHSFMQWFOQKPGTSPKLMIVSTSNLAS 55
    |||||

Qy 61 GVPARFSGSGSGTYSYSLTISRMEAEADAATYYCCQSNEDPYTFGSGDQAGNKR 111
    |||||
Db 61 GVPARFSGSGSGTYSYSLTISRMEAEADAATYYCCQSSSYPYTFGSGDQAGNKR 106
    |||||

RESULT 5
US-09-976-787-8
/ Sequence 8, Application US/09976787
/ Patent No. US20020064528A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhu, Zhenping
/ TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
/ FILE REFERENCE: 11245/46505
/ CURRENT APPLICATION NUMBER: US/09/976,787
/ CURRENT FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: US 09/493,539
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/117,726
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 8
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-976-787-8

Query Match          78.1%; Score 460.5; DB 3; Length 108;
Best Local Similarity 82.1%; Pred. No. 7.4e-33;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

Qy 1 DIELTQSPAIMSASPGKRVTTTCRASGSYDVSYGHSFMQWFOQKPGTSPKLMIVSTSNLAS 60
    |||||
Db 1 DIELTQSPAIMSASPGKRVTTTCRASGSYDVSYGHSFMQWFOQKPGTSPKLMIVSTSNLAS 55
    |||||

Qy 61 GVPARFSGSGSGTYSYSLTISRMEAEADAATYYCCQSNEDPYTFGSGDQAGNKR 112
    |||||
Db 61 GVPARFSGSGSGTYSYSLTISRMEAEADAATYYCCQSSSYPYTFGSGDQAGNKR 107
    |||||

RESULT 6
US-09-865-198-8
/ Sequence 8, Application US/09865198
/ Patent No. US20020103345A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhu, Zhenping
/ TITLE OF INVENTION: Bisppecific Immunoglobulin-like Antigen Binding Proteins and Method
/ TITLE OF INVENTION: Production
/ FILE REFERENCE: 11245/47102
/ CURRENT APPLICATION NUMBER: US/09/865,198
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CURRENT FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 60/206,749  
PRIOR FILING DATE: 2000-05-24  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 8  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Mouse  
US-09-865-198-8

Query Match 78.1%; Score 460.5; DB 3; Length 108;  
Best Local Similarity 82.1%; Pred. No. 7.4e-33;  
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIELTOSPAIMASGEGKVTTCRASBSVDYSGHSPMQFOOKPQTSPLKMIYSTSNLAS 60  
DB 1 DIELTOSPAIMASGEGKVTTCRASBSV-----SYNMFQOKPQTSPLKMIYSTSNLAS 55  
QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSGDDQGNKR 112  
DB 56 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSSSYPTFGSGTKLEIKR 107

RESULT 7  
US-10-482-630-8  
Sequence 8, Application US/10482630  
Publication No. US20040242851A1  
GENERAL INFORMATION:  
APPLICANT: Zhu, Zhenping  
TITLE OF INVENTION: Bispecific Antibodies That Bind to VEGF Receptors  
FILE REFERENCE: 11245/48502  
CURRENT APPLICATION NUMBER: US/10/482,630  
CURRENT FILING DATE: 2003-12-23  
PRIOR APPLICATION NUMBER: PCT/US02/20332  
PRIOR FILING DATE: 2002-06-26  
PRIOR APPLICATION NUMBER: US 60/301,299  
PRIOR FILING DATE: 2001-06-26  
NUMBER OF SEQ ID NOS: 137  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 8  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Mouse  
US-10-482-630-8

Query Match 78.1%; Score 460.5; DB 5; Length 108;  
Best Local Similarity 82.1%; Pred. No. 7.4e-33;  
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;  
QY 1 DIELTOSPAIMASGEGKVTTCRASBSVDYSGHSPMQFOOKPQTSPLKMIYSTSNLAS 60  
DB 1 DIELTOSPAIMASGEGKVTTCRASBSV-----SYNMFQOKPQTSPLKMIYSTSNLAS 55  
QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSGDDQGNKR 112  
DB 56 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSSSYPTFGSGTKLEIKR 107

RESULT 8  
US-10-203-399B-8  
Sequence 8, Application US/10203399B  
Publication No. US20040248781A1  
GENERAL INFORMATION:  
APPLICANT: Kerbel, Robert  
TITLE OF INVENTION: Therapeutic Method for Reducing Angiogenesis  
FILE REFERENCE: 11245/47002  
CURRENT APPLICATION NUMBER: US/10/203,399B  
CURRENT FILING DATE: 2002-08-08  
PRIOR APPLICATION NUMBER: 60/178,791  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 09/539,692  
PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: PCT/US01/02839  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Mouse  
US-10-203-399B-8

Query Match 78.1%; Score 460.5; DB 5; Length 108;  
Best Local Similarity 82.1%; Pred. No. 7.4e-33;  
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIELTOSPAIMASGEGKVTTCRASBSVDYSGHSPMQFOOKPQTSPLKMIYSTSNLAS 60  
DB 1 DIELTOSPAIMASGEGKVTTCRASBSV-----SYNMFQOKPQTSPLKMIYSTSNLAS 55  
QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSGDDQGNKR 112  
DB 56 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSSSYPTFGSGTKLEIKR 107

RESULT 9  
US-10-778-910-8  
Sequence 8, Application US/10778910  
Publication No. US20040259156A1  
GENERAL INFORMATION:  
APPLICANT: Zhu, Zhenping  
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Method  
FILE REFERENCE: 11245/47102  
CURRENT APPLICATION NUMBER: US/10/778,910  
CURRENT FILING DATE: 2004-02-13  
PRIOR APPLICATION NUMBER: US/09/865,198  
PRIOR FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 60/206,749  
PRIOR FILING DATE: 2000-05-24  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 8  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Mouse  
US-10-778-910-8

Query Match 78.1%; Score 460.5; DB 5; Length 108;  
Best Local Similarity 82.1%; Pred. No. 7.4e-33;  
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;  
QY 1 DIELTOSPAIMASGEGKVTTCRASBSVDYSGHSPMQFOOKPQTSPLKMIYSTSNLAS 60  
DB 1 DIELTOSPAIMASGEGKVTTCRASBSV-----SYNMFQOKPQTSPLKMIYSTSNLAS 55  
QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSGDDQGNKR 112  
DB 56 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSSSYPTFGSGTKLEIKR 107

RESULT 10  
US-10-809-387-8  
Sequence 8, Application US/10809387  
Publication No. US20050214860A1  
GENERAL INFORMATION:  
APPLICANT: Zhu, Zhenping  
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
FILE REFERENCE: 11245/46506  
CURRENT APPLICATION NUMBER: US/10/809,387  
CURRENT FILING DATE: 2004-03-23  
PRIOR APPLICATION NUMBER: 09/976,787  
PRIOR FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 09/493,539

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/ PRIOR FILING DATE: 2000-01-28
/ SOFTWARE: WordPerfect 8.0 for Windows
/ PRIOR APPLICATION NUMBER: 60/117,726
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 8
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-809-387-8

Query Match      78.1%; Score 460.5; DB 5; Length 108;
Best Local Similarity 82.1%; Pred. No. 7.4e-33;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIETGSPAIMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTNLAS 60
DB 1 DIETGSPAIMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTNLAS 55
61 GVPARFSGSGSGTSTLTSRMEADATYYCOOSNEDPYTFSGGDAQNKR 112
DB 56 GVPARFSGSGSGTSTLTSRMEADATYYCOORSSYPTFGSGTKLEIKR 107

RESULT 11
US-09-976-787-28
/ Sequence 28, Application US/09976787
/ Patent No. US20020064528A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhu, Zhenping
/ TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
/ FILE REFERENCE: 11245/46505
/ CURRENT APPLICATION NUMBER: US/09/976,787
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: US 09/493,539
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/117,726
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 28
/ LENGTH: 240
/ TYPE: PRT
/ ORGANISM: Mouse
US-09-976-787-28

Query Match      78.1%; Score 460.5; DB 3; Length 240;
Best Local Similarity 82.1%; Pred. No. 1.7e-32;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIETGSPAIMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTNLAS 60
DB 133 DIETGSPAIMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTNLAS 187
61 GVPARFSGSGSGTSTLTSRMEADATYYCOOSNEDPYTFSGGDAQNKR 112
DB 188 GVPARFSGSGSGTSTLTSRMEADATYYCOORSSYPTFGSGTKLEIKR 239

RESULT 12
US-09-865-198-27
/ Sequence 27, Application US/09865198
/ Patent No. US20020103345A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhu, Zhenping
/ TITLE OF INVENTION: Bispesfic Immunoglobulin-Like Antigen Binding Proteins and Methc
/ FILE REFERENCE: 11245/47102
/ CURRENT APPLICATION NUMBER: US/09/865,198
/ PRIOR FILING DATE: 2001-05-24
/ PRIOR APPLICATION NUMBER: US 60/206,749
/ PRIOR FILING DATE: 2000-05-24
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/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 27
/ LENGTH: 240
/ TYPE: PRT
/ ORGANISM: Mouse
US-09-865-198-27

Query Match      78.1%; Score 460.5; DB 3; Length 240;
Best Local Similarity 82.1%; Pred. No. 1.7e-32;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIETGSPAIMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTNLAS 60
DB 133 DIETGSPAIMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTNLAS 187
61 GVPARFSGSGSGTSTLTSRMEADATYYCOOSNEDPYTFSGGDAQNKR 112
DB 188 GVPARFSGSGSGTSTLTSRMEADATYYCOORSSYPTFGSGTKLEIKR 239

RESULT 13
US-10-482-630-27
/ Sequence 27, Application US/10482630
/ Publication No. US20040242851A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhu, Zhenping
/ TITLE OF INVENTION: Bispesfic Antibodies That Bind to VEGF Receptors
/ FILE REFERENCE: 11245/48502
/ CURRENT APPLICATION NUMBER: US/10/482,630
/ PRIOR FILING DATE: 2003-12-23
/ PRIOR APPLICATION NUMBER: PCT/US02/20332
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: US 60/301,299
/ PRIOR FILING DATE: 2001-06-26
/ NUMBER OF SEQ ID NOS: 137
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 27
/ LENGTH: 240
/ TYPE: PRT
/ ORGANISM: Mouse
US-10-482-630-27

Query Match      78.1%; Score 460.5; DB 5; Length 240;
Best Local Similarity 82.1%; Pred. No. 1.7e-32;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIETGSPAIMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTNLAS 60
DB 133 DIETGSPAIMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTNLAS 187
61 GVPARFSGSGSGTSTLTSRMEADATYYCOOSNEDPYTFSGGDAQNKR 112
DB 188 GVPARFSGSGSGTSTLTSRMEADATYYCOORSSYPTFGSGTKLEIKR 239

RESULT 14
US-10-778-910-27
/ Sequence 27, Application US/10778910
/ Publication No. US20040259156A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhu, Zhenping
/ TITLE OF INVENTION: Bispesfic Immunoglobulin-Like Antigen Binding Proteins and Methoc
/ FILE REFERENCE: 11245/47102
/ CURRENT APPLICATION NUMBER: US/10/778,910
/ PRIOR FILING DATE: 2004-02-13
/ PRIOR APPLICATION NUMBER: US/09/865,198
/ PRIOR FILING DATE: 2001-05-24
/ PRIOR APPLICATION NUMBER: US 60/206,749
/ PRIOR FILING DATE: 2000-05-24
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: WordPerfect 8.0 for Windows
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SEQ ID NO 27  
LENGTH: 240  
TYPE: PRT  
ORGANISM: Mouse  
US-10-778-910-27

Query Match 78.1% Score 460.5; DB 5; Length 240;  
Best Local Similarity 82.1%; Pred. No. 1.7e-32;  
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIETOSPAINASAPGKVTTCRASBSVDSYGHSPQWFOQKPGTSPKLMYSTSNLAS 60  
133 DIETOSPAINASAPGKVTTCRASBSV-----SYMHWFOQKPGTSPKLMYSTSNLAS 187

QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPTFTFGSGDQAGNR 112  
DB 188 GVPARFSGSGSGTSTSLTISRMEADATYYCCQRSSYPTFTFGSGTKLEIKR 239

## RESULT 15

US-10-809-387-28  
Sequence 28, Application US/10809387  
Publication No. US20050214860A1  
GENERAL INFORMATION:  
APPLICANT: Zhu, Zhenping  
APPLICANT: Wille, Larry  
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof  
FILE REFERENCE: 11245/46506  
CURRENT APPLICATION NUMBER: US/10/809,387  
PRIOR FILING DATE: 2004-03-23  
PRIOR APPLICATION NUMBER: 09/976,787  
PRIOR FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 09/493,539  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/117,726  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 28  
LENGTH: 240  
TYPE: PRT  
ORGANISM: Mouse  
US-10-809-387-28

Query Match 78.1% Score 460.5; DB 5; Length 240;  
Best Local Similarity 82.1%; Pred. No. 1.7e-32;  
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIETOSPAINASAPGKVTTCRASBSVDSYGHSPQWFOQKPGTSPKLMYSTSNLAS 60  
DB 133 DIETOSPAINASAPGKVTTCRASBSV-----SYMHWFOQKPGTSPKLMYSTSNLAS 187

QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPTFTFGSGDQAGNR 112  
DB 188 GVPARFSGSGSGTSTSLTISRMEADATYYCCQRSSYPTFTFGSGTKLEIKR 239

Search completed: November 21, 2005, 12:33:33  
Job time : 139.667 secs

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OM protein - protein search, using SW model

Run on: November 21, 2005, 12:04:27 ; Search time 2.05128 Seconds  
(without alignments)  
61.686 Million cell updates/sec

Title: US-10-632-706-86

Perfect score: 530  
Sequence: 1 DIETQSPALMSAPGKVT.....QSNEDPYTGGSDQGNKR 112

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*



PRIM. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404	68.5	543	1	US-10-495-664-3
2	394.5	66.9	106	7	US-11-174-186-1
3	388	65.8	111	7	US-11-077-978-1
4	386.5	65.5	106	7	US-11-174-186-8
5	385.5	65.3	213	7	US-11-174-186-42
6	381.5	64.7	106	7	US-11-174-186-9
7	370.5	62.8	248	1	US-10-512-184-36
8	370.5	62.8	615	1	US-10-512-184-50
9	369.5	62.6	106	7	US-11-174-186-15
10	368.5	62.5	106	7	US-11-174-186-16
11	359	60.8	111	7	US-11-077-978-4
12	358.5	60.8	106	7	US-11-174-186-10
13	358.5	60.4	106	7	US-11-174-186-14
14	356.5	60.4	106	7	US-11-174-186-12
15	355.5	60.3	106	7	US-11-174-186-13
16	354.5	60.1	106	7	US-11-174-186-7
17	352.5	59.7	106	7	US-11-174-186-11
18	343	58.1	128	1	US-10-721-763-31
19	342	58.0	110	1	US-10-648-816-2
20	342	58.0	110	1	US-10-648-816-3
21	342	58.0	110	1	US-10-648-816-4
22	342	58.0	110	1	US-10-648-816-6
23	342	58.0	110	1	US-10-648-816-7
24	342	58.0	110	1	US-10-648-816-8
25	342	58.0	129	1	US-10-721-763-19

26	339	57.5	129	1	US-10-721-763-23	Sequence 23, Appl
27	338	57.3	110	1	US-10-648-816-5	Sequence 5, Appl
28	336	56.9	110	1	US-10-648-816-1	Sequence 1, Appl
29	334.5	56.7	213	7	US-11-172-340-4	Sequence 4, Appl
30	333	56.4	131	1	US-10-721-763-27	Sequence 27, Appl
31	332	56.3	263	1	US-10-512-184-29	Sequence 29, Appl
32	330	55.9	236	7	US-11-144-248-48	Sequence 48, Appl
33	329.5	55.8	106	7	US-11-174-186-5	Sequence 5, Appl
34	329.5	55.8	213	7	US-11-172-320-8	Sequence 8, Appl
35	327	55.4	96	7	US-11-144-248-42	Sequence 42, Appl
36	326	55.3	236	7	US-11-144-248-52	Sequence 52, Appl
37	323	54.7	107	7	US-11-144-248-14	Sequence 14, Appl
38	318.5	54.0	113	1	US-10-932-334-61	Sequence 61, Appl
39	317	53.7	126	1	US-10-839-799-47	Sequence 47, Appl
40	317	53.7	126	1	US-10-839-799-65	Sequence 65, Appl
41	316	53.6	126	1	US-10-839-799-85	Sequence 85, Appl
42	315	53.4	107	7	US-11-077-978-6	Sequence 6, Appl
43	314	53.2	236	7	US-11-144-248-51	Sequence 51, Appl
44	313.5	53.1	251	1	US-10-512-184-30	Sequence 30, Appl
45	313.5	53.1	320	1	US-10-512-184-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1  
US-10-495-664-3  
; Sequence 3, Application US/10495664  
; Publication No. US20050244416A1  
; GENERAL INFORMATION:  
; APPLICANT: JUNG, GUNDRAM  
; TITLE OF INVENTION: BISPECIFIC ANTI-CD28 ANTIBODY MOLECULE  
; FILE REFERENCE: 034258-0801  
; CURRENT APPLICATION NUMBER: US/10/495, 664  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: PCT/EP02/12545  
; PRIOR FILING DATE: 2002-11-09  
; PRIOR APPLICATION NUMBER: DE 101 56 482.1  
; PRIOR FILING DATE: 2001-11-12  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patent In Ver. 3.3  
; SEQ ID NO 3  
; LENGTH: 543  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: protein construct  
US-10-495-664-3  
Query Match 68.5%; Score 404; DB 1; Length 543;  
Best Local Similarity 68.8%; Pred. No. 4; 8e-21;  
Matches 77; Conservative 13; Mismatches 22; Indels 0; Gaps 0;  
QY 1 DIETQSPALMSAPGKVTTCRAESVDYGHFSFMQFOCKPRTSPKLTWYTSNLS 60  
DB 423 DIETQSPALMSAPGKVTTCRAESVDYGHFSFMQFOCKPRTSPKLTWYTSNLS 482  
QY 61 GVPARFSGSGSTSYSLTISRMEADATYYCQSNEDPYTGGSDQGNKR 112  
DB 483 GVPARFSGSGSTSYSLTISRMEADATYYCQSNEDPYTGGSDQGNKR 534  
RESULT 2  
US-11-174-186-1  
; Sequence 1, Application US/11174186  
; Publication No. US20050244418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Olan, Xiang  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019

```
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: KS VK mouse
US-11-174-186-1
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Query Match          66.9%; Score 394.5; DB 7; Length 106;
Best Local Similarity 76.0%; Pred. No. 3.7e-21;
Matches 79; Conservative 5; Mismatches 15; Indels 5; Gaps 1;
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Qy 2 IEILTQSPATMSASPGKVTTCRASBSVDYSGHSFMQFQKPKQTSFKLWYSTSNLASG 61
Db 2 ILILQSPATMSASPGKVTTCRASBSVDYSGHSFMQFQKPKQTSFKLWYSTSNLASG 56
Qy 62 VPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFGSG 105
Db 57 FPARFSGSGSGTSTSLTISRMEADATYYCHGRSGYPYTFGSG 100
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## RESULT 3

```
US-11-077-978-1
/ Sequence 1, Application US/11077978
/ Publication No. US2005024433A1
/ GENERAL INFORMATION:
/ APPLICANT: Yasaki, Paul J.
/ APPLICANT: Sherman, Mark A.
/ APPLICANT: Shively, John B.
/ APPLICANT: Raubitschek, Andrew A.
/ APPLICANT: Wu, Anna M.
/ TITLE OF INVENTION: A Humanized Anti-CEA T84.66 Antibody and Uses Thereof
/ FILE REFERENCE: 54435, 8012, US01
/ CURRENT APPLICATION NUMBER: US/11/077,978
/ CURRENT FILING DATE: 2005-03-11
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1
/ LENGTH: 111
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Artificially constructed variable light chain of M5A and M5B
US-11-077-978-1
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```
Query Match          65.8%; Score 388; DB 7; Length 111;
Best Local Similarity 67.6%; Pred. No. 1e-20;
Matches 71; Conservative 15; Mismatches 19; Indels 0; Gaps 0;
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Qy 1 DIEILTQSPATMSASPGKVTTCRASBSVDYSGHSFMQFQKPKQTSFKLWYSTSNLAS 60
Db 1 DIELTQSPATMSASPGKVTTCRASBSVDYSGHSFMQFQKPKQTSFKLWYSTSNLAS 60
Qy 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFGSG 105
Db 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFGSG 105
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## RESULT 4

```
US-11-174-186-8
/ Sequence 8, Application US/11174186
/ Publication No. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xiang
```

```
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 8
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: VK7 light chain
US-11-174-186-8
```

```
Query Match          65.5%; Score 386.5; DB 7; Length 106;
Best Local Similarity 74.0%; Pred. No. 1.2e-20;
Matches 77; Conservative 6; Mismatches 16; Indels 5; Gaps 1;
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Qy 2 IEILTQSPATMSASPGKVTTCRASBSVDYSGHSFMQFQKPKQTSFKLWYSTSNLASG 61
Db 2 ILILQSPATMSASPGKVTTCRASBSVDYSGHSFMQFQKPKQTSFKLWYSTSNLASG 56
Qy 62 VPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFGSG 105
Db 57 FPARFSGSGSGTSTSLTISRMEADATYYCHGRSGYPYTFGSG 100
```

## RESULT 5

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US-11-174-186-42
/ Sequence 42, Application US/11174186
/ Publication No. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xiang
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 42
/ LENGTH: 213
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: light chain
US-11-174-186-42
```

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Query Match          65.3%; Score 385.5; DB 7; Length 213;
Best Local Similarity 68.8%; Pred. No. 2.3e-20;
Matches 77; Conservative 9; Mismatches 21; Indels 5; Gaps 1;
```

```
Qy 1 DIEILTQSPATMSASPGKVTTCRASBSVDYSGHSFMQFQKPKQTSFKLWYSTSNLAS 60
Db 1 EILVLTQSPATMSASPGKVTTCRASBSVDYSGHSFMQFQKPKQTSFKLWYSTSNLAS 55
Qy 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFGSGDQAGNKR 112
Db 56 GVPARFSGSGSGTSTSLTISRMEADATYYCHGRSGYPYTFGSGTLEIKR 107
```

## RESULT 6

```
US-11-174-186-9
/ Sequence 9, Application US/11174186
/ Publication No. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
```

APPLICANT: Qian, Xiang  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT FILING DATE: 2005-07-01  
PRIORITY FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 9  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: VK8 light chain  
US-11-174-186-9

Query Match 64.7% Score 381.5; DB 7; Length 106;  
Best Local Similarity 71.4%; Pred. No. 2.6e-20;  
Matches 75; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

QY 1 DIELTOSPAIMASGEGKVTTCRASSEVDYGHSMQFOOKPQTSFKLMTYSTNLS 60  
DB 1 EIVLTQSPALISLQGERVTLTCSASSV-----SYLMYQOKPSSSPKRWIPDTSKLAS 55  
QY 61 GVPARFSGSGGTSTLTISRMEADATYYCQGSNEDPYTFGSG 105  
DB 56 GVPARFSGSGGTSTLTISRMEADATYYCQGSNEDPYTFGSG 100

RESULT 7  
US-10-512-184-36  
Sequence 36, Application US/10512184  
Publication No. US20050244901A1

GENERAL INFORMATION:  
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.  
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant  
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease  
TITLE OF INVENTION: resistance against fungi  
FILE REFERENCE: 3581.01US01  
CURRENT APPLICATION NUMBER: US/10/512,184  
CURRENT FILING DATE: 2004-10-22  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1.  
SEQ ID NO 36  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: scFv SS2 with  
OTHER INFORMATION: specificity against Sclerotinia sclerotiorum,  
OTHER INFORMATION: originates from Mus musculus.  
US-10-512-184-36

Query Match 62.8% Score 370.5; DB 1; Length 248;  
Best Local Similarity 67.0%; Pred. No. 2.4e-19;  
Matches 75; Conservative 9; Mismatches 23; Indels 5; Gaps 1;

QY 1 DIELTOSPAIMASGEGKVTTCRASSEVDYGHSMQFOOKPQTSFKLMTYSTNLS 60  
DB 141 DVLTPQSPVIMASGPEKVTTCRASSEVDYGHSMQFOOKPQTSFKLMTYSTNLS 195  
QY 61 GVPARFSGSGGTSTLTISRMEADATYYCQGSNEDPYTFGSGQDQGNKR 112  
DB 196 GVPARFSGSGGTSTLTISRMEADATYYCQGSNEDPYTFGSGQDQGNKR 247

RESULT 8  
US-10-512-184-50  
Sequence 50, Application US/10512184  
Publication No. US20050244901A1  
GENERAL INFORMATION:  
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.

TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant  
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease  
FILE REFERENCE: 3581.01US01  
CURRENT FILING DATE: 2004-10-22  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 50  
LENGTH: 615  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: fusion protein  
OTHER INFORMATION: comprising the leader peptide - chitinase - linker  
OTHER INFORMATION: - scFv SS2 - cmvC/H16c.  
US-10-512-184-50

Query Match 62.8% Score 370.5; DB 1; Length 615;  
Best Local Similarity 67.0%; Pred. No. 4.6e-19;  
Matches 75; Conservative 9; Mismatches 23; Indels 5; Gaps 1;

QY 1 DIELTOSPAIMASGEGKVTTCRASSEVDYGHSMQFOOKPQTSFKLMTYSTNLS 60  
DB 482 DVLTPQSPVIMASGPEKVTTCRASSEVDYGHSMQFOOKPQTSFKLMTYSTNLS 536  
QY 61 GVPARFSGSGGTSTLTISRMEADATYYCQGSNEDPYTFGSGQDQGNKR 112  
DB 537 GVPARFSGSGGTSTLTISRMEADATYYCQGSNEDPYTFGSGQDQGNKR 588

RESULT 9  
US-11-174-186-15  
Sequence 15, Application US/11174186  
Publication No. US20050244418A1

GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
APPLICANT: Lo, Kin-Ming  
APPLICANT: Qian, Xiang  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/11/174,186  
CURRENT FILING DATE: 2005-07-01  
PRIORITY FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 15  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: KS de-immunized VK5  
US-11-174-186-15

Query Match 62.6% Score 369.5; DB 7; Length 106;  
Best Local Similarity 68.3%; Pred. No. 1.6e-19;  
Matches 71; Conservative 11; Mismatches 17; Indels 5; Gaps 1;

QY 2 IELTOSPAIMASGEGKVTTCRASSEVDYGHSMQFOOKPQTSFKLMTYSTNLS 61  
DB 2 IELTOSPAIMASGEGKVTTCRASSEVDYGHSMQFOOKPQTSFKLMTYSTNLS 56  
QY 62 GVPARFSGSGGTSTLTISRMEADATYYCQGSNEDPYTFGSG 105  
DB 57 GVPARFSGSGGTSTLTISRMEADATYYCQGSNEDPYTFGSG 100

RESULT 10  
US-11-174-186-16  
Sequence 16, Application US/11174186  
Publication No. US20050244418A1  
GENERAL INFORMATION:



Search completed: November 21, 2005, 12:33:50  
Job time : 3.15128 secs

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US-11-174-186-12
; Sequence 12, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VK2
US-11-174-186-12

Query Match      60.4%; Score 356.5; DB 7; Length 106;
Best Local Similarity 65.4%; Pred. No. 1.1e-18;
Matches 68; Conservative 12; Mismatches 19; Indels 5; Gaps 1;

QY      2 IELTQSPALMSAPGKXTTTCRASEVDSYGHSEFMQWFOOKPGTSPKLMITYSTSNLASG 61
DB      2 IVLQSPALMSAPGQKATITCSASSV-----SYLWYQKPGQPPKWIPTDSNLASG 56

QY      62 VPARFSGSGGTSTYSLTISRMEDADATYYCOQSNEDPYTFGSG 105
DB      57 FPRFSGSGGTSTYTLTINSLEADADATYYCHGRSGYPTTFGSG 100

RESULT 15
US-11-174-186-13
; Sequence 13, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS-deimmunized VK3
US-11-174-186-13

Query Match      60.3%; Score 355.5; DB 7; Length 106;
Best Local Similarity 65.4%; Pred. No. 1.3e-18;
Matches 68; Conservative 12; Mismatches 19; Indels 5; Gaps 1;

QY      2 IELTQSPALMSAPGKXTTTCRASEVDSYGHSEFMQWFOOKPGTSPKLMITYSTSNLASG 61
DB      2 IVLQSPALMSAPGQKATITCSASSV-----SYLWYQKPGQPPKWIPTDSNLASG 56

QY      62 VPARFSGSGGTSTYSLTISRMEDADATYYCOQSNEDPYTFGSG 105
DB      57 FPRFSGSGGTSTYTLTINSLEADADATYYCHGRSGYPTTFGSG 100
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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:32; Search time 143.255 Seconds  
(without alignments)  
328.182 Million cell updates/sec

Title: US-10-632-706-87

Perfect score: 553  
Sequence: 1 DTBLTQSPALMSASPERKVT.....QWSSNPITFGSGTKLEIKR 107

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseq\_21:1\*  
2: geneseqp1980s:\*  
3: geneseqp1990s:\*  
4: geneseqp2000s:\*  
5: geneseqp2001s:\*  
6: geneseqp2002s:\*  
7: geneseqp2003as:\*  
8: geneseqp2003bs:\*  
9: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	107	8	ADR38685
2	518	99.7	109	8	ADR38686
3	516	99.3	107	8	ADR38673
4	516	99.3	129	5	ABR75616
5	515	99.1	107	9	ADW86126
6	515	99.1	210	8	ADU86565
7	515	99.1	210	8	ADU86571
8	510	92.2	108	8	ADU74993
9	506	91.5	107	8	ADR38670
10	506	91.5	244	2	AAR79867
11	505	91.3	242	2	AAR79871
12	502	90.8	106	5	ABG32682
13	502	90.8	106	5	ABG32682
14	502	90.8	128	2	AAR27050
15	501	90.6	106	4	AA669673
16	501	90.6	106	4	AD047720
17	501	90.6	128	4	AA669655
18	501	90.6	128	4	AD047747
19	499	90.2	242	2	AAR79870
20	499	90.2	242	2	AAR79872
21	498.5	90.1	108	8	ADW86127
22	498.5	90.1	214	8	ADW86519
23	497	89.9	106	8	AD016879
24	496	89.7	246	2	AAR79869

25	491.5	88.9	117	3	AA93891	AA93891 The kappa
26	489	88.4	108	2	AAR21293	Aar21293 Murine VL
27	489	88.4	259	9	AA629819	Aa629819 Mouse hlg
28	488	88.2	110	6	AA633326	Aa633326 128 antib
29	488	88.2	110	9	AD221524	Ad221524 Anti-Muc-
30	488	88.2	110	9	AD221532	Ad221532 Anti-Muc-
31	488	88.2	128	2	AAR12327	Aar12327 Light (ka
32	488	88.2	244	2	AAR79868	Aar79868 Anti-EGFR
33	488	88.2	244	2	AAR79873	Aar79873 Anti-EGFR
34	488	88.2	260	9	AD221541	Ad221541 Anti-Muc-
35	488	88.2	260	9	AA633333	Aa633333 128 antib
36	488	88.2	281	6	AA633333	Aa633333 128 antib
37	486	87.9	110	9	AD221534	Ad221534 Anti-Muc-
38	486	87.9	128	4	AA665521	AA665521 Mouse ant
39	486	87.9	260	9	AD221542	Ad221542 Anti-Muc-
40	486	87.9	304	9	ADX69520	Adx69520 Mouse ICA
41	485	87.7	107	4	ADW80852	Adw80852 Anti-CD3
42	485	87.7	108	2	AAR21301	Aar21301 Murine VL
43	484	87.5	246	9	ADW64805	Adw64805 Murine si
44	484	87.5	246	9	ADW64803	Adw64803 Murine si
45	484	87.5	252	8	ADH77287	Adh77287 Yeast k11

#### ALIGNMENTS

RESULT 1  
ADR38685  
ID ADR38685 standard; peptide; 107 AA.

AC ADR38685;

DT 02-DEC-2004 (first entry)

DE Mouse light chain variable region scFv seqid 87.

KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
KW light chain variable region; single chain antibody; scFv.

OS Mus sp.

PN US2004175385-A1.

PD -09-SEP-2004.

PP 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

PA (REGC) UNIV CALIFORNIA.

PI Marks JD, Amerdorfer P;

PS WPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.

PT with botulinum neurotoxin poisoning.

PS Example 1; SEQ ID NO 87; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds  
CC to an epitope specifically bound by an antibody expressed by a specific  
CC clone where (I) binds to and neutralises botulinum neurotoxin type A

CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone

CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, A1, Ar2, W1 (V), W1 (F), 3-1,  
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum

CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
CC comprising BoNT/A neutralising epitope having an epitope that is

CC	specifically bound by an antibody expressed by clones as mentioned in (I)	
CC	; producing (I); and a composition (II) comprising several anti-	
CC	botulinum neurotoxin antibodies, where each antibody is specific for a	
CC	different epitope of a botulinum neurotoxin and the combination of	
CC	antibodies show greater toxin neutralisation than the single antibodies	
CC	in surplus. The following are disclosed: a pharmaceutical composition	
CC	comprising (I); and a kit comprising (I). (I) is useful for neutralising	
CC	BoNT/A antibody and for neutralising a botulinum neurotoxin which	
CC	involves contacting neurotoxin with (I) in surplus, where each of (I) is	
CC	specific for a different epitope of the botulinum neurotoxin and the	
CC	combination of antibodies shows greater toxin neutralisation than the	
CC	single antibodies in surplus. (I) is useful for diagnosing the botulinum	
CC	or for treating pathologies associated with botulinum neurotoxin	
CC	poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)	
CC	enables rapid detection or diagnosis of botulism. This is the amino acid	
CC	sequence of a mouse light chain variable fragment anti-botulinum toxin	
CC	scfv.	
XX		
XX	Sequence 107 AA;	
Qy	Query Match	100.0%; Score 553; DB 8; Length 107;
Db	Best Local Similarity	100.0%; Pred. No. 2,1e-34;
	Matches 107; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Qy	1 DTEITGSPAIMSASPGEKVTTTCSASSSVSYMTYQKFGSSPLLIDTSTNLASGVPR	60
Db	1 DTEITGSPAIMSASPGKVTTCSSASSSVYMTYQKFGSSPLLIDTSTNLASGVPR	60
Qy	61 FSGSGGCTSYSLTISRMEADATYYCOQWSSNPLTFGSGTGLFLNR	107
Db	61 FSGSGGCTSYSLTISRMEADATYYCOQWSSNPLTFGSGTGLFLNR	107
RESULT 2		
ID	ADR38686	standard, peptide; 109 AA.
XX	ADR38686;	
AC	02-DEC-2004	(first entry)
DT		
XX	Mouse light chain variable region scfv seqid 88.	
DE		
XX	antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;	
KW	BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;	
KW	toxin neutralisation; botulinum neurotoxin poisoning; mouse;	
KW	light chain variable region; single chain antibody; scfv.	
OS	Mus sp.	
XX	US2004175385-A1.	
PN	09-SEP-2004.	
XX		
PD	01-AUG-2003; 2003US-00632706.	
XX		
PP	31-AUG-1998; 98US-00144886.	
XX		
PR	01-AUG-2002; 2002US-0400721P.	
XX		
PA	(REGC ) UNIV CALIFORNIA.	
XX		
P1	Marks JD, Ameradorfer P;	
XX		
DR	WPI; 2004-652009/63.	
XX		
PT	New isolated antibody that neutralizes botulinum neurotoxin type A,	
XX	useful for diagnosing botulism or for treating pathologies associated	
PT	with botulinum neurotoxin poisoning.	
XX		
PS	Example 1, SEQ ID NO 88; 110pp; English.	
XX		
CC	The invention describes an isolated antibody (I) that specifically binds	
CC	to an epitope specifically bound by an antibody expressed by a specific	

```
CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed from a clone chosen from clone  
CC S22, C25, C39, I06, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
CC 3-8, 3-10 and INGL, where (I) binds to and neutralizes botulinum  
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
CC comprising BoNT/A neutralising epitope having an epitope that is  
CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I); and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of a mouse light chain variable fragment anti-botulinum toxin  
CC scFv.  
CC  
CC XX  
SQ Sequence 109 AA;  
  
Query Match          93.7%; Score 518; DB 8; Length 109;  
Best Local Similarity 94.5%; Pred. No. 9,3e-32;  
Matches 103; Conservative 1; Mismatches 3; Indels 2; Gaps 1;  
  
Qy      1 DTELTPGPAIMASAPGEKVTTCSSASSV--SYWYRTOOKFGSSPRLLIYTSTNLASGP 58  
Db      1 DIETLPGPAIMASAPGEKVTTTCTCASSSVSS86YGWYQCKGSSPRLLIYDTSNLASGP 60  
  
Qy      59 VRFSGSGSGTYSYSLTISRMEADATYYCOQMSNPILTFGGTGLELKR 107  
Db      61 VRFGSGSGTSYSTLTISRMEADATYYCOQMSNPILTFGGTGLELKR 109  
  
RESULT 3  
ADR38673  
ID      ADR38673 standard; peptide; 107 AA.  
XX  
XX      ADR38673;  
XX  
DT      02-DEC-2004 (first entry)  
DS  
XX      Mouse light chain variable region scFv seqid 75.  
XX  
XX      antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
KW      BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KW      toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
KW      light chain variable region; single chain antibody; scFv.  
XX  
OS      Mus sp.  
PN      US2004175385-A1.  
PD      09-SEP-2004.  
PF      01-AUG-2003; 2003US-00632706.  
PR      31-AUG-1998; 98US-00144886.  
PR      01-AUG-2002; 2002US-0400721P.  
XX  
XX      (REGC ) UNIV CALIFORNIA.  
XX      PA  
XX      Marks JD, Ameradorfer P;  
XX      WPI; 2004-652009/63.  
XX  
PT      New isolated antibody that neutralizes botulinum neurotoxin type A,
```



PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.

PS Example 1, SEQ ID NO 75, 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C35, 1C6, 3D12, B4, 1F3, huc25, At1, At2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralises botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC , producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of a mouse light chain variable fragment anti-botulinum toxin  
 CC scFv.

SO Sequence 107 AA:

Query Match 93.3%; Score 516; DB 8; Length 107;  
 Best Local Similarity 94.4%; Pred. No. 1.3e-31;  
 Matches 101; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DTELTPAIVMSASGKGVTTTCSSASSSVSYMYWYQQRGSSPRLLIYDTSNLASGVPR 60

DB 1 DIELTPAIVMSASGKGVTTTCSSASSSVSYMYWYQQRGSSPRLLIYDTSNLASGVPR 60

QY 61 FSGSGSTSYSLTISRMEADAAATYYCOQWSNPLTFSSGRTLEIKR 107

DB 61 FSGSGSTSYSLTISRMEADAAATYYCOQWSNPLTFSSGRTLEIKR 107

RESULT 4

ID ABB75616 standard; protein; 129 AA.

AC ABB75616;

DT 10-JUN-2002 (first entry)

XX Anti-RANK ligand mAb 19H22 light chain variable region.

XX RANK ligand; RANK-L; monoclonal antibody; mAb; 19H22; antibody;  
 XX complementarity determining region; CDR; rheumatoid arthritis;  
 XX osteoporosis; bone cancer; metastasis; osteoarthritis;  
 XX psoriasis; inflammatory bowel disease; multiple sclerosis; diabetes;  
 XX cystic acid; inflammatory; antineoplastic; osteoporosis; antidiabetic;  
 XX antirheumatic; immunosuppressive; antipsoriatic; neuroprotective;  
 XX light chain; VL; mouse.

XX Mus musculus.

XX Key Location/Qualifiers

XX Region 24..33

XX /label= CDR1

XX /note= "complementarity determining region 1"

XX Region 49..55

XX /label= CDR2

FT /note= "complementarity determining region 2"

FT Region 88..96

FT /label= CDR3

FT /note= "complementarity determining region 3"

XX WO200215846-A2.

XX 28-FEB-2002.

XX 21-AUG-2001; 2001WO-US026161.

XX 21-AUG-2000; 2000US-0226524P.

XX 07-SEP-2000; 2000US-0220639P.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Sweet RW, Tornetta MA, Truneh A, Wattam TA;

XX WPI; 2002-242022/29.

XX N-PSDB; ABL53530.

XX A mouse monoclonal antibody 19H22 for treating or preventing osteopenic

XX diseases including rheumatoid arthritis and osteoporosis.

XX Claim 6; Page 7; 45pp; English.

XX The present sequence is that of the light chain variable region of  
 CC claimed anti-human RANK ligand (RANK-L) murine monoclonal antibody (mAb)  
 CC 19H22 (isotype IgG2b/kappa). The mAb is produced by hybridoma cells  
 CC obtained by immunising C57BL/6 mice with human RANK-L protein, and fusing  
 CC spleen cells with X63-Ag8.653 myeloma cells. 19H22 mAb is specific for  
 CC human RANK-L, having a binding affinity characterised by a dissociation  
 CC constant of about 10 power -10 M. RANK-L is a member of the tumour  
 CC necrosis factor family of proteins and a key regulator of the immune  
 CC system, bone development and homeostasis. The invention provides altered,  
 CC fragment, antibodies comprising the light and heavy chain variable  
 CC regions of 19H22, and antibodies comprising the complementarity  
 CC determining regions of 19H22. These are used in methods for the  
 CC diagnosis, treatment and prevention of osteopenic diseases, including  
 CC rheumatoid arthritis, osteoporosis, metastatic and primary bone cancer,  
 CC wear debris induced osteolysis or osteoarthritis, and immune diseases  
 CC including psoriasis, insulin dependent diabetes, inflammatory bowel  
 CC disease or multiple sclerosis. Methods are also provided for the  
 CC recombinant production of the antibodies, using isolated nucleic acids  
 CC and transfected host (preferably mammalian) host cells, and a method of  
 CC diagnosing conditions associated with Th1 T-cell activity or osteoclast  
 CC development and activation, in particular those listed above

SO Sequence 129 AA:

Query Match 93.3%; Score 516; DB 5; Length 129;  
 Best Local Similarity 96.2%; Pred. No. 1.6e-31;  
 Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LTQSPAINASGKGVTTTCSSASSSVSYMYWYQQRGSSPRLLIYDTSNLASGVPRSG 63

DB 4 LTQSPAINASGKGVTTTCSSASSSVSYMYWYQQRGSSPRLLIYDTSNLASGVPRSG 63

QY 64 GSGGTSYSLTISRMEADAAATYYCOQWSNPLTFSSGRTLEIKR 107

DB 64 GSGGTSYSLTISRMEADAAATYYCOQWSNPLTFSSGRTLEIKR 107

RESULT 5

ID ADM86126 standard; protein; 107 AA.

AC ADM86126;

DT 21-APR-2005 (first entry)



RESULT 7  
ID ADU86571 standard; protein; 210 AA.  
AC ADU86571;  
XX 10-FEB-2005 (first entry)  
XX  
DE Immunoglobulin variable domain protein seqid 60.  
XX  
XX antiinflammatory; antibacterial; virucide; cytostatic; antipsoriatic;  
KM antidiabetic; vasotropic; vaccine; protein purification; protein folding;  
KM diagnosis; inflammation; immune disorder; allergic hypersensitivity;  
KM infection; autoimmune disease; asthma; psoriasis;  
KM insulin dependent diabetes; multiple sclerosis; rheumatoid arthritis;  
KM systemic lupus erythematosus; myasthenia gravis; hematological disease;  
KM neoplasm; immunoglobulin; variable region.  
XX  
XX Homo sapiens.  
XX  
XX MO2004101790-A1.  
XX  
XX 25-NOV-2004.  
XX  
XX 14-MAY-2004; 2004WO-GB002102.  
XX  
XX 14-MAY-2003; 2003US-0470340P.  
XX 17-MAR-2004; 2004US-0554021P.  
XX  
XX (DOMA-) DOMANTIS LTD.  
XX  
XX Jespers LS, Jones PC, Famm KHJ, Winter GP;  
PI WPI; 2004-82188/81.  
XX  
XX Recovering a polypeptide that unfolds reversibly from a repertoire of  
PT polypeptides for treating e.g., cancer, by unfolding a portion of the  
PT displayed polypeptides and refolding a portion of the unfolded  
PT polypeptides.  
XX  
XX Disclosure; SEQ ID NO 60; 222pp; English.  
XX  
XX The invention describes a method of recovering a polypeptide that unfolds  
CC reversibly from a repertoire of polypeptides that unfolds reversibly and  
CC has a common selectable characteristic that distinguishes folded  
CC polypeptides from unfolded or misfolded polypeptides. The method  
CC comprises: providing a polypeptide display system comprising the  
CC repertoire of displayed polypeptides; unfolding at least a portion of the  
CC displayed polypeptides; refolding at least a portion of the unfolded  
CC polypeptides; and recovering at least one polypeptide that unfolds  
CC reversibly and has the selectable characteristic from the refolded  
CC portion. The method is useful in recovering a polypeptide that unfolds  
CC reversibly from a repertoire of polypeptides that unfolds reversibly. The  
CC library or repertoire is useful for selecting a polypeptide comprising an  
CC antibody variable domain that unfolds reversibly or a polypeptide that  
CC refolds reversibly and comprising an antibody format. The polypeptide is  
CC useful in the manufacture of a medicament for diagnosing, treating or  
CC preventing a disease or medical condition mediated by a cytokine,  
CC cytokine receptor, enzyme, enzyme co-factor or DNA binding protein, such  
CC as an inflammatory state, allergic hypersensitivity, cancer, bacterial or  
CC viral infection or an autoimmune disorder, e.g., asthma, psoriasis, Type  
CC I diabetes, multiple sclerosis, rheumatoid arthritis, systemic lupus  
CC erythematosus, Crohn's disease, myasthenia gravis, leukemia or solid  
CC tumor. This is the amino acid sequence of an immunoglobulin variable  
CC region associated with the protein purification method of the invention.  
XX  
XX Sequence 210 AA;  
SQ

Query Match 93.1%; Score 515; DB 8; Length 210;  
Best Local Similarity 91.6%; Pred. No. 2, 9e-31;  
Matches 98; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTELTPSPAIMSASPGKXTTTCASSSVSYMYWYOOKPGSSPRLILYDTSNLASGVPR 60  
DB 1 DIQMTSPAIMSASPGKXTTTCASSSVSYMYWYOOKPGSSPRLILYDTSNLASGVPR 60  
QY 61 FSGSGSGTSTSLTISRMEADAAATYYCOQWSSNPLTFGSGTKLEKR 107  
DB 61 FSGSGSGTSTSLTISRMEADAAATYYCOQWSTYPLTFGAQTKLEKR 107  
RESULT 8  
ID ADT74993 standard; protein; 108 AA.  
XX ADT74993;  
XX  
AC ADT74993;  
XX  
XX 13-JAN-2005 (first entry)  
XX  
XX Light chain murine anti-hL-SIGN scFv antibody protein A2LC Seq 39.  
DE  
XX  
XX autoimmune disease; antibody; antigen presenting cell; APC;  
KM diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive;  
KM vaccine; hL-SIGN.  
XX  
XX Mus sp.  
XX  
XX WO2004091543-A2.  
XX  
XX 28-OCT-2004.  
XX  
XX 04-MAR-2004; 2004WO-US006570.  
XX  
XX 04-MAR-2003; 2003US-0451816P.  
XX 15-DEC-2003; 2003US-0529500P.  
XX 28-FEB-2004; 2004US-0548385P.  
XX  
XX (ALEX-) ALEXION PHARM INC.  
XX  
XX Bowditch KS, Kretz-Rommel A, Dakappagari N;  
PI WPI; 2004-758274/74.  
XX  
XX Treating an autoimmune disease comprises providing an  
PT antibody/autocanigen construct containing an autocanigen linked to an  
PT antibody to a receptor of an antigen presenting cell and administering  
PT the construct to a subject.  
XX  
XX Example 9; Fig 8; 71pp; English.  
XX  
XX This invention relates to the novel treatment of an autoimmune disease  
CC that utilizes an antibody/autocanigen construct. Specifically, it refers  
CC to a peptide autocanigen that is linked to an antibody raised against an  
CC antigen presenting cell (APC) receptor. The present invention describes a  
CC method for treating diabetes mellitus by inducing an immune tolerance to  
CC an autocanigen, which can be chosen from glutamic acid decarboxylase  
CC (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived  
CC from each thereof or beta cell antigens that are linked to an APC  
CC receptor antibody. In particular, the antibody recognises a receptor  
CC chosen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst  
CC others, which is expressed on the surface of the APC. The antibody/  
CC autocanigen construct then works to interfere with the interaction  
CC between the APC and immune cells such as autoreactive T cells, and hence  
CC inhibits T-cell proliferation. Accordingly, such compositions exhibit  
CC antidiabetic and immunosuppressive activities and can be used in the  
CC development of vaccines. Note that the single chain antibodies (scFvs)  
CC used in this specification contain both variable light and heavy chain  
CC regions connected by a linker, their short length makes these antibody  
CC fragments particularly suitable for antigen linkage, and the capacity for  
CC binding to the receptor is preserved. This polypeptide sequence is a  
CC light chain murine anti-human L-SIGN (hL-SIGN) antibody protein of the  
CC invention.  
XX  
XX Sequence 108 AA;  
SQ

Query Match 92.2%; Score 510; DB 8; Length 108;  
 Best Local Similarity 95.2%; Pred. No. 3.7e-31;  
 Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASPGKRVTTTTCASASSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRFSG 63  
 DB 4 LTGSPAIMSASPGKRVTTTTCASASSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRFSG 63  
 QY 64 SGGSGSTSYSLTISRMEADATYYCCQWMSNPLTFGSGTKLELR 107  
 DB 64 SGGSGSTSYSLTISRMEADATYYCCQWMSNPLTFGSGTKLELR 107

RESULT 9  
 ADR38670 ID ADR38670 standard; peptide: 107 AA.  
 AC ADR38670;  
 XX 02-DEC-2004 (first entry)  
 DT Mouse light chain variable region scFv seqid 72.  
 DE  
 XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
 KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 KM light chain variable region; single chain antibody; scFv.  
 OS Mus sp.  
 XX US2004175385-A1.  
 PN 09-SEP-2004.  
 PD 01-AUG-2003; 2003US-00632706.  
 PF 31-AUG-1998; 98US-0014886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA Marks JD, Amersdorfer P;  
 PI WPI; 2004-652009/63.  
 DR  
 XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 PS Example 1; SEQ ID NO 72; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, IC6, 3012, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralises botulinum  
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
 CC comprising BONT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin

CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of a mouse light chain variable fragment anti-botulinum toxin  
 CC scFv.  
 CC  
 SQ Sequence 107 AA;  
 QY Query Match 91.5%; Score 506; DB 8; Length 107;  
 DB Best Local Similarity 91.6%; Pred. No. 7.4e-31;  
 DB Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DRELQSPAIMSASPGKRVTTTTCASASSVSYMYWYQOKPGSSPRLIYDTSNLASGVPR 60  
 DB 1 DRELQSPAIMSASPGKRVTTTTCASASSVSYMYWYQOKPGSSPRLIYDTSNLASGVPR 60  
 QY 61 FSGSGSGTSYSLTISRMEADATYYCCQWMSNPLTFGSGTKLELR 107  
 DB 61 FSGSGSGTSYSLTISRMEADATYYCCQWMSNPLTFGSGTKLELR 107

RESULT 10  
 AAR79867 ID AAR79867 standard; protein: 244 AA.  
 AC AAR79867;  
 XX 02-JUL-1996 (first entry)  
 DT Anti-EGFR single chain antibody (Clone 10 D 2).  
 DE  
 XX Single chain antibody; antibody; epidermal growth factor receptor; EGFR;  
 KM tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;  
 KM phage antibody library.  
 OS Mus musculus.  
 XX WO9525167-A1.  
 PN 21-SEP-1995.  
 PD 16-MAR-1995; 95WO-EP000978.  
 PF 17-MAR-1994; 94EP-00104160.  
 PR 02-DEC-1994; 94EP-00118970.  
 XX (MERE ) MERCK PATENT GMBH.  
 PA Kettlborough AC, Bendig MM, Ansell KH, Guessow D, Adan J;  
 PI Miltjans F, Rosell E, Biasco F, Plutats J;  
 DR WPI; 1995-336972/43.  
 DR N-PSDB; AAT04020.  
 PS Anti-EGFR antibodies and single chain Fv antibody fragments - obtained  
 PT from phage-antibody libraries, useful for diagnosis and therapy of  
 PT tumours.  
 XX Claim 4; Page 60-61; 93pp; English.

CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies and  
 CC antibodies constructed from anti-EGFR antibody fragments can be used for  
 CC diagnosis of tumours and assessment of tumour growth in vitro and in  
 CC vivo. They may also be used in a pharmaceutical composition for the  
 CC therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and  
 CC fragments are derived from mice but are humanised so as to cause minimum  
 CC reaction against them. They are produced using the phage antibody  
 CC library. AAT04020 and AAR79858-R79873)  
 CC AAT04020 and AAR79858-R79873)  
 XX Sequence 244 AA;  
 SQ Query Match 91.5%; Score 506; DB 2; Length 244;  
 Best Local Similarity 92.6%; Pred. No. 1.6e-30;

Matches 100; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 DTELTPSAIMASPGKVTTCSSASSSVYMYWQKRGSSPRLIYDTSNLASGVPR 60  
 DB 137 DIELTPSAIMASPGKVTTCSSASSSVYMYWQKRGSSPRLIYDTSNLASGVPR 196  
 QY 61 FSGSGSGTSYSLTISRMEADATYCCQWSSNP--LTFSGTKLEIK 106  
 DB 197 FSGSGSGTSYSLTISRMEADATYCCQWSSNPMPYFGGTGLEIK 244

## RESULT 11

AAR79871  
 ID AAR79871 standard; protein; 242 AA.

AC AAR79871;  
 XX  
 AC AAR79871;  
 XX

DT 02-JUL-1996 (first entry)  
 XX

DE Anti-EGFR single chain antibody (Clone 7 G 1).  
 XX

KM Single chain antibody; antibody; epidermal growth factor receptor; EGFR;  
 KW tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;  
 KW phage antibody library.  
 XX

OS Mus musculus.  
 XX

XX WO9525167-A1.  
 XX

PD 21-SEP-1995.  
 XX

PF 16-MAR-1995; 95WO-EP000978.  
 XX

PR 17-MAR-1994; 94EP-00104160.  
 PR 02-DEC-1994; 94EP-00118970.  
 XX

PA (MERE ) MERCK PATENT GMBH.  
 XX

PI Kettleborough AC, Bendig MW, Ansell KH, Guesow D, Adan J,  
 PI Mitjans F, Rosell E, Blasco F, Pizlats J;  
 DR N-PSDB; AAT04024.  
 XX

XX WPI; 1995-336972/43.  
 DR  
 XX

PT Anti-EGFR antibodies and single chain Fv antibody fragments - obtained  
 PT from phage-antibody libraries, useful for diagnosis and therapy of  
 PT tumours.  
 PT  
 PS  
 PS

Claim 4; Page 70; 93pp; English.

CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies and  
 CC antibodies constructed from anti-EGFR antibody fragments can be used for  
 CC diagnosis of tumours and assessment of tumour growth in vitro and in  
 CC vivo. They may also be used in a pharmaceutical composition for the  
 CC therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and  
 CC fragments are derived from mice but are humanised so as to cause minimum  
 CC reaction against them. They are produced using the phage antibody  
 CC library. They are produced using the phage antibody library. (See  
 CC AAT04011-T04024 and AAR79858-R79873)  
 CC  
 CC

CC Sequence 242 AA;  
 SQ

Query Match 91.3%; Score 505; DB 2; Length 242;  
 Best Local Similarity 92.5%; Pred. No. 1.9e-30;

Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DTELTPSAIMASPGKVTTCSSASSSVYMYWQKRGSSPRLIYDTSNLASGVPR 60  
 DB 137 DIELTPSAIMASPGKVTTCSSASSSVYMYWQKRGSSPRLIYDTSNLASGVPR 196

QY 61 FSGSGSGTSYSLTISRMEADATYCCQWSSNP-LTFSGTKLEIK 106  
 DB 197 FSGSGSGTSYSLTISRMEADATYCCQWSSNP-LTFSGTKLEIK 244

## RESULT 12

ABG32682  
 ID ABG32682 standard; protein; 106 AA.

AC ABG32682;  
 XX

DT 29-NOV-2002 (first entry)  
 XX

DE Murine anti-EGFR antibody, MAb425, VK polypeptide.  
 XX

KM Mouse; variable kappa light chain; VK; epidermal growth factor receptor;  
 KW EGFR; antibody; Her 1; immunogenic; immune system; T cell epitope;  
 KW immunogenicity; major histocompatibility complex; MHC; allotype;  
 KW MHC class II; antibody therapy; cancer; tumour; murine;  
 KW anti-EGFR antibody; MAb425.  
 XX

OS Mus sp.  
 XX

PN WO20026058-A1.  
 XX

PD 29-AUG-2002.  
 XX

PF 18-FEB-2002; 2002WO-BP001687.  
 XX

PR 19-FEB-2001; 2001EP-00103954.  
 XX

PA (MERE ) MERCK PATENT GMBH.  
 XX

PI Carr RJ, Carter G, Jones T, Williams S, Hamilton A;  
 PI WPI; 2002-674898/72.  
 DR

PT New modified anti-epidermal growth factor receptor antibodies which are  
 PT non-immunogenic or less immunogenic compared with non-modified  
 PT antibodies, useful for treating cancers or tumors, e.g. tumor of the  
 PT breast, heart or lung.  
 PT  
 PS  
 PS

PS Disclosure; Page 20; 47pp; English.

CC The invention discloses a modified antibody (or fragment) directed to the  
 CC epidermal growth factor receptor (EGFR or Her 1). The antibody is  
 CC substantially non-immunogenic, or less immunogenic, than any original  
 CC immunogenically non-modified antibody directed to the same receptor when  
 CC exposed to the immune system of a given species and compared with the non  
 CC -modified antibody. Compared with a non-modified antibody, the modified  
 CC antibody does not have, or has a reduced number, of T cell epitope  
 CC sequences and/or major histocompatibility complex (MHC) allotypes having  
 CC the ability to bind peptides derived from the non-modified antibody. The  
 CC 13-mer T-cell epitope peptide, or a sequence having at least 9  
 CC consecutive amino acid residues of the 13-mer T-cell epitope having a  
 CC potential MHC class II binding activity, is useful in the manufacture of  
 CC an immunogenically modified antibody having substantially no or less  
 CC immunogenicity, when used in vivo, compared to the non-modified antibody.  
 CC The modified antibody is useful in antibody therapy to treat cancers or  
 CC tumours. The modified antibody is substantially non-immunogenic or less  
 CC immunogenic than any original immunogenically non-modified antibody  
 CC directed to the same receptor when exposed to the immune system of a  
 CC given species, has enhanced properties and with reduced or absent  
 CC potential to induce an immune response in the human subject. The modified  
 CC antibody displays an increased circulation time within the human subject  
 CC and would be of particular benefit in chronic or recurring disease  
 CC settings. The sequence presented is the murine anti-EGFR antibody,  
 CC MAb425, variable kappa light chain (VK) polypeptide  
 CC  
 CC

CC Sequence 106 AA;  
 SQ

Query Match 90.8%; Score 502; DB 5; Length 106;  
 Best Local Similarity 94.2%; Pred. No. 1.5e-30;

Matches 97; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTPSAIMASPGKVTTCSSASSSVYMYWQKRGSSPRLIYDTSNLASGVPRFSG 63

Db 4 LTGSPAIMSASPGKVTMTCSASSVTYMWYQKPPSSPRLIYDTSNLASGVPRFSG 63  
 QY 64 SGGSTSYSLTISRMEADATYTCQOWSSNPLTFGSGTKLEIK 106  
 Db 64 SGGSTSYSLTISRMEADATYTCQOWSSHIFTFGSGTKLEIK 106

## RESULT 13

AAE27810  
 ID AAE27810 standard; protein; 106 AA.

AAE27810;  
 AC AAE27810;

DT 13-DEC-2002 (first entry)  
 XT Mouse 425 antibody VK protein.

DE Mouse 425 antibody VK protein.

XX Mouse; fusion protein; immunological; major histocompatibility complex;  
 KM MHC; nausea; gastric upset; antibody; VK region.

OS Mus sp.

XX WO200266514-A2.

PD 29-AUG-2002.

PF 18-FEB-2002; 2002MO-EP001690.

PR 19-FEB-2001; 2001EP-00103955.

PR 05-APR-2001; 2001EP-00108291.

PA (MERE ) MERCK PATENT GMBH.

PI Gallies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S,  
 PI Hanlon M, Watkins J, Baker M, May JC;

DR WPI; 2002-667054/71.

PT New modified fusion protein with reduced immunogenicity, useful for  
 PT combining favorable properties of a composition, comprises an  
 PT immunoglobulin molecule linked to a non-immunoglobulin target  
 PT polypeptide.

PS Example 18; Page 68; 92pp; English.

CC The invention relates to an immunogenically modified fusion protein  
 CC derived from a parent fusion protein, comprising first and second  
 CC proteins/polypeptides, where the first protein is an immunoglobulin  
 CC molecule or its fragment and the second protein is non-immunoglobulin  
 CC target polypeptide each linked to the other directly or by a linker  
 CC molecule. The immunogenically modified fusion protein is useful in  
 CC combining known favourable properties of a composition or in creating new  
 CC properties of a composition which elicits biological or pharmacological  
 CC efficacy without having undesirable physiological effects such as nausea  
 CC or gastric upset. The present sequence is mouse 425 antibody VK protein.  
 CC This sequence is used in the exemplification of the invention

XX Sequence 106 AA;

Query Match 90.8%; Score 502; DB 5; Length 106;  
 Best Local Similarity 94.2%; Pred. No. 1.5e-30;  
 Matches 97; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASPGKVTMTCSASSVTYMWYQKPPSSPRLIYDTSNLASGVPRFSG 63

Db 4 LTGSPAIMSASPGKVTMTCSASSVTYMWYQKPPSSPRLIYDTSNLASGVPRFSG 63

QY 64 SGGSTSYSLTISRMEADATYTCQOWSSNPLTFGSGTKLEIK 106

Db 64 SGGSTSYSLTISRMEADATYTCQOWSSHIFTFGSGTKLEIK 106

RESULT 14  
 AAR27050  
 ID AAR27050 standard; protein; 128 AA.

AC AAR27050;  
 XX AAR27050;

DT 25-MAR-2003 (revised)

DT 01-MAR-1993 (first entry)

XX VLA425 antibody cloned into pUC18.

XX Monoclonal antibody; complementarity determining region; framework;  
 KM antigens; tumour; melanoma; carcinoma; glioma; light; heavy; variable;  
 KM chain.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..22 /note="signal peptide"

FT Protein 23..128 /note="mature peptide"

FT Region 46..55 /label="CDR1"

FT Region 71..77 /label="CDR2"

FT Region 110..118 /label="CDR3"

XX WO9215683-A1.

PD 17-SEP-1992.

PF 04-MAR-1992; 92WO-EP000480.

PR 06-MAR-1991; 91BP-00103389.

PA (MERE ) MERCK PATENT GMBH.

PI Bendig MM, Kettieborough CA, Saldanha V;

DR WPI; 1992-331729/40.

DR N-PADB; AAQ28740.

PT Human monoclonal antibodies binding to human receptors - for treatment  
 PT and diagnosis of tumours, e.g. melanoma and carcinoma.

PS Disclosure; Fig 2; 89pp; English.

CC The variable light chain of monoclonal antibody 425 was prep'd. from a  
 CC synthetic cDNA sequence in which mutatoche had been made to the 5' and 3'  
 CC ends to allow for cloning into HCV expression vectors. Donor splice  
 CC sites were recreated in the 3' flanking regions to allow correct splicing  
 CC of the variable and constant regions. The 5' sequence was altered to  
 CC introduce an initiation codon. The cloned antibody may be used int the  
 CC prodn. of reshaped or humanised antibodies which are less immunogenic than  
 CC native antibodies and may be used to combat e.g. glioma, melanoma or  
 CC carcinoma. See also AAR27299-300 and AAR27037-41. (Updated on 25-MAR-2003  
 CC to correct PN field.)

XX Sequence 128 AA;

Query Match 90.8%; Score 502; DB 2; Length 128;  
 Best Local Similarity 94.2%; Pred. No. 1.8e-30;  
 Matches 97; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASPGKVTMTCSASSVTYMWYQKPPSSPRLIYDTSNLASGVPRFSG 63

Db 26 LTGSPAIMSASPGKVTMTCSASSVTYMWYQKPPSSPRLIYDTSNLASGVPRFSG 85

QY 64 SGGSTSYSLTISRMEADATYTCQOWSSNPLTFGSGTKLEIK 106

Db 86 SGGSTSYSLTISRMEADATYTCQOWSSHIFTFGSGTKLEIK 128

## RESULT 15

AAB69673  
ID AAB69673 standard; protein; 106 AA.

XX AAB69673;

XX 30-APR-2001 (first entry)

XX Murine mlk-beta1 antibody light chain SEQ ID NO: 58.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;  
XX light chain; graft versus host disease; transplant; autoimmune disease;  
XX multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;  
XX myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX Mus sp.

XX US6180370-B1.

XX 30-JAN-2001.

XX 07-JUN-1995; 95US-00484537.

XX 28-DEC-1988; 88US-00290975.

XX 13-FEB-1989; 89US-00310252.

XX 28-SEP-1990; 90US-00590274.

XX 19-DEC-1990; 90US-00634278.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Queen Cl, Selick HB;

XX WPI; 2001-190856/19.

XX Producing humanized immunoglobulin, involves producing a cell containing  
XX DNA segments encoding humanized heavy and light chain variable regions,  
XX and expressing the DNA segments in the cell.

XX Disclosure; Fig 5; 145pp; English.

XX The present invention describes a method of producing humanised  
XX immunoglobulins involving expressing in a cell a nucleic acid encoding a  
XX humanised version of an immunoglobulin. This is obtained by comparing a  
XX donor and human immunoglobulin and producing a combined antibody which  
XX contains part of each. These are useful in the treatment of graft-versus-  
XX host disease, transplant rejection, autoimmune diseases such as diabetes,  
XX rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic  
XX lupus erythematosus, herpes infections, CMV virus infections and myeloid  
XX leukaemia. The present sequence is an antibody used to demonstrate the  
XX method of the invention

XX Sequence 106 AA;

Query Match 90.6%; Score 501; DB 4; Length 106;  
Best Local Similarity 93.2%; Pred. No. 1.7e-30;  
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPAINASPGKVTTCASASSVSYMYQOKPGSSPRLIYDTSNLASGVPRFSG 63  
DB 4 LTQSPAINASPGKVTTCASASSVSYMYQOKPGSSPRLIYDTSNLASGVPRFSG 63  
QY 64 SSGSGTYSYSLTISRMEADAATYCCQMSNPITFGSGTLELK 106  
DB 64 SSGSGTYSYSLTISRMEADAATYCCQMSNPITFGSGTLELK 106

Search completed: November 21, 2005, 12:19:55  
Job time : 144.255 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 ; Search time 26.0641 Seconds  
(without alignments)  
394.995 Million cell updates/sec

Title: US-10-632-706-87

Sequence: 1 DTELQSPAIMSASPEKVT.....QWSSNPDTFGSGTKLBKLR 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	481	87.0	107 2 PC4405	Ig kappa chain V r
2	473	85.5	107 2 A30562	Ig kappa chain V r
3	472	85.4	107 2 B30562	Ig kappa chain V r
4	471	85.2	130 1 JL0079	Ig kappa chain pre
5	469.5	84.9	108 2 S38720	Ig light chain V r
6	467	84.4	103 2 S29591	Ig kappa chain V r
7	466	84.3	235 2 S25058	Ig kappa chain - m
8	465	84.1	106 2 PS0071	Ig kappa chain V r
9	463	83.7	104 2 B49049	Ig kappa chain V r
10	462	83.5	140 2 PL0013	Ig kappa chain pre
11	460.5	83.3	108 2 G30560	Ig kappa chain V r
12	460	83.0	107 2 A42848	Ig light chain V r
13	459	83.0	107 2 PD0011	Ig kappa chain V r
14	457	82.6	107 2 G11119	Ig kappa chain V r
15	456	82.5	106 2 B54378	Ig light chain V r
16	455	82.3	107 2 S11118	Ig kappa chain V r
17	455	82.1	108 2 S11125	Ig kappa chain V r
18	454	82.1	130 2 A32513	Ig kappa chain pre
19	449	81.2	107 2 S11121	Ig kappa chain V r
20	448	81.0	105 2 S26338	Ig kappa chain V r
21	447	80.8	107 2 PT0406	Ig kappa chain V r
22	443	80.1	106 2 G27887	Ig kappa chain V r
23	442	79.9	107 2 S11117	Ig kappa chain V r
24	442	79.9	113 2 S03410	Ig kappa chain pre
25	442	79.9	120 2 S66536	Ig light chain V r
26	441	79.7	97 2 S26341	Ig light chain V r
27	441	79.7	100 2 S29590	Ig kappa chain V r
28	439	79.4	106 2 PL0082	Ig kappa chain V r
29	438	79.2	107 2 S11112	Ig kappa chain V r

30	438	79.2	132 2 S05268	Ig kappa chain pre
31	437.5	79.1	106 2 S11114	Ig kappa chain V r
32	437	79.0	130 2 S04573	Ig kappa chain pre
33	436	78.8	106 2 PS0070	Ig kappa chain V r
34	435	78.7	97 2 PH1084	Ig light chain V r
35	434	78.5	104 2 JC6076	anti-D-dimer monoc
36	433	78.3	108 2 PL0278	Ig kappa chain V r
37	433	78.3	123 2 S05269	Ig kappa chain pre
38	432	78.1	130 2 B32456	Ig kappa chain pre
39	430	77.8	108 2 PS0069	Ig kappa chain V r
40	429	77.6	108 2 PL0277	Ig kappa chain V r
41	429	77.6	108 2 PL0276	Ig kappa chain V r
42	429	77.6	108 2 S29581	Ig kappa chain V r
43	428	77.4	107 2 S11113	Ig kappa chain V r
44	427	77.2	107 2 S11123	Ig kappa chain V r
45	425	76.9	124 2 S05267	Ig kappa chain pre

#### ALIGNMENTS

##### RESULT 1

PC4405  
Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)

C/Species: Mus musculus (house mouse)  
C/Date: 10-Nov-1997 #sequence\_revision 23-Jan-1998 #text\_change 09-Jul-2004

C/Accession: PC4405  
R/Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.

Chinese Biochem. J. 12, 648-653, 1996  
A/Title: Generation of a phage display library of the immunoglobulin repertoire from hum

A/Reference number: PC4405  
A/Accession: PC4405

A/Molecule type: mRNA  
A/Residues: 1-107 <DEN>

A/Cross-references: UNIPROT:O8KLF0; UNIPARC:UPI00001767B8

A/Experimental source: spleen cell  
C/Suprafamily: immunoglobulin V region; immunoglobulin homology

F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 481; DB 2; Length 107;  
Best Local Similarity 85.0%; Pred. No. 8.9e-35;

Matches 91; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY	1	DTELQSPAIMSASPEKVTTCASSSVSITMYTQKPGSSPLLITDTSILASGVPR	60
DB	1	DIELTQSPAIMSASPEKVTTCASSSISYTHWYQKPGTSPKRWIDTSKLSGVPR	60
QY	61	PSGSGSGSYSLTTSRMAREDAATYTCOWASNPITFGSGTKLBKLR	107
DB	61	PSGSGSGSYSLTTSRVAEDAAATYTCOWMDNPITFGSGTKLBKLR	107

##### RESULT 2

A30562  
Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse

C/Species: Mus musculus (house mouse)  
C/Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000

C/Accession: A30562  
R/Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.

J. Immunol. 142, 888-893, 1989  
A/Title: Amino acid substitutions in V-H CDR3 change the idiotype but not the antigen-bir

A/Reference number: A30562; MUID:89110066; PMID:2464031  
A/Status: preliminary

A/Accession: A30562  
A/Molecule type: mRNA

A/Cross-references: UNIPARC:UPI00001767B0

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 473; DB 2; Length 107;  
Best Local Similarity 87.5%; Pred. No. 4.4e-34;

```

Matches 91; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASPGKVTTCGASSSVSVMYVYQKPGSSPRLIYDTSNLAGVPRFSG 63
    |||||
Db 4 LTGSPAIMSASPGKVTTCGASSSVSVMYVYQKPGSSPRLIYDTSNLAGVPRFSG 63
    |||||

QY 64 SGGSTSYSLTISRMEADATATYTCQWSSNPLTFGSGTKLEIKR 107
    |||||
Db 64 SGGSTSYSLTISRMEADATATYTCQWSSNPLTFGSGTKLEIKR 107
    |||||

RESULT 3
Ig kappa chain V region (27.10.2) - mouse (fragment)
B30562
C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C/Accession: B30562
R/Sikder, S.K.; Borden, P.; Grzesio, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A/Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
A/Reference number: A30562; MUID:89110066; PMID:2464031
A/Accession: B30562
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-107 <SIK>
A/Cross-references: UNIPARC:UPI00001767BA
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 85.4%; Score 472; DB 2; Length 107;
Best Local Similarity 86.5%; Pred. No. 5.3e-34;
Matches 90; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASPGKVTTCGASSSVSVMYVYQKPGSSPRLIYDTSNLAGVPRFSG 63
    |||||
Db 4 LTGSPAIMSASPGKVTTCGASSSVSVMYVYQKPGSSPRLIYDTSNLAGVPRFSG 63
    |||||

QY 64 SGGSTSYSLTISRMEADATATYTCQWSSNPLTFGSGTKLEIKR 107
    |||||
Db 64 SGGSTSYSLTISRMEADATATYTCQWSSNPLTFGSGTKLEIKR 107
    |||||

RESULT 4
Ig kappa chain precursor V region (anti-phenylloxazone 6F6) - mouse
JL0079
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C/Accession: JL0079; A49044; B49044
R/Karltun, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A/Title: Combinatorial association of V genes: one VH gene codes for three non-cross-re
A/Reference number: JL0076; MUID:89096973; PMID:3211160
A/Accession: JL0079
A/Molecule type: mRNA
A/Residues: 1-130 <KAA>
A/Cross-references: UNIPARC:UPI000017371F; GB:M27792; NID:G197159
A/Experimental source: mRNA clones for anti-phenylloxazone antibody 6F6
A/Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10
R/Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
Eur. J. Immunol. 22, 1627-1634, 1992
A/Title: Non-random features of the repertoire expressed by the members of one V kappa g
A/Reference number: A49044; MUID:92289826; PMID:1601044
A/Accession: A49044
A/Molecule type: DNA
A/Residues: 1-25 <MI1>
A/Cross-references: UNIPARC:UPI000011760C; GB:S37663; NID:G250214; PIDN:AA22331.1; PID:
A/Accession: B49044
A/Molecule type: DNA
A/Residues: 114-116 <MI12>
A/Cross-references: UNIPARC:UPI0000118E85; GB:S37664; NID:G250215; PIDN:AA22332.1; PID:

```

```

A/Experimental source: BAB/c germ-line
A/Note: sequences extracted from NCBI backbone, partial nucleotide sequences of 13 addit
A/Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBI:P:106822)
C/Genetics:
A/Gene: V(kappa)Ox1
A/Insertion: 17/1
C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F/38-111/Domain: immunoglobulin homology <IMM>
F/45-109/Disulfide bonds: #status predicted

Query Match 85.2%; Score 471; DB 1; Length 130;
Best Local Similarity 87.5%; Pred. No. 7.9e-34;
Matches 91; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASPGKVTTCGASSSVSVMYVYQKPGSSPRLIYDTSNLAGVPRFSG 63
    |||||
Db 26 LTGSPAIMSASPGKVTTCGASSSVSVMYVYQKPGSSPRLIYDTSNLAGVPRFSG 85
    |||||

QY 64 SGGSTSYSLTISRMEADATATYTCQWSSNPLTFGSGTKLEIKR 107
    |||||
Db 86 SGGSTSYSLTISRMEADATATYTCQWSSNPLTFGSGTKLEIKR 129
    |||||

RESULT 5
S38720
Ig light chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C/Accession: S38720
R/Cimani, A.V.
submitted to the EMBL Data Library, November 1993
A/Reference number: S38713
A/Accession: S38720
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <CIM>
A/Cross-references: UNIPARC:UPI0000117544; EMBL:X76023; NID:G416104; PIDN:CAA53610.1; PI
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 84.9%; Score 469.5; DB 2; Length 108;
Best Local Similarity 88.6%; Pred. No. 8.8e-34;
Matches 93; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 4 LTGSPAIMSASPGKVTTCGASSSVSVMYVYQKPGSSPRLIYDTSNLAGVPRFSG 63
    |||||
Db 4 LTGSPAIMSASPGKVTTCGASSSVSVMYVYQKPGSSPRLIYDTSNLAGVPRFSG 63
    |||||

QY 64 SGGSTSYSLTISRMEADATATYTCQWSSNPLTFGSGTKLEIKR 107
    |||||
Db 64 SGGSTSYSLTISRMEADATATYTCQWSSNPLTFGSGTKLEIKR 108
    |||||

RESULT 6
Ig kappa chain V region - mouse
S29591
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S29591
R/Kavaler, J.
submitted to the EMBL Data Library, April 1991
A/Reference number: S26459
A/Accession: S29591
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-103 <KAV>
A/Cross-references: UNIPARC:UPI0000115F57; EMBL:X59094; NID:G52227; PIDN:CAA41820.1; PID:

```

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
P:15-88/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 467; DB 2; Length 103;  
Best Local Similarity 89.1%; Pred. No. 1.4e-33;  
Matches 90; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRFSG 63  
|||||  
DB 3 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKSGSPKRWYDTSKLASGVPRFSG 62  
|||||

QY 64 SSGGTSYSLTISRMEADDAATYYCOQMSNPITFGSGTKLE 104  
|||||  
DB 63 SSGGTSYSLTISRMEADDAATYYCOQMSNPITFGAGTKLE 103  
|||||

#### RESULT 7

S25058  
Ig kappa chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000

C:Accession: S25058  
R: Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992

A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neocytospecific protein

A:Reference number: S25057

A:Accession: S25058

A:Status: Preliminary

A:Residue type: mRNA

A:Residues: 1-235 <FIS>

A:Cross-references: UNIPARC:UPI0000116096; EMBL:X67211; NID:G54828; PIDN:CAA47650.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
P:38-111/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 466; DB 2; Length 235;  
Best Local Similarity 88.5%; Pred. No. 3.9e-33;  
Matches 92; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRFSG 63  
|||||  
DB 26 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKSGSPKRWYDTSKLASGVPRFSG 85  
|||||

QY 64 SSGGTSYSLTISRMEADDAATYYCOQMSNPITFGSGTKLE 107  
|||||  
DB 86 SSGGTSYSLTISRMEADDAATYYCOQMSNPITFGAGTKLE 129  
|||||

#### RESULT 8

PS0071

Ig kappa chain V region (38C13 V8) - mouse

C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000

C:Accession: PS0071  
R: Levy, S.; Campbell, M.J.; Levy, R.

J. Exp. Med. 170, 1-13, 1989

A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement

A:Reference number: A92781; MUID:89310348; PMID:2501443

A:Accession: PS0071

A:Status: translation not shown

A:Residue type: DNA

A:Residues: 1-106 <LEV>

A:Cross-references: UNIPARC:UPI00001767C9

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
P:16-89/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 465; DB 2; Length 106;  
Best Local Similarity 87.4%; Pred. No. 2.1e-33;  
Matches 90; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRFSG 63  
|||||

DB 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKSGTSPKRWYDTSKLASGVPRFSG 63

QY 64 SSGGTSYSLTISRMEADDAATYYCOQMSNPITFGSGTKLE 106  
|||||  
DB 64 SSGGTSYSLTISRMEADDAATYYCOQMSNPITFGAGTKLE 106  
|||||

#### RESULT 9

B49049  
Ig kappa chain V region (anti-Idiotypic) - mouse

C:Species: Mus musculus (house mouse)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000

C:Accession: B49049  
R: Armadillo, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.

Eur. J. Immunol. 22, 2893-2899, 1992

A:Title: Molecular analysis of anti-Idiotypic monoclonal antibodies in the HLA-DR antigen

A:Reference number: A49049; MUID:93049629; PMID:11425914

A:Accession: B49049

A:Status: Preliminary

A:Residue type: nucleic acid

A:Residues: 1-104 <ARM>

A:Cross-references: UNIPARC:UPI00001767AD

A:Experimental source: BALB/c

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
P:16-89/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 463; DB 2; Length 104;  
Best Local Similarity 88.1%; Pred. No. 3.1e-33;  
Matches 89; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRFSG 63  
|||||  
DB 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKSGTSPKRWYDTSKLASGVPRFSG 63  
|||||

QY 64 SSGGTSYSLTISRMEADDAATYYCOQMSNPITFGSGTKLE 104  
|||||  
DB 64 SSGGTSYSLTISRMEADDAATYYCOQMSNPITFGAGTKLE 104  
|||||

#### RESULT 10

PI0013

Ig kappa chain precursor V region (4C11) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000

C:Accession: PI0013  
R: Cheng, H.L.; Sood, A.K.; Ward, R.B.; Kleber-Emmmons, T.; Kohler, H.

Mol. Immunol. 25, 33-40, 1988

A:Title: Structural basis of stimulatory anti-Idiotypic antibodies.

A:Reference number: PI0011; MUID:88142863; PMID:3125424

A:Accession: PI0013

A:Residue type: mRNA

A:Residues: 1-140 <CHR>

A:Cross-references: UNIPARC:UPI00001767A6

A:Experimental source: cell line 4C11

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin

P:1-22/Domain: signal sequence #status predicted <SIG>

F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>

F:38-111/Domain: immunoglobulin homology <IMM>

F:46-55/Region: complementarity-determining 1

F:71-77/Region: complementarity-determining 2

F:110-118/Region: complementarity-determining 3

P:130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 83.5%; Score 462; DB 2; Length 140;  
Best Local Similarity 87.5%; Pred. No. 5.1e-33;  
Matches 91; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRFSG 63  
|||||

Db 26 LTOSPAIMSAPGEKVTITCSASSSVSYMMFOOKDPISPKMIYSTSLAGVPVRFEG 85

Qy 64 SGSGTSYSLTISRMEADATYYCOOMSNPLTFGSGTKLEMR 107  
|||||  
86 SGSGTSYSLTISRMEADATYYCOOMSSYPPFGGSGTKLEMR 129

## RESULT 11

G30560  
IG kappa chain V region (35.8.2H) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
C/Accession: G30560  
R/MacLuda, T.; Kabat, E.A.  
U./Immunol. 142, 863-870, 1989  
A./Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal  
. .  
A./Reference number: A30560; MUID:89110062; PMID:2464028  
A./Accession: G30560  
A./Status: preliminary; not compared with conceptual translation  
A./Molecule type: mRNA  
A./Residues: 1-108 <MAT>  
A./Cross-references: UNIPARC:UPI00001767B8  
C./Superfamily: Immunoglobulin V region; immunoglobulin homology  
C./Keywords: heterotetramer; immunoglobulin  
C./16-89/Domain: immunoglobulin homology <IM>

Query Match	83.3%	Score 460.5;	DB 2;	Length 108;
Best Local Similarly	85.7%	Pred. NO. 5.2e-33;		
Matches 90; Conservative .	5;	Mismatches 9;	Indels 1;	Gaps 1;

```
Oy      4 LTQSPAIMSASPGEKVTTCSSASSSVSTMWYQQPKGSSRRLLIDTSLNLSAGVPRFSG 63
        |||||
Db      4 LTQSPAIMSASPGEKVTTCSSASSSVSTMWYQQKGSSSKRTWIDTSKLASGVPRFSG 63
```

```
Qy      64 SGGSTSYSLTISRMEADATYYCOOMSSN-PLTFGSGTKLEIKR 107
        |||||
Db      64 SGGSTSYSLTISRMEADATYYCOOMTRNPPFTFGSGTKLEIKR 108
        |||||
```

## RESULT 12

A42848  
Ig1light chain V region - mouse (fragment)  
N/Alternate names: I6 anti-tumor antibody  
C/Species: Mus musculus (house mouse)  
C/Date: 27-Apr-1993 #sequence revision 18-Nov-1994 #text change 21-Jan-2000  
C/Accession: A42848; S33902  
R/Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsitch, L.; Schieven, G.L.; Marken, J.S.; Arnfield  
J. Biol. Chem. 267, 15552-15558, 1992  
A/Title: Chimeric I6 anti-tumor antibody. Genomic construction, expression, and character  
A/Reference number: A42848; MUID:92348410; PMID:1639794  
A/Accession: A42848  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-107 <FEI>  
A/Cross-references: UNIPARC:UPI0000115334; EMBL:M90690  
A/Note: sequence extracted from NCBI database (NCBI:109958, NCBI:P:109959)  
C/Superfamily: immunoglobulin V region, immunoglobulin homology  
C/Keywords: immunoglobulin  
C/KeyWords: immunoglobulin homology <IMM>  
/16-89/Domain: immunoglobulin homology

Query Match 83.2%; Score 460; DB 2; Length 107;

```
Oy      4 LTQSPALMSAEPGEKVTITTCSSASSVSVMYMQCKPGSSPRLIYDTSNLTAAGVPRFSG 63
         :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      4 LQSPPAILSAEPGEKVTILTRASSSVSFNMYYQCKPGSSSKPMWATSNLNASGVPRGFSG 63
```

	64	S G S G T S Y S L T I R M E A B D A T Y Y C Q O M S N P L T F G S G T K L E K R	1077
Oy	:	:          :	
Dd	64	S G S G T S Y S L A I S R V E A B D A T Y Y C Q O M S N P L T F G A G T K L E K R	1077

**DEC 11 1972**

Accession: 15  
 PD0011  
 Ig kappa chain V region (VLBI0, anti-AFP) - mouse (fragment)  
 CSpecies: Mus musculus (house mouse)  
 CDate: 10-Jul-1998 #sequence\_rev10n 10-Jul-1998 #text\_change 21-Jan-2000  
 CAccession: PD0011  
 RIdeng, J.B., Han, H., Su, C.Z., Chen, C.Q.  
 Chinese Biochem. J. 12, 648-653, 1996  
 ATitle: Generation of a phage display library of the immunoglobulin repertoire from human spleen  
 AReference number: PC4405  
 AContents: Spleen  
 AAccession: PD0011  
 A.Molecule type: mRNA  
 A.Residues: 1-107 <DEN>  
 C8Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 F16-89/Domain: Immunoglobulin homology <IMM>

Query Match	83.0%	Score 459	DB 2	Length 107
Best Local Similarly	82.2%	Pred. No. 7e-33	12	Indels 0
Matches 88		Conservative	7	Mismatches 0

```
QY      1 DTELTPAINTSASPGKEVTTTCSASSSVSYMYWYQQKGGSSPLLIIYDTSNLTASGVPR    60C
        | ||||| ||||| ||||| : ||| : ||||| : ||| ||||| :
Db      1 DIETLPATINSASPGKEVTMTCSASSISYMYHYQQKGTSTPKMVIYDTSKLASGVPAK    60C
```

```

QY      61  PGGSGGTSYSTLTISRMEADDAATYYCQOWSNPLTFGGGKLEIKR  107
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  GSGSGGTSYSTLTISRVEADDAATYYCQQRNDNPPFGGKLEIKR  107

```

## RESULT 14

S1119  
Ig kappa chain V region (clone NO6-8.3.1) - mouse (fragment)  
C|Species: Mus musculus (house mouse)  
C|Date: 19-Mar-1997 #sequence\_rev|sion 23-Aug-1997 #text\_change 21-Jan-2000  
C|Accession: S1119  
R|Kaerliren, M.; Griffiths, G.M.; Markham, A.P.; Milstein, C.  
N|ature 304, 320-324, 1983  
A|Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone  
A|Reference number: S07331; MUID:83271467; PMID:687353  
A|Accession: S1119  
A|Molecule type: mRNA  
A|Residues: 1-107 <NAT>  
A|Cross-references: UNIPARC:UPI00001767E0  
C|Superfamily: immunoglobulin V region; immunoglobulin homology  
P116-89|Domain: immunoglobulin homology <IMM>

Query Match	82.6%	Score 457	DB 2	Length 107
Best Local Similarity	84.6%	Pred. No. 18-32		
Matches 88; Conservative	4	Mismatches 12	Indels 0	Gaps 0

QY 4 LTSPAIMSASPGEKYTTTCSASSSVSYMYWYQOKPGSSPRLLIYDTSNLASGVPYRFSG 633

Db 4 LTSPAIMSASPGEKYMTTCSASSSVSYMHYQOKSGSPKRWIYDTSKLASGVPARFSG 633

Dy 64 SSGSTSYSLTISRMEADATYYCQOWSSNPITFGSGTKLELR 107  
| | | | | : | | | | |  
Db 64 XGSGTSYSLTISMPAADAATYYCQOWSSNPITFGAGTKLELR 107

## RESULT 15

B54378  
Ig light chain V region anti-triplex DNA - mouse (fragment)  
CISpecies: Mus musculus (house mouse)  
CDate: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
CAccession: B54378  
RAgazie, Y.M.; Lee, J.S.; Burkholder, G.D.  
J Biol. Chem. 269, 7019-7023, 1994  
ATitle: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence labeling of triplex DNA  
AReference number: A54378; MUID:94I65109; PMID:7509814  
AAccession: B54378

A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-106 <AG>  
A/Cross-references: UNIPARC:UPI00001767AC; GB:S68985; NID:G545746; PID:AB30096.1; PID:  
A/Experimental source: spleen and myeloma cell line M08C 315.43  
A/Note: sequence inconsistent with nucleotide translation  
A/Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBI:144175)  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin  
F:16-89/Domain: immunoglobulin homology <IM>

Query Match 82.5%; Score 456; DB 2; Length 106;  
Best Local Similarity 86.4%; Pred. No. 1.3e-32;  
Matches 89; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY	4	LTGSPATMSASPGKVTTCSSASSSVSYWYQOKRGSSPRLTYDTSNLASGVVPRPSG	63
DB	4	LTGSPATMSASPGKVTTCSSASSSVSYWYQOKRGSPKLTWYSTKSLASGVVPRPSG	63
QY	64	SGSGTYSILITSRMEADATYCCQWSSNPLTFGSGTKLEIK	106
DB	64	SGSGTYSILITSRMEADATYCCQWSSNPLTFGSGTKLEIK	106

Search completed: November 21, 2005, 12:22:12  
Job time : 26.0641 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55; Search time 158.344 Seconds  
(without alignments)  
476.756 Million cell updates/sec

Title: US-10-632-706-87  
Perfect score: 553  
Sequence: 1 DTBLTQSPALWASPGKRVLT.....QQWSSNPVTFGGSTKLEIKR 107

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: uniprotc\_05.80.\*  
2: uniprotc\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	500	90.4	106 2	Q9U410_MOUSE
2	489	88.4	108 1	KV6K_MOUSE
3	475	85.9	112 2	Q8K1F2_MOUSE
4	471	85.2	235 2	Q58EV6_MOUSE
5	466	84.3	107 1	KV6P_MOUSE
6	463	83.7	112 2	Q8K1F3_MOUSE
7	461	83.4	107 1	KV6I_MOUSE
8	460	83.2	107 1	KV6G_MOUSE
9	460	83.2	107 1	KV6H_MOUSE
10	460	83.2	107 1	KV6J_MOUSE
11	457	82.6	235 2	Q5XFF8_MOUSE
12	456	82.5	112 2	Q8K1F0_MOUSE
13	452	81.7	114 2	Q8VDD0_MOUSE
14	443.5	80.2	131 2	Q811C3_MOUSE
15	440	79.6	114 2	Q8K1F1_MOUSE
16	426	77.0	237 2	Q569Y8_MOUSE
17	414	74.9	107 1	KV6B_MOUSE
18	413.5	74.8	97 2	Q9J176_MOUSE
19	413	74.8	107 1	KV6C_MOUSE
20	410	74.1	107 1	KV6D_MOUSE
21	408	73.8	129 1	KV4A_MOUSE
22	406	73.4	107 1	KV6A_MOUSE
23	398	72.0	107 1	KV6E_MOUSE
24	390.5	70.6	101 2	Q9J178_MOUSE
25	375	67.8	109 2	Q9UL78_MOUSE
26	364	65.8	129 1	KV3L_HUMAN
27	363.5	65.7	129 1	Q6PIH7_HUMAN
28	363	65.6	109 1	KV3D_HUMAN
29	361	65.3	109 1	KV3M_HUMAN
30	360.5	65.2	189 2	Q569I7_HUMAN
31	360	65.1	109 1	KV3B_HUMAN

32	358.5	64.8	111 1	KV3N_MOUSE	P01666 mus musculus
33	358.5	64.8	244 2	Q65ZC8_HUMAN	O65ZC8 homo sapien
34	357.5	64.6	108 1	KV1B_HUMAN	P01594 homo sapien
35	355.5	64.3	108 1	KV1O_HUMAN	P01607 homo sapien
36	355.5	64.3	111 1	KV3M_MOUSE	P01665 mus musculus
37	354.5	64.1	108 1	KV1P_HUMAN	P01608 homo sapien
38	354.5	64.1	108 2	Q9UL70_HUMAN	Q9UL70 homo sapien
39	354.5	64.1	111 1	Q9J170_MOUSE	P01667 mus musculus
40	354.5	64.1	236 2	Q6PIH8_HUMAN	O65I18 homo sapien
41	354.5	64.1	240 2	Q65ZC9_HUMAN	O65ZC9 homo sapien
42	354	64.0	107 2	Q96SA9_HUMAN	Q96SA9 homo sapien
43	353	63.8	109 1	KV3E_HUMAN	P01623 homo sapien
44	352.5	63.7	108 2	Q9UL77_HUMAN	Q9UL77 homo sapien
45	352.5	63.7	111 1	KV3K_MOUSE	P01663 mus musculus

## ALIGNMENTS

```

RESULT 1
Q9U410_MOUSE
ID Q9U410_MOUSE PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30
DE Immunoglobulin light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12567627;
RA Song X.T., Feng Z.O., Qiu Z.N., Li Y.Q., Yu X.C., Xiong Y., Yin C.C.,
RA Huang H.L., Guan X.H.;
RT "Cloning and sequence analysis of the light chain variable region
RT gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma
RT japonicum.";
RL Zhongguo Ji Sheng Chong Xue Yu Ji Sheng Chong Bing Za Zhi
RL 18:257-259(2000); AAF19434.1; -, Genomic_DNA.
DR EMBL; AF207620; AAF19434.1; -, Genomic_DNA.
DR HSSP; P01679; 2FBJ.
DR SMR; Q9U410; 4-106.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544436BA63E CRC64;

Query Match 90.4%; Score 500; DB 2; Length 106;
Best Local Similarity 94.2%; Pred. No. 36-42;
Matches 97; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LTQSPALWASPGKRVLTTCSSASSSVSYMYVQQRGSGSPRLLIYDTSNLASGVPRFSG 63
DB 4 LTQSPALWASPGKRVLTTCSSASSSVSYMYVQQRGSGSPRLLIYDTSNLASGVPRFSG 63
QY 64 SSGGTSYSLTISRMEADATYTCQOWSNPVTFFSGTLEIK 106
DB 64 SSGGTSYSLTISRMEADATYTCQOWSNPVTFFSGTLEIK 106
DB 64 SSGGTSYSLTISRMEADATYTCQOWSNPVTFFSGTLEIK 106

RESULT 2
KV6K_MOUSE
ID KV6K_MOUSE STANDARD; PRT; 108 AA.
AC P04945;
DT 13-AUG-1987 (rel. 05, Created)
DT 13-AUG-1987 (rel. 05, Last sequence update)

```

```

DT 10-MAY-2005 (Ref. 47, last annotation update)
DE IG kappa chain V-VI region N02-6.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
ON NCBI_TaxId=10090;
RX NUCLEOTIDE SEQUENCE.
RX Medline=83271467; PubMed=6877353;
RA Kaartinen M., Giffiths G.M., Mathiam A.F., Milestein C.;
RT "Mammal sequences define an unusually restricted Igg response to 2-
RT phenylloxazone and its early diversification."
RL Nucleic Acids Res. 30:320-324(1983).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; K00746; AAA38691.1; -; mRNA.
CC -----
DR HSSP; Q91W12; 1A11.
DR SMR; P04945; 1-108.
DR Ensembl; ENSMUSG0000062686; Mus musculus.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_Like; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 98 Framework-4.
FT REGION 99 108 Complementarity-determining-3.
FT DISULFID 23 87 By similarity.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;

Query Match 88.4%; Score 489; DB 1; Length 108;
Best Local Similarity 91.4%; Pred. No. 4.7e-41;
Matches 96; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Cy 4 LTGSPAIMSASPEKRYTTTCASASSVSYMYWYQOKPSSPRLIYDTSNLASGVPRFSG 63
Db 4 LTGSPAIMSASPEKRYTTTCASASSVSYMYWYQOKPSSPRLIYDTSNLASGVPRFSG 63
64 SGGSTSYSLTISRMEADATYTCOQMSNP--LTPSGTGLRLK 106
64 SGGSTSYSLTISRMEADATYTCOQMSNP--LTPSGTGLRLK 106
64 SGGSTSYSLTISRMEADATYTCOQMSNP--LTPSGTGLRLK 106
64 SGGSTSYSLTISRMEADATYTCOQMSNP--LTPSGTGLRLK 106

RESULT 3
08K1F2_MOUSE PRELIMINARY; PRT; 112 AA.
AC Q8K1F2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-viase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
ON NCBI_TaxId=10090;
RX NUCLEOTIDE SEQUENCE.
RX STRAIN=BAHB/C; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

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RP NUCLEOTIDE SEQUENCE.
RX PubMed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Terryck T., Avramas S.;
RT "Two murine natural polypeptide autoantibodies are encoded by
RT nonmated germ-line genes."
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR EMBL; AF516283; AAM64201.1; -; Genomic_DNA.
DR PIR; H33932; H33932.
DR HSSP; P01837; 25C8.
DR SMR; Q8K1F2; 2-112.
DR Ensembl; ENSMUSG0000064150; Mus musculus.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_Like; 1.
FT NON_TER 1 1
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 11953 MW; 4716B87FAD543BD CRC64;

Query Match 85.9%; Score 475; DB 2; Length 112;
Best Local Similarity 86.9%; Pred. No. 1.2e-39;
Matches 93; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Cy 1 DTELQSPAIMSASPEKRYTTTCASASSVSYMYWYQOKPSSPRLIYDTSNLASGVPR 60
Db 1 DTELQSPAIMSASPEKRYTTTCASASSVSYMYWYQOKPSSPRLIYDTSNLASGVPR 60
61 FSGSGSGTSTSLTISRMEADATYTCOQMSNP-LTPSGTGLRLK 107
61 FSGSGSGTSTSLTISRMEADATYTCOQMSNP-LTPSGTGLRLK 107
61 FSGSGSGTSTSLTISRMEADATYTCOQMSNP-LTPSGTGLRLK 107
61 FSGSGSGTSTSLTISRMEADATYTCOQMSNP-LTPSGTGLRLK 107

RESULT 4
08E8V6_MOUSE PRELIMINARY; PRT; 235 AA.
AC Q8E8V6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
ON NCBI_TaxId=10090;
RX NUCLEOTIDE SEQUENCE.
RX STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Bhennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schaefer T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RX NUCLEOTIDE SEQUENCE.
RX STRAIN=FVB/N; TISSUE=Colon;

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RG NIH MGC Project;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC091738; AAH91738.1; -; mRNA.  
 DR SMR: O588Y6; 23-235.  
 DR GO: GO:0003823; F:antigen binding; IBA.  
 DR InterPro: IPR003599; IG\_1.  
 DR InterPro: IPR007110; IG\_1like.  
 DR InterPro: IPR003597; IG\_C1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF07654; CI-sect; 1.  
 DR SMART: SM00409; IG; 2.  
 DR SMART: SM00407; IGc1; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 2.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN 1.  
 SO SEQUENCE 235 AA; 25719 MW; BR4E4ABDD2578252 CRC64;

Query Match 85.2%; Score 471; DB 2; Length 235;  
 Best Local Similarity 86.5%; Pred. No. 7.6e-39;  
 Matches 90; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 4 LTGSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRPSG 63  
 |||||  
 DB 26 LTGSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRPSG 85  
 |||||  
 OY 64 SGSGTYSGLTISRMEADATYTCQOWSNPLTFGSGTKLELKR 107  
 |||||  
 DB 86 SGSGTYSGLTISRMEADATYTCQOWSNPLTFGAGTKLELKR 129  
 |||||

## RESULT 5

KY6F\_MOUSE  
 ID KY6F\_MOUSE STANDARD; PRT; 107 AA.

AC P04940;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-VI region NQ2-17.4.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=83271467; PubMed=6877353;  
 RA Kaartinen M., Griffiths G.M., Martham A.F., Milstein C.;  
 RT "mRNA sequences define an unusually restricted Igg response to 2-  
 phenylloxazalone and its early diversification";  
 RL Nature 304:320-324(1983).  
 CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL: K00735; AAA38680.1; -; mRNA.  
 DR HSSP: P04940; 1-107.  
 DR Ensemble: ENSMUSG0000062047; Mus musculus.  
 DR InterPro: IPR007110; IG\_1like.  
 DR InterPro: IPR003596; IG\_V.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.  
 FT REGION 1 23 Framework-1.  
 FT REGION 24 33 Complementarity-determining-1.  
 FT REGION 34 48 Framework-2.  
 FT REGION 49 55 Complementarity-determining-2.  
 FT REGION 56 87 Framework-3.

FT REGION 88 96 Complementarity-determining-3.  
 FT REGION 97 106 Framework-4.  
 FT DISULFID 23 87 By similarity.  
 FT NON TER 107 107  
 SO SEQUENCE 107 AA; 11561 MW; 6F694284BCFA68B6 CRC64;

Query Match 84.3%; Score 466; DB 1; Length 107;  
 Best Local Similarity 85.6%; Pred. No. 9.2e-33;  
 Matches 89; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 4 LTGSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRPSG 63  
 |||||  
 DB 4 LTGSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRPSG 63  
 |||||  
 OY 64 SGSGTYSGLTISRMEADATYTCQOWSNPLTFGSGTKLELKR 107  
 |||||  
 DB 64 SGSGTYSGLTISRMEADATYTCQOWSNPLTFGAGTKLELKR 107  
 |||||

## RESULT 6

OBK1F3\_MOUSE  
 ID OBK1F3\_MOUSE PRELIMINARY; PRT; 112 AA.

AC OBK1F3;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Anti-VIPase light chain variable region. (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BA1B/c; TISSUE=Hyperimmunized spleen;  
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=2499887;  
 RA Baccala R., Quang T.V., Gilbert M., Terrynck T., Avrameas S.;  
 RT "Two murine natural polyclonal autoantibodies are encoded by  
 RT nonmutated germ-line genes";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;  
 RA Tillman D.M., You N.T., Hill R.J., Marich T.N.;  
 RT "Both Igm and Igg anti-DNA antibodies are the products of clonally  
 RT selective B cell stimulation in (NZB x NZW) F1 mice.";  
 RL J. Exp. Med. 176:761-779(1992).  
 DR EMBL: AF516282; AAM64200.1; -; Genomic\_DNA.  
 DR PIR: A33933; A33933.  
 DR PIR: PH1085; PH1085.  
 DR HSSP: P01837; 25C8.  
 DR SMR: Q8K1F3; 2-112.  
 DR Ensemble: ENSMUSG0000063156; Mus musculus.  
 DR InterPro: IPR007110; IG\_1like.  
 DR InterPro: IPR003596; IG\_V.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 FT NON TER 1 1  
 FT NON TER 112 112  
 SO SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

Query Match 83.7%; Score 463; DB 2; Length 112;  
 Best Local Similarity 85.0%; Pred. No. 1.9e-38;  
 Matches 91; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

OY 1 DTELQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPR 60  
 |||||  
 DB 1 DVLQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPKPMIYRTSNLASGVPR 60  
 |||||

Qy 61 FSGSGSGTSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107  
 |||||  
 Db 61 FSGSGSGTSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107

## RESULT 7

KV6H MOUSE

ID KV6H MOUSE STANDARD; PRT; 107 AA.

AC P04943;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE IG kappa chain V-VI region NQ6-8.3.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=83271467; PubMed=6877353;  
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.  
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification."  
 RL Nature 304:320-324(1983).  
 CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.

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CC -----  
 CC EMBL, K00740; AAA38685.1; -, mRNA.  
 DR HSSP; P01679; ZFBU.  
 DR SMR; P04943; 1-107.  
 DR Ensembl; ENSMUSG0000062047; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV, 1.  
 DR PROSITE; PS50835; IG\_LIKE, 1.  
 KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.  
 FT REGION 1 23 Framework-1.  
 FT REGION 24 33 Complementarity-determining-1.  
 FT REGION 34 48 Framework-2.  
 FT REGION 49 55 Complementarity-determining-2.  
 FT REGION 56 87 Framework-3.  
 FT REGION 88 96 Complementarity-determining-3.  
 FT REGION 97 106 Framework-4.  
 FT DISULFID 23 87 By similarity.  
 FT NON TER 107 107  
 SQ SEQUENCE 107 AA; 11573 MW; 6694824BCFC886 CRC64;

Query Match 83.4%; Score 461; DB 1; Length 107;  
 Best Local Similarity 84.6%; Pred. No. 2.9e-38;  
 Matches 88; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 4 LTGSPALMSAPGKATTTTCSASSSVYMWYQKQKSSPRLLYDTSNLASGVPARFSG 63  
 |||||  
 Db 4 LTGSPALMSAPGKATTTTCSASSSVYMWYQKQKSSPRLLYDTSNLASGVPARFSG 63  
 |||||  
 Qy 64 SSGSGTSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107  
 |||||  
 Db 64 SSGSGTSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107

## RESULT 8

KV6G MOUSE

ID KV6G MOUSE STANDARD; PRT; 107 AA.

AC P04941;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE IG kappa chain V-VI region NQ2-48.2.2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=83271467; PubMed=6877353;  
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.  
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification."  
 RL Nature 304:320-324(1983).  
 CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.

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CC -----  
 CC EMBL, K00737; AAA38682.1; -, mRNA.  
 DR HSSP; Q91W12; IAYI.  
 DR SMR; P04941; 1-103.  
 DR Ensembl; ENSMUSG0000062047; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV, 1.  
 DR PROSITE; PS50835; IG\_LIKE, 1.  
 KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.  
 FT REGION 1 23 Framework-1.  
 FT REGION 24 33 Complementarity-determining-1.  
 FT REGION 34 48 Framework-2.  
 FT REGION 49 55 Complementarity-determining-2.  
 FT REGION 56 87 Framework-3.  
 FT REGION 88 96 Complementarity-determining-3.  
 FT DISULFID 23 87 By similarity.  
 FT NON TER 107 107  
 SQ SEQUENCE 107 AA; 11557 MW; 72488DA9BF54934 CRC64;

Query Match 83.2%; Score 460; DB 1; Length 107;  
 Best Local Similarity 84.6%; Pred. No. 3.7e-38;  
 Matches 88; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 4 LTGSPALMSAPGKATTTTCSASSSVYMWYQKQKSSPRLLYDTSNLASGVPARFSG 63  
 |||||  
 Db 4 LTGSPALMSAPGKATTTTCSASSSVYMWYQKQKSSPRLLYDTSNLASGVPARFSG 63  
 |||||  
 Qy 64 SSGSGTSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107  
 |||||  
 Db 64 SSGSGTSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107

## RESULT 9

KV6H MOUSE

ID KV6H MOUSE STANDARD; PRT; 107 AA.

AC P04942;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE IG kappa chain V-VI region NQ5-61.1.2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=83271467; PubMed=6877353;  
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.  
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification."

RL Nature 304:320-324(1983).  
 CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL: K00739; AAA38684.1; -; mRNA.  
 DR HSP; P01679; 2PBJ.  
 DR SMR; P04942; 1-107.  
 DR Ensembl; ENSMUSG0000062047; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IG\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Hydroloma; Immunoglobulin domain; Immunoglobulin V region.  
 FT REGION 1 23 Framework-1.  
 FT REGION 24 33 Complementarity-determining-1.  
 FT REGION 34 48 Framework-2.  
 FT REGION 49 55 Complementarity-determining-2.  
 FT REGION 56 87 Framework-3.  
 FT REGION 88 96 Complementarity-determining-3.  
 FT REGION 97 106 Framework-4.  
 FT DISULFID 23 87 By similarity.  
 FT NON TER 107 107  
 SQ SEQUENCE 107 AA; 11605 MW; CA6C484BFCB550 CRC64;  
 Query Match 83.2%; Score 460; DB 1; Length 107;  
 Best Local Similarity 84.6%; Pred. No. 3.7e-38;  
 Matches 88; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
 Oy 4 LTOSPAIMASPGKVTTCSSASSSVSYMYQQKPSPPRLIYDTSNLASGVPRFG 63  
 Db 4 LTOSPAIMASPGKVTTCSSASSSVSYMYQQKPSPPRLIYDTSNLASGVPRFG 63  
 Oy 64 SSGSTSYSLTISRMEDADATYTCQOWSNPLTFGSGTKLELR 107  
 Db 64 SSGSTSYSLTISRMEDADATYTCQOWSNPLTFGSGTKLELR 107  
 RESULT 10  
 KV6J MOUSE STANDARD; PRT; 107 AA.  
 ID \_KV6J\_MOUSE  
 AC P04944; 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-VI region NQ5-78.2.6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=83271467; PubMed=6877353;  
 RA Kaartinen M., Griffiths G.W., Martham A.P., Milstein C.;  
 RA "mRNA sequences define an unusually restricted IgG response to 2-  
 RA phenylloxazolone and its early diversification".  
 RT Nature 304:320-324(1983).  
 RL Nature 304:320-324(1983).  
 CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.  
 CC -----  
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 CC removed.  
 CC -----  
 CC EMBL: K00744; AAA38689.1; -; mRNA.  
 DR HSP; G91W12; IAYI.  
 DR SMR; P04944; 1-106.

DR Ensembl; ENSMUSG0000062047; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IG\_1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Hydroloma; Immunoglobulin domain; Immunoglobulin V region.  
 FT REGION 1 23 Framework-1.  
 FT REGION 24 33 Complementarity-determining-1.  
 FT REGION 34 48 Framework-2.  
 FT REGION 49 55 Complementarity-determining-2.  
 FT REGION 56 87 Framework-3.  
 FT REGION 88 96 Complementarity-determining-3.  
 FT REGION 97 106 Framework-4.  
 FT DISULFID 23 87 By similarity.  
 FT NON TER 107 107  
 SQ SEQUENCE 107 AA; 11613 MW; A38290781F3C30D3 CRC64;  
 Query Match 83.2%; Score 460; DB 1; Length 107;  
 Best Local Similarity 84.6%; Pred. No. 3.7e-38;  
 Matches 88; Conservative 6; Mismatches 10; Indels 0; Gaps 0;  
 Oy 4 LTOSPAIMASPGKVTTCSSASSSVSYMYQQKPSPPRLIYDTSNLASGVPRFG 63  
 Db 4 LTOSPAIMASPGKVTTCSSASSSVSYMYQQKPSPPRLIYDTSNLASGVPRFG 63  
 Oy 64 SSGSTSYSLTISRMEDADATYTCQOWSNPLTFGSGTKLELR 107  
 Db 64 SSGSTSYSLTISRMEDADATYTCQOWSNPLTFGSGTKLELR 107  
 RESULT 11  
 Q5XF8\_MOUSE PRELIMINARY; PRT; 235 AA.  
 ID Q5XF8\_MOUSE  
 AC Q5XF8;  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max 9.I., Wang J., Hsieh F.,  
 RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Ueda T.B., Toshitsugu S., Carrin P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Aramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.W.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC [2]  
 CC NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RA Director MGC Project;  
 RL Submitted (Oct-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC084683; AA84683.1; -; mRNA.

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DR SMR; Q5XFY8; 23-235.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGCL; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein.
KM HYPOTHETICAL PROTEIN.
SQ SEQUENCE 235 AA; 25835 MM; 8285BD277FDC667 CRC64;

Query Match 82.6%; Score 457; DB 2; Length 235;
Best Local Similarity 83.7%; Pred. No. 1.9e-37;
Matches 87; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 4 LTOSPAIMASPGKVTTCSSASSSVSYMWYQOKPGSSPRLTYDTSNLASGVPRFSG 63
Db 26 LTOSPALISGPGKVTTCSSASSSVYMWYQOKPGSSPSPWYATSKLASGVPRFSG 85

64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107
86 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGATGRLLELR 129

RESULT 12
Q8K1F0 MOUSE PRELIMINARY; PRT; 112 AA.
AC O8K1F0;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN 1;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
RN 2;
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Tennyck T., Avrameas S.;
RT "Two murine natural polypeptide autoantibodies are encoded by
RT nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR EMBL; AF516285; AAM64203.1; -; Genomic_DNA.
DR PIR; A33933; A33933.
DR PIR; PC4405; PC4405.
DR HSSP; P01837; IOR0.
DR SMK; Q8K1F0; 3-112.
DR Ensemble; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 11901 MM; F6644663201AA239 CRC64;

Query Match 82.5%; Score 456; DB 2; Length 112;
Best Local Similarity 84.6%; Pred. No. 9.8e-38;
Matches 88; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 4 LTOSPAIMASPGKVTTCSSASSSVSYMWYQOKPGSSPRLTYDTSNLASGVPRFSG 63
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Db 4 LTOSPAIMASPGKVTTCSSASSSVSYMWYQOKPGSTPKRWIYDTSKLASGVPRFSG 63
Qy 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107
Db 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107

RESULT 13
Q8VDD0 MOUSE PRELIMINARY; PRT; 134 AA.
ID Q8VDD0;
AC Q8VDD0;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Anti-MOG z12 variable light chain (Fragment).
OS Name=Gm1502; Synonyms=anti-MOG kappa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN 1;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Semb P.;
RL Submitted (Jan-2002) to the EMBL/GenBank/DBJ databases.
RN 2;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Chernajovsky Y.;
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
RN 3;
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2427335;
RA Caton A.v., Brownlee G.G., Staudt L.M., Gerhard W.;
RT "Structural and functional implications of a restricted antibody
RT response to a defined antigenic region on the influenza virus
RT haemagglutinin.";
RL EMBL J. 5:1577-1587(1986).
DR EMBL; A016331; CAC94866.1; -; mRNA.
DR PIR; G27887; G27887.
DR HSSP; P01834; 1MIM.
DR SMK; Q8VDD0; 23-134.
DR Ensemble; ENSMUSG0000062047; Mus musculus.
DR MGI; MGI:2686348; Gm1502.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 134
FT NON_TER 134
SQ SEQUENCE 134 AA; 14525 MM; CFDF8E2236E2D0CF CRC64;

Query Match 81.7%; Score 452; DB 2; Length 134;
Best Local Similarity 84.6%; Pred. No. 3e-37;
Matches 88; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 4 LTOSPAIMASPGKVTTCSSASSSVSYMWYQOKPGSSPRLTYDTSNLASGVPRFSG 63
Db 26 LTOSPALISGPGKVTTCSSASSSVYMWYQOKPGSTPKRWIYDTSKLASGVPRFSG 85

64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107
86 SSGSTSYSLTISRMEADATYYCHGRSSYPWTFGGSTKLELR 129

RESULT 14
Q81IC3 MOUSE PRELIMINARY; PRT; 131 AA.
ID Q81IC3;
AC Q81IC3;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
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DE Immunoglobulin gamma-3 kappa chain precursor (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=MRL-MpJ-1pr/1pr; TISSUE=Spleen;  
RX MEDLINE=93156722; PubMed=8429833; DOI=10.1016/0161-5890(93)90089-T;  
RA Takahashi S., Itoh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;  
RT "Cloning and cDNA sequence analysis of nephritic monoclonal  
RL antibodies derived from an MRL/lpr lupus mouse.";  
RM Mol. Immunol. 30:177-182(1993).  
DR EMBL; D14629; BAA03482.1; -; mRNA.  
DR HSSP; P01679; 2PRJ  
DR SMR; Q81IC3; 23-131.  
DR Ensemble; ENSMUSG0000058987; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KM Signal.  
FT CHAIN 23 >131 Potential.  
FT NON TER 131 Immunoglobulin gamma-3 kappa chain.  
SQ SEQUENCE 131 AA; 14083 MW; 5E8365695466E98 CRC64;  
Query Match 80.2%; Score 443.5; DB 2; Length 131;  
Best Local Similarity 84.0%; Pred. No. 2,1e-36;  
Matches 89; Conservative 8; Mismatches 6; Indels 3; Gaps 2;  
QY 4 LTQSPALMSASPGKVTTCASASSV--SYWYWOOKPGSSPRLTIYDTSNLASGVPRF 61  
DB 26 LTQSPALMSASPGKVTTCASASSVSSSYLHWYQKPGSSPKLMIYTSNLASGVPRF 85  
QY 62 SGGSGSGTYSYLTISRMEADATYYCQOWSNP-LTFGSGTLELR 106  
DB 86 SGGSGSGTYSYLTISRMEADATYYCQOWSNP-LTFGSGTLELR 131  
RESULT 15  
Q8K1F1 MOUSE PRT; 114 AA.  
AC 08K1F1\_002 (TREMblrel. 22, Created)  
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)  
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
DE Anti-VIPase light chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;  
RX Zhou Y.-X., Taguchi H., Plaque S., Karle S., Nishiyama Y., Paul S.;  
RT Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
RN (2)  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2499887;  
RA Baccala R., Quang T.V., Gilbert M., Tennyck T., Avrameas S.;  
RT "Two murine natural polyreactive autoantibodies are encoded by  
RL nonmutated germ-line genes.";  
RM Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).  
RN (3)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;  
RA Tildeman D.W., Jon N.T., Hill R.J., Marion T.N.,  
RT "Both IgM anti-DNA antibodies are the products of clonally  
RL selective B cell stimulation in (NZB x NZM)F1 mice.";  
RM J. Exp. Med. 176:761-779(1992).

DR EMBL; AF516284; AAM64202.1; -; genomic\_DNA.  
DR PIR; A33933; A33933.  
DR PIR; PH1058; PH1058.  
DR HSSP; P01837; 25C8.  
DR SMR; Q8K1F1; 2-114.  
DR Ensemble; ENSMUSG0000059896; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 1 1  
FT NON TER 114 114  
SQ SEQUENCE 114 AA; 12163 MW; 8BD9833DBF38EPD1 CRC64;  
Query Match 79.6%; Score 440; DB 2; Length 114;  
Best Local Similarity 80.7%; Pred. No. 4e-36;  
Matches 88; Conservative 6; Mismatches 13; Indels 2; Gaps 1;  
QY 1 DTELQSPALMSASPGKVTTCASASSV--SYWYWOOKPGSSPRLTIYDTSNLASGV 58  
DB 1 DIVLTQSPALMSASPGKVTTCASASSVSSSYLHWYQKSGASPKLMIYTSNLASGV 60  
QY 59 VRFSGSGSGTYSYLTISRMEADATYYCQOWSNP-LTFGSGTLELR 107  
DB 61 ARFSGSGSGTYSYLTISRMEADATYYCQOWSNP-LTFGSGTLELR 109  
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Job time : 159.344 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:31 / Search time 40.37 Seconds  
(without alignments)  
219.131 Million cell updates/sec

Title: US-10-632-706-87

Perfect score: 553  
Sequence: 1 DTELTQSPAIMSAPGKVT.....QWSSNPLRTGGSTKELKR 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/1/1aa/5.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/6.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/H.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PCUTS.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RE.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	506	91.5	244	1	US-08-553-497A-20 Sequence 20, Appl
2	505	91.3	242	1	US-08-553-497A-28 Sequence 28, Appl
3	502	90.8	128	1	US-07-946-421-26 Sequence 26, Appl
4	501	90.6	106	1	US-07-634-278-58 Sequence 58, Appl
5	501	90.6	106	1	US-08-477-728-58 Sequence 58, Appl
6	501	90.6	106	1	US-08-474-040-58 Sequence 58, Appl
7	501	90.6	106	1	US-08-487-200-58 Sequence 58, Appl
8	501	90.6	106	2	US-08-484-537-58 Sequence 58, Appl
9	501	90.6	128	1	US-07-634-278-31 Sequence 31, Appl
10	501	90.6	128	1	US-08-477-728-31 Sequence 31, Appl
11	501	90.6	128	1	US-08-474-040-31 Sequence 31, Appl
12	501	90.6	128	1	US-08-487-200-31 Sequence 31, Appl
13	501	90.6	128	2	US-08-484-537-31 Sequence 31, Appl
14	499	90.2	242	1	US-08-553-497A-26 Sequence 26, Appl
15	496	89.7	246	1	US-08-553-497A-24 Sequence 24, Appl
16	490.5	88.7	108	2	US-09-232-290-2 Sequence 2, Appl
17	489	88.4	108	2	US-09-196-522-243 Sequence 243, App
18	489	88.4	108	2	US-09-196-522-243 Sequence 243, App
19	488	88.2	244	1	US-08-553-497A-22 Sequence 22, Appl
20	485	87.7	108	2	US-09-726-219A-251 Sequence 251, App
21	485	87.7	108	2	US-09-196-522-251 Sequence 251, App
22	479	86.6	108	2	US-09-171-945-9 Sequence 9, Appl
23	479	86.6	108	2	US-09-910-059-9 Sequence 9, Appl
24	478	86.4	108	2	US-09-726-219A-253 Sequence 253, App
25	478	86.4	108	2	US-09-196-522-253 Sequence 253, App
26	477	86.3	106	2	US-09-198-689-8 Sequence 8, Appl
27	477	86.3	235	2	US-09-171-945-17 Sequence 17, Appl

#### ALIGNMENTS

28	477	86.3	235	2	US-09-910-059-17	Sequence 17, Appl
29	477	86.3	238	2	US-09-798-689-21	Sequence 21, Appl
30	475	85.9	107	1	US-08-211-202-3	Sequence 3, Appl
31	475	85.9	108	2	US-09-726-219A-241	Sequence 241, App
32	475	85.9	108	2	US-09-196-522-241	Sequence 2, App
33	475	85.9	128	2	US-08-619-491-2	Sequence 2, Appl
34	475	85.9	128	1	PCT-US95-07302-2	Sequence 57, Appl
35	475	85.9	246	1	US-08-469-486-57	Sequence 57, Appl
36	475	85.9	246	1	US-08-469-658-57	Sequence 8, Appl
37	475	85.9	255	2	US-09-553-498-8	Sequence 8, Appl
38	475	85.9	255	2	US-09-618-869-8	Sequence 16, Appl
39	475	85.9	270	1	US-08-652-507-2	Sequence 16, Appl
40	475	85.9	553	1	US-08-661-052-16	Sequence 16, Appl
41	475	85.9	553	2	US-09-188-082-16	Sequence 16, Appl
42	475	85.9	553	2	US-09-364-088-16	Sequence 16, Appl
43	475	85.9	553	2	US-09-102-716-16	Sequence 16, App
44	474	85.7	108	2	US-09-726-219A-240	Sequence 240, App
45	474	85.7	108	2	US-09-196-522-240	Sequence 240, App

RESULT 1  
US-08-553-497A-20  
Sequence 20, Application US/08553497A  
Patent No. 5844093  
GENERAL INFORMATION:  
APPLICANT: KETLEBOROUGH, C. A.  
APPLICANT: BENDIG, MARY M.  
APPLICANT: ANSELL, KEITH H.  
APPLICANT: GUSLOW, DETLEF  
APPLICANT: ADAM, JADME  
APPLICANT: MITJANS, FRANCESCA  
APPLICANT: ROSELL, ELISABET  
APPLICANT: BLASCO, FRANCESC  
APPLICANT: PIUTATS, JADME  
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR  
NUMBER OF SEQUENCES: 30  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLER, WHITE, ZELANO & BRANTIGAN, P. C.  
STREET: 2200 CLARENDON BLVD. SUITE 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,497A  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/00978  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94104160.0  
FILING DATE: 17-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94118970.6  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1726  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-553-497A-20

Query Match 91.5%; Score 506; DB 1; Length 244;  
Best Local Similarity 92.6%; Pred. No. 6,6e-42;  
Matches 100; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 DTETLQSPAIMSAPGKRYTTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPR 60  
137 DIELTQSPAIMSAPGKRYTTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPR 136

QY 61 FSGSGSGTSTSLTISRMEADATYTCQOMSSNP--LTFSGTKLEIK 106  
197 FSGSGSGTSTSLTISRMEADATYTCQOMSSNPMTTFGQTKLEIK 244

RESULT 2  
US-08-553-497A-28

Sequence 28, Application US/08553497A  
Patent No. 5844093

GENERAL INFORMATION:

APPLICANT: KETLEBOROUGH, C. A.

APPLICANT: BENDIG, MARY M.

APPLICANT: ANSELL, KATH H.

APPLICANT: GUSSOW, DETLEF

APPLICANT: ADAM, JAUWE

APPLICANT: MITTANS, FRANCES

APPLICANT: ROSEIL, ELISABET

APPLICANT: BLASCO, FRANCESC

APPLICANT: PIVULAT, JAUWE

TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR

TITLE OF INVENTION: ANTIBODIES

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.

STREET: 2200 CLARENDON BLVD. SUITE 1400

CITY: ARLINGTON

STATE: VA

COUNTRY: US

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,497A

FILING DATE: 17-NOV-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP95/00978

FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94104160.0

FILING DATE: 17-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94118970.6

FILING DATE: 02-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAMES: HAMLET-KING, DIANA

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1726

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 242 amino acids

TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-553-497A-28

Query Match 91.3%; Score 505; DB 1; Length 242;  
Best Local Similarity 92.5%; Pred. No. 8,2e-42;  
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DTETLQSPAIMSAPGKRYTTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPR 60  
137 DIELTQSPAIMSAPGKRYTTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPR 136

QY 61 FSGSGSGTSTSLTISRMEADATYTCQOMSSNP-LTFSGTKLEIK 106  
197 FSGSGSGTSTSLTISRMEADATYTCQOMSSNPMTTFGQTKLEIK 242

Db

RESULT 3  
US-07-946-421-26

Sequence 26, Application US/07946421  
Patent No. 555864

GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.

APPLICANT: Ketleborough, Catherine A.

APPLICANT: Saldanha, Jose

TITLE OF INVENTION: Humanized and Chimeric Monoclonal

TITLE OF INVENTION: Antibodies

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Miller, White, Zelano & Branigan, P.C.

STREET: 2200 Clarendon Boulevard, Suite 1400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/946,421

FILING DATE: 06-NOV-1992

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP92/00480

FILING DATE: 04-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 911933892

FILING DATE: 06-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAMES: Hamlet-King, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: Merck 1430

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 128 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-07-946-421-26

Query Match 90.8%; Score 502; DB 1; Length 128;  
Best Local Similarity 94.2%; Pred. No. 7,5e-42;  
Matches 97; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPAIMSAPGKRYTTTCSSASSSVSYMYWYQOKGSSPRLIYDTSNLSAGVPRFSG 63  
26 LTQSPAIMSAPGKRYTTTCSSASSSVSYMYWYQOKGSSPRLIYDTSNLSAGVPRFSG 85

Db



QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106  
Db 86 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 128

## RESULT 4

US-07-634-278-58  
Sequence 58, Application US/07634278  
Patent No. 5530101  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COBLINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend Kourile and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-07-634-278-58

Query Match 90.6%; Score 501; DB 1; Length 106;  
Best Local Similarity 93.2%; Pred. No. 7,6e-42;  
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPAINASPGKVTTCASASSVSYWYVYQQRGSSPRLIYDTSNLTASGVPRFSG 63  
Db 4 LTQSPAINASPGKVTTCSSSSVSFWYVYQQRGSSPRLIYDTSNLTASGVPRFSG 63

QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106  
Db 64 SSGSTSYSLTISRMEADATYYCOQWSTYPLTFGAGTKLEIK 106

RESULT 5

US-08-477-728-58  
Sequence 58, Application US/08477728  
Patent No. 5585089  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,728  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-08-477-728-58

Query Match 90.6%; Score 501; DB 1; Length 106;  
Best Local Similarity 93.2%; Pred. No. 7,6e-42;  
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPAINASPGKVTTCASASSVSYWYVYQQRGSSPRLIYDTSNLTASGVPRFSG 63  
Db 4 LTQSPAINASPGKVTTCSSSSVSFWYVYQQRGSSPRLIYDTSNLTASGVPRFSG 63

QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106  
Db 64 SSGSTSYSLTISRMEADATYYCOQWSTYPLTFGAGTKLEIK 106

## RESULT 6

US-08-474-040-58  
Sequence 58, Application US/08474040  
Patent No. 5693761  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.  
 APPLICANT: LANDOLFI, Nicholas F.  
 APPLICANT: COELINGH, Kathleen L.  
 APPLICANT: SELICK, Harold B.  
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 NUMBER OF SEQUENCES: 113  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend Kourie and Crew  
 STREET: 379 Lytton Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: US  
 ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/474,040  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/634,278  
 FILING DATE: 19-DEC-1990  
 APPLICATION NUMBER: US-07/590,274  
 FILING DATE: 28-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/310,252  
 FILING DATE: 13-FEB-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/290,975  
 FILING DATE: 28-DEC-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, William M  
 REGISTRATION NUMBER: 30,223  
 REFERENCE/DOCKET NUMBER: 11823-002600  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 326-2400  
 TELEFAX: (415) 326-2422  
 INFORMATION FOR SEQ ID NO: 58:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 106 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IS-08-474-040-58

```

Query Match      90.6%; Score 501; DB 1; Length 106;
Best Local Similarity 93.2%; Fred. No. 7.6e-42;
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      4      LTGSPALMSAGPGRKVTTCCTCASSSVSYMYWYQOKRPGSSPLLITDTSNLASGVVPRFSG 63
          |||
Db      4      LTGSPALMSAPGRKRVITTCGSSSVSYMYWYQQRPGSSPLLITDTSNLASGVVPRFSG 63

Qy      64      SGGSTSYSLTISRMEADPATYYCOQMSNPITFGSGYKLEIK 106
          |||
Db      64      SGGSTSYSLTISRMEADPATYYCOQMSNPITFGAGYKLEIK 106

RESULT 7
US-08-487-200-58
; Sequence 58, Application US/08487200
; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.

```

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 NUMBER OF SEQUENCES: 113  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew  
 STREET: 379 Lytton Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: US  
 ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,200  
 FILING DATE: 7-JUN-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/634,278  
 FILING DATE: 19-DEC-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/590,274  
 FILING DATE: 28-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/310,252  
 FILING DATE: 13-FEB-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/290,975  
 FILING DATE: 28-DEC-1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, William M  
 REGISTRATION NUMBER: 30,223  
 REFERENCE/DOCKET NUMBER: 11823-002610  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 326-2400  
 TELEFAX: (415) 326-2422  
 INFORMATION FOR SEQ ID NO: 58:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 106 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-487-200-58

```

Query Match          90.64; Score 501; DB 1; Length 106;
Best Local Similarity 93.24; Pred. No. 7, 66-42;
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Cy 4 LTOSPATMSAPGKXKTTTSCASSSSVYMYWYQKPGSSPRLLTYDPSNLASGVVAFSSG 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 LTOSPATMSAPGKXKVTTCSSGSSSVFPMYVQQRPPSSPRLLTYDPSNLASGVVAFSSG 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Cy 64 SGSGTYSLTISRMEADATYYTCQWSSNPLTFGSGTKLELK 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 SGSGTYSLTISRMEADATYYTCQWSTYPLTFGAGATKLELK 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-08-484-537-58
; Sequence 58, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold B.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSER: Townsend and Townsend Kourile and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,537  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US/07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-537-58

Query Match 90.6%; Score 501; DB 2; Length 106;  
Best Local Similarity 93.2%; Pred. No. 7.6e-42;  
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASGPERVTTTCASASSVSVMYVYQOKPGSSPRLIYDTSNLASGVVPRFSG 63  
DB 4 LTGSPAIMSASGPERVTTTCASASSVSVMYVYQOKPGSSPRLIYDTSNLASGVVPRFSG 63  
QY 64 SSGGTSYSLTISRMEADATYTCOOMSSNPLTFGSGTGLBLK 106  
DB 64 SSGGTSYSLTISRMEADATYTCOOMSSNPLTFGSGTGLBLK 106

RESULT 9  
US-07-634-278-31  
Sequence 31, Application US/07634278  
Patent No. 5530101  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas P.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend Kourile and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California

COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-634-278-31

Query Match 90.6%; Score 501; DB 1; Length 128;  
Best Local Similarity 93.2%; Pred. No. 9.5e-42;  
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASGPERVTTTCASASSVSVMYVYQOKPGSSPRLIYDTSNLASGVVPRFSG 63  
DB 26 LTGSPAIMSASGPERVTTTCASASSVSVMYVYQOKPGSSPRLIYDTSNLASGVVPRFSG 85  
QY 64 SSGGTSYSLTISRMEADATYTCOOMSSNPLTFGSGTGLBLK 106  
DB 86 SSGGTSYSLTISRMEADATYTCOOMSSNPLTFGSGTGLBLK 128

RESULT 10  
US-08-477-728-31  
Sequence 31, Application US/08477728  
Patent No. 5585089  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th floor  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,728  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-728-31

Query Match 90.6%; Score 501, DB 1; Length 128;  
Best Local Similarity 93.2%; Pred. No. 9.5e-42;  
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTGSPAIMSAPBPKYTTTSSASSSVSYMYQKPGSSPRLIYDTSNLSAGVPVRFSG 63  
DB 26 LTGSPAIMSAPBPKYTTTSSASSSVSYMYQKPGSSPRLIYDTSNLSAGVPVRFSG 85

QY 64 SSGSTSYSLTISRMEADATYTCQWSSNPLTFGSGTKLEK 106  
DB 86 SSGSTSYSLTISRMEADATYTCQWSTYPLTFGAGTKLEK 128

RESULT 11  
US-08-474-040-31  
Sequence 31, Application US/08474040  
Patent No. 5693761  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: CORLINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend Kourile and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,040  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-040-31

Query Match 90.6%; Score 501, DB 1; Length 128;  
Best Local Similarity 93.2%; Pred. No. 9.5e-42;  
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTGSPAIMSAPBPKYTTTSSASSSVSYMYQKPGSSPRLIYDTSNLSAGVPVRFSG 63  
DB 26 LTGSPAIMSAPBPKYTTTSSASSSVSYMYQKPGSSPRLIYDTSNLSAGVPVRFSG 85

QY 64 SSGSTSYSLTISRMEADATYTCQWSSNPLTFGSGTKLEK 106  
DB 86 SSGSTSYSLTISRMEADATYTCQWSTYPLTFGAGTKLEK 128

RESULT 12  
US-08-487-200-31  
Sequence 31, Application US/08487200  
Patent No. 5693762  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: CORLINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,200  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-487-200-31

Query Match 90.6%; Score 501; DB 1; Length 128;  
Best Local Similarity 93.2%; Pred. No. 9.5e-42;  
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LTGSPAIMSASPGKVTTCGASSSVSMTYQKPGSSPRLIYDTSNLASGVPRFSG 63  
Db 26 LTGSPAIMSASPGKVTTCGASSSVSMTYQKPGSSPRLIYDTSNLASGVPRFSG 85

Qy 64 SGSGTYSILTISRMEADPAATYYCOQWSSNPLTFGSGTKLELK 106  
Db 86 SGSGTYSILTISRMEADPAATYYCOQWSSNPLTFGAGTKLELK 128

RESULT 13  
US-08-484-537-31  
Sequence 31, Application US/08484537  
Patent No. 6180370  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELING, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,537  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-537-31

Query Match 90.6%; Score 501; DB 2; Length 128;  
Best Local Similarity 93.2%; Pred. No. 9.5e-42;  
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LTGSPAIMSASPGKVTTCGASSSVSMTYQKPGSSPRLIYDTSNLASGVPRFSG 63  
Db 26 LTGSPAIMSASPGKVTTCGASSSVSMTYQKPGSSPRLIYDTSNLASGVPRFSG 85

Qy 64 SGSGTYSILTISRMEADPAATYYCOQWSSNPLTFGSGTKLELK 106  
Db 86 SGSGTYSILTISRMEADPAATYYCOQWSSNPLTFGAGTKLELK 128

RESULT 14  
US-08-553-497A-26  
Sequence 26, Application US/08553497A  
Patent No. 5844093  
GENERAL INFORMATION:  
APPLICANT: KETTLERBOUGH, C. A.  
APPLICANT: BENDIG, MARY M.  
APPLICANT: ANSELL, KEITH H.  
APPLICANT: GUSLOW, DETLEF  
APPLICANT: ADAM, JAUDE  
APPLICANT: MITCHELL, FRANCESCA  
APPLICANT: ROSELL, ELISABETH  
APPLICANT: BLASCO, FRANCESC  
APPLICANT: PIULATS, JAUME  
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANNIGAN, P. C.  
STREET: 2200 CLARENDON BLVD. SUITE 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,497A  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/00978  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94104160.0  
FILING DATE: 17-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94118970.6  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1726



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:50:51 / Search time 132.476 Seconds  
(without alignments)  
337.478 Million cell updates/sec

Title: US-10-632-706-87

Perfect score: 553

Sequence: 1 DTELQSPAINASPGKRVT.....QQWSSNPITFGSGTLEIKR 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	107	4	US-10-632-706-87
2	524	94.8	107	3	US-09-144-886-78
3	520	94.0	107	3	US-09-144-886-90
4	518	93.7	109	4	US-10-632-706-88
5	516	93.3	107	4	US-10-632-706-75
6	516	93.3	129	4	US-10-344-779-2
7	516	93.3	129	4	US-10-738-809-2
8	515	92.1	107	5	US-10-895-135-46
9	514	92.9	107	3	US-09-144-886-75
10	506	91.5	107	4	US-10-632-706-72
11	502	90.8	106	4	US-10-468-370-643
12	502	90.8	106	4	US-10-468-528-2
13	501	90.6	106	4	US-10-389-155-17
14	501	90.6	106	4	US-10-389-417-17
15	501	90.6	106	4	US-10-452-357-58
16	498.5	90.5	108	5	US-10-895-135-47
17	498.5	90.5	108	5	US-10-895-135-44
18	495	89.1	128	4	US-10-389-417-44
19	485	89.5	108	4	US-10-803-622-243
20	489	88.4	108	4	US-10-803-653-243
21	488	88.2	110	4	US-10-112-788-2
22	488	88.2	110	4	US-10-435-614-2
23	488	88.2	110	4	US-10-435-614-10
24	488	88.2	110	4	US-10-435-614-19
25	488	88.2	281	4	US-10-112-788-9
26	488	88.2	281	4	US-10-112-788-9
27	488	88.2	281	4	US-10-435-614-15

28	487	88.1	109	3	US-09-144-886-91	Sequence 91, Appl
29	486	87.9	110	4	US-10-435-614-12	Sequence 12, Appl
30	486	87.9	128	3	US-09-772-103-6	Sequence 6, Appl
31	486	87.9	260	4	US-10-435-614-20	Sequence 20, Appl
32	485	87.7	107	3	US-09-144-886-82	Sequence 82, Appl
33	485	87.7	107	3	US-09-144-886-83	Sequence 83, Appl
34	485	87.7	109	4	US-10-803-622-251	Sequence 251, Appl
35	485	87.7	108	4	US-10-803-653-251	Sequence 251, Appl
36	484	87.5	246	5	US-10-861-617-15	Sequence 15, Appl
37	484	87.5	246	5	US-10-861-617-17	Sequence 17, Appl
38	482	87.2	108	3	US-09-976-787-8	Sequence 8, Appl
39	482	87.2	108	3	US-09-865-198-8	Sequence 8, Appl
40	482	87.2	108	5	US-10-482-630-8	Sequence 8, Appl
41	482	87.2	108	5	US-10-203-398-8	Sequence 8, Appl
42	482	87.2	108	5	US-10-778-910-8	Sequence 8, Appl
43	482	87.2	108	5	US-10-809-387-8	Sequence 8, Appl
44	482	87.2	240	3	US-09-976-787-28	Sequence 28, Appl
45	482	87.2	240	3	US-09-865-198-27	Sequence 27, Appl

#### ALIGNMENTS

```
RESULT 1
US-10-632-706-87
; Sequence 87, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-87
Query Match 100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.9e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DTELQSPAINASPGKRVTTTCSASSSVSYHYVYQKRGSSPRLIYDTSLAGVPVR 60
DB 1 DTELQSPAINASPGKRVTTTCSASSSVSYHYVYQKRGSSPRLIYDTSLAGVPVR 60
QY 61 FSGSGSTYSYLTISRMEADATYYCOQWSSNPITFGSGTLEIKR 107
DB 61 FSGSGSTYSYLTISRMEADATYYCOQWSSNPITFGSGTLEIKR 107
RESULT 2
US-09-144-886-78
; Sequence 78, Application US/09144886
; Patent No. US2002015514A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
```





APPLICANT: TRUNEH, ALEMSEGED  
APPLICANT: WATTAM, TREVOR A.  
TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS  
FILE REFERENCE: GP50033  
CURRENT APPLICATION NUMBER: US/10/344,779  
PRIOR FILING DATE: 2003-02-17  
PRIOR APPLICATION NUMBER: PCT/US01/26161  
PRIOR FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: US 60/226,524  
PRIOR FILING DATE: 2000-08-21  
PRIOR APPLICATION NUMBER: US 60/230,639  
PRIOR FILING DATE: 2000-09-07  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 129  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-344-779-2

Query Match 93.3%; Score 516; DB 4; Length 129;  
Best Local Similarity 96.2%; Pred. No. 1.7e-38;  
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LTQSPAINASPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPRFSG 63  
DB 4 LTQSPAINASPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPRFSG 63

QY 64 SGGSTSYSLTISRMEADPAATYCCQMSNPITFGSGTKLEIKR 107  
DB 64 SGGSTSYSLTISRMEADPAATYCCQMSNPITFGSGTKLEIKR 107

RESULT 7  
US-10-738-809-2

Sequence 2, Application US/10738809  
Publication No. US2004017117A1  
GENERAL INFORMATION:  
APPLICANT: SWEET, RAYMOND W.  
APPLICANT: TORNETTA, MARK A.  
APPLICANT: TRUNEH, ALEMSEGED  
APPLICANT: WATTAM, TREVOR A.  
TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES  
TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS  
FILE REFERENCE: GP50033  
CURRENT APPLICATION NUMBER: US/10/738,809  
PRIOR FILING DATE: 2003-12-17  
PRIOR APPLICATION NUMBER: US/10/344,779  
PRIOR FILING DATE: 2003-02-19  
PRIOR APPLICATION NUMBER: PCT/US01/26161  
PRIOR FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: US 60/226,524  
PRIOR FILING DATE: 2000-08-21  
PRIOR APPLICATION NUMBER: US 60/230,639  
PRIOR FILING DATE: 2000-09-07  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 129  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-738-809-2

Query Match 93.3%; Score 516; DB 4; Length 129;  
Best Local Similarity 96.2%; Pred. No. 1.7e-38;  
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LTQSPAINASPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPRFSG 63  
DB 4 LTQSPAINASPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPRFSG 63

QY 64 SGGSTSYSLTISRMEADPAATYCCQMSNPITFGSGTKLEIKR 107

DB 64 SGGSTSYSLTISRMEADPAATYCCQMSNPITFGSGTKLEIKR 107

RESULT 8  
US-10-895-135-46  
Sequence 46, Application US/10895135  
Publication No. US20050123549A1  
GENERAL INFORMATION:  
APPLICANT: Immunogen, Inc.  
APPLICANT: PAYNE, Gallian  
APPLICANT: CHUN, Philip  
APPLICANT: TAYARS, Daniel  
TITLE OF INVENTION: A C6 ANTIGEN-SPECIFIC CYTOTOXIC CONJUGATE AND METHODS OF USING  
TITLE OF INVENTION: THE SAME  
FILE REFERENCE: A8621  
CURRENT APPLICATION NUMBER: US/10/895,135  
PRIOR FILING DATE: 2004-07-21  
PRIOR APPLICATION NUMBER: 60/488,447  
PRIOR FILING DATE: 2003-07-21  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 46  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-895-135-46

Query Match 93.1%; Score 515; DB 5; Length 107;  
Best Local Similarity 91.6%; Pred. No. 1.7e-38;  
Matches 98; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTELQSPAINASPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPR 60  
DB 1 DTELQSPAINASPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPR 60

QY 61 FSGSGSTSYSLTISRMEADPAATYCCQMSNPITFGSGTKLEIKR 107  
DB 61 FSGSGSTSYSLTISRMEADPAATYCCQMSNPITFGSGTKLEIKR 107

RESULT 9  
US-09-144-886-75  
Sequence 75, Application US/09144886  
Patent No. US20020155114A1  
GENERAL INFORMATION:  
APPLICANT: Marks, James D  
APPLICANT: Amersdorfer, Peter  
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
TITLE OF INVENTION: Botulinum Neurotoxins  
FILE REFERENCE: 2500.117USO  
CURRENT APPLICATION NUMBER: US/09/144,886  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 75  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
OTHER INFORMATION: C15 region VL epitope 1  
US-09-144-886-75

Query Match 92.9%; Score 514; DB 3; Length 107;  
Best Local Similarity 92.5%; Pred. No. 2.1e-38;  
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DTELQSPAINASPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPR 60  
DB 1 DTELQSPAINASPGKVTTCSSASSSVSHMYWYQKPGSSPRLIYDTSNLASGVPR 60

QY 61 FSGSGSTSYSLTISRMEADPAATYCCQMSNPITFGSGTKLEIKR 107

Db 61 FSGSGSTSYSLTISRMEADDAATYYCQWSSYPTFGSGTKLEIKR 107

RESULT 10  
US-10-632-706-72  
Sequence 72, Application US/10632706  
Publication No. US20040175385A1  
GENERAL INFORMATION:  
APPLICANT: MARKS, JAMES D.  
APPLICANT: AMERSDORFER, PETER  
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
FILE REFERENCE: 407T-895120US  
CURRENT APPLICATION NUMBER: US/10/632,706  
CURRENT FILING DATE: 2003-08-01  
PRIOR APPLICATION NUMBER: US 60/400,721  
PRIOR FILING DATE: 2002-08-01  
PRIOR APPLICATION NUMBER: US 09/144,806  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 278  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 72  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: single chain antibody  
US-10-632-706-72

Query Match 91.5%; Score 506; DB 4; Length 107;  
Best Local Similarity 91.6%; Pred. No. 1.1e-37;  
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
QY 1 DTSLTSPAIMSASPEKXTTTCASASSSVYMTWYQKPGSSPRLTIYDTSNLSAGVPVRFSG 60  
DB 1 DILTOSPAIMASPGKXVMTCSASSSVHMYWYQKPGSSPRLTIYDTSNLSAGVPVRFSG 60  
QY 61 FSGSGSTSYSLTISRMEADDAATYYCQWSSNPFTFGSGTKLEIKR 107  
DB 61 FSGSGSTSYSLTISRMEADDAATYYCQWSSNPFTFGSGTKLEIKR 107

RESULT 11  
US-10-468-370-643  
Sequence 643, Application US/10468370  
Publication No. US20040082039A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
APPLICANT: Carr, Francis J.  
APPLICANT: Jones, Tim  
APPLICANT: Carter, Graham  
APPLICANT: Hamilton, Anita  
APPLICANT: Williams, Stephen  
APPLICANT: Hanlon, Marian  
APPLICANT: Watkins, John  
APPLICANT: Baker, Matthew  
APPLICANT: Kay, Jeffrey  
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED  
TITLE OF INVENTION: IMMUNOGENICITY  
FILE REFERENCE: MER-118  
CURRENT APPLICATION NUMBER: US/10/468,370  
CURRENT FILING DATE: 2003-08-19  
PRIOR APPLICATION NUMBER: BP 01103955.9  
PRIOR FILING DATE: 2001-02-19  
PRIOR APPLICATION NUMBER: BP 01108291.4  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: PCT/EP02/01690  
PRIOR FILING DATE: 2002-02-18  
NUMBER OF SEQ ID NOS: 689  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 643  
LENGTH: 106

TYPE: PRT  
ORGANISM: Mus Musculus  
US-10-468-370-643

Query Match 90.8%; Score 502; DB 4; Length 106;  
Best Local Similarity 94.2%; Pred. No. 2.5e-37;  
Matches 97; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTOSPAIMASPEKXTTTCASASSSVYMTWYQKPGSSPRLTIYDTSNLSAGVPVRFSG 63  
DB 4 LTOSPAIMASPEKXTTTCASASSSVYMTWYQKPGSSPRLTIYDTSNLSAGVPVRFSG 63  
QY 64 SSGSTSYSLTISRMEADDAATYYCQWSSNPFTFGSGTKLEIKR 106  
DB 64 SSGSTSYSLTISRMEADDAATYYCQWSSNPFTFGSGTKLEIKR 106

RESULT 12  
US-10-468-528-2  
Sequence 2, Application US/10468528  
Publication No. US20040096442A1  
GENERAL INFORMATION:  
APPLICANT: Carr, Francis J.  
APPLICANT: Carter, Graham  
APPLICANT: Jones, Tim  
APPLICANT: Hamilton, Anita  
APPLICANT: Williams, Stephen  
TITLE OF INVENTION: MODIFIED ANTI-BCFR ANTIBODIES WITH  
TITLE OF INVENTION: REDUCED IMMUNOGENICITY  
FILE REFERENCE: MER-116  
CURRENT APPLICATION NUMBER: US/10/468,528  
CURRENT FILING DATE: 2003-08-19  
PRIOR APPLICATION NUMBER: BP 01103954.2  
PRIOR FILING DATE: 2001-02-19  
PRIOR APPLICATION NUMBER: PCT/EP02/01687  
PRIOR FILING DATE: 2002-02-19  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antibody fragment  
US-10-468-528-2

Query Match 90.8%; Score 502; DB 4; Length 106;  
Best Local Similarity 94.2%; Pred. No. 2.5e-37;  
Matches 97; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTOSPAIMASPEKXTTTCASASSSVYMTWYQKPGSSPRLTIYDTSNLSAGVPVRFSG 63  
DB 4 LTOSPAIMASPEKXTTTCASASSSVYMTWYQKPGSSPRLTIYDTSNLSAGVPVRFSG 63  
QY 64 SSGSTSYSLTISRMEADDAATYYCQWSSNPFTFGSGTKLEIKR 106  
DB 64 SSGSTSYSLTISRMEADDAATYYCQWSSNPFTFGSGTKLEIKR 106

RESULT 13  
US-10-389-155-17  
Sequence 17, Application US/10389155  
Publication No. US20030229208A1  
GENERAL INFORMATION:  
APPLICANT: Queen, Cary L.  
APPLICANT: Co, Man Sung  
APPLICANT: Schneider, William P.  
APPLICANT: Landolfi, Nicholas F.  
APPLICANT: Coalingh, Kathleen L.  
APPLICANT: Selick, Harold E.  
TITLE OF INVENTION: Improved Humanized Immunoglobulins  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/389,155  
FILING DATE: 13-Mar-2003

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/325,000  
FILING DATE: 01-JUN-1999  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 08/484,537  
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-002650US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-10-389-155-17

Query Match 90.6%; Score 501; DB 4; Length 106;  
Best Local Similarity 93.2%; Pred. No. 3,1e-37;  
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPAINASPGKVTTCSSASSSVSYMYTQOKRGSSPRLIYDTSNLAGVPRFSG 63  
DB 4 LTQSPAINASPGKVTTCSSASSSVSYMYTQOKRGSSPRLIYDTSNLAGVPRFSG 63  
QY 64 SSGSGTSLTISRMEAEADATYYCOQWSSNPITFGSGTKLEIK 106  
DB 64 SSGSGTSLTISRMEAEADATYYCOQWSTYPLTFAGTKLEIK 106

RESULT 14  
US-10-389-417-17  
Sequence 17, Application US/10389417  
Publication No. US2004009014A1  
GENERAL INFORMATION:  
APPLICANT: Queen, Cary L.  
Co. Man Sung  
Schneider, William P.  
Landolfi, Nicholas F.  
Coeligh, Kathleen L.  
Selick, Harold B.

TITLE OF INVENTION: Improved Humanized Immunoglobulins  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/389,417  
FILING DATE: 13-Mar-2003  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/325,000  
FILING DATE: 01-JUN-1999  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 08/484,537  
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-002650US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-10-389-417-17

Query Match 90.6%; Score 501; DB 4; Length 106;  
Best Local Similarity 93.2%; Pred. No. 3,1e-37;  
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPAINASPGKVTTCSSASSSVSYMYTQOKRGSSPRLIYDTSNLAGVPRFSG 63  
DB 4 LTQSPAINASPGKVTTCSSASSSVSYMYTQOKRGSSPRLIYDTSNLAGVPRFSG 63  
QY 64 SSGSGTSLTISRMEAEADATYYCOQWSSNPITFGSGTKLEIK 106  
DB 64 SSGSGTSLTISRMEAEADATYYCOQWSTYPLTFAGTKLEIK 106

RESULT 15  
US-10-452-357-58  
Sequence 58, Application US/10452357  
Publication No. US2004005841A1  
GENERAL INFORMATION:  
APPLICANT: Queen, Cary  
Co. Man Sung  
Schneider, William  
Landolfi, Nicholas  
Coeligh, Kathleen  
Selick, Harold

TITLE OF INVENTION: Improved Humanized Immunoglobulins  
FILE REFERENCE: 05882,0078,CNUS01  
CURRENT APPLICATION NUMBER: US/10/452,357  
CURRENT FILING DATE: 2003-05-30  
PRIOR APPLICATION NUMBER: 09/718,993  
PRIOR FILING DATE: 2000-11-22

! PRIOR APPLICATION NUMBER: 09/487,200  
! PRIOR FILING DATE: 1995-06-07  
! PRIOR APPLICATION NUMBER: 07/634,278  
! PRIOR FILING DATE: 1990-12-19  
! PRIOR APPLICATION NUMBER: 07/590,275  
! PRIOR FILING DATE: 1990-09-28  
! PRIOR APPLICATION NUMBER: 07/310,252  
! PRIOR FILING DATE: 1989-02-13  
! PRIOR APPLICATION NUMBER: 07/290,975  
! PRIOR FILING DATE: 1988-12-28  
! NUMBER OF SEQ ID NOS: 113  
! SOFTWARE: PatentIn version 3.2  
! SEQ ID NO 58  
! LENGTH: 106  
! TYPE: PRT  
! ORGANISM: Artificial  
! FEATURE:  
! OTHER INFORMATION: murine mlk-1 beta light chain antibody  
US-10-452-357-58

Query Match 90.6%; Score 501; DB 4; Length 106;  
Best Local Similarity 93.2%; Pred. No. 3.1e-37;  
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLSAGVPRFSG 63  
DB 4 LTQSPAIMSASPGKVTMTCSGSSSVSFMYWYQKPGSSPRLIYDTSNLSAGVPRFSG 63  
  
QY 64 SGSGTYSYLTISRMEADATYYCQWNSNPITFGSGTKLELK 106  
DB 64 SGSGTYSYLTISRMEADATYYCQWNSNPITFGAGTKLELK 106

Search completed: November 21, 2005, 12:33:34  
Job time : 133.476 secs

GenCore version 5.1.6  
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OM protein - protein search, using BW model

Run on: November 21, 2005, 12:04:27 ; Search time 1.95971 Seconds  
(without alignments)  
61.686 Million cell updates/sec

Title: US-10-632-706-87  
Perfect score: 553  
Sequence: 1 DTELQSPALMSASGPKVKT.....QOWSSNPLTFSGTLEIKR 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New+  
1: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/ECT\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	447	80.8	248 1	US-10-512-184-36 Sequence 36, Appl
2	447	80.8	615 1	US-10-512-184-50 Sequence 50, Appl
3	435	78.7	106 7	US-11-174-186-1 Sequence 1, Appl
4	427	77.2	106 7	US-11-174-186-1 Sequence 8, Appl
5	426	77.0	213 7	US-11-172-320-4 Sequence 4, Appl
6	424	76.7	213 7	US-11-174-186-42 Sequence 42, Appl
7	419	75.8	106 7	US-11-174-186-9 Sequence 9, Appl
8	416	75.2	213 7	US-11-172-320-8 Sequence 8, Appl
9	409	74.0	106 7	US-11-174-186-7 Sequence 7, Appl
10	409	74.0	106 7	US-11-174-186-16 Sequence 16, Appl
11	407	73.6	106 7	US-11-174-186-15 Sequence 15, Appl
12	394	71.2	106 7	US-11-174-186-10 Sequence 10, Appl
13	394	71.2	106 7	US-11-174-186-14 Sequence 14, Appl
14	392	70.9	106 7	US-11-174-186-12 Sequence 12, Appl
15	392	70.9	106 7	US-11-174-186-13 Sequence 13, Appl
16	388	70.2	106 7	US-11-174-186-11 Sequence 11, Appl
17	377.5	68.3	128 1	US-10-721-763-31 Sequence 31, Appl
18	375	67.8	106 7	US-11-174-186-5 Sequence 5, Appl
19	370.5	67.0	110 1	US-10-648-816-5 Sequence 5, Appl
20	369.5	66.8	110 1	US-10-721-763-19 Sequence 19, Appl
21	368.5	66.6	129 1	US-10-648-816-1 Sequence 1, Appl
22	366.5	66.3	543 1	US-10-495-664-3 Sequence 3, Appl
23	365.5	66.1	131 1	US-10-721-763-27 Sequence 27, Appl
24	363.5	65.7	129 1	US-10-721-763-23 Sequence 23, Appl
25	360.5	65.2	110 1	US-10-648-816-2 Sequence 2, Appl

26	360.5	65.2	110 1	US-10-648-816-3 Sequence 3, Appl
27	360.5	65.2	110 1	US-10-648-816-4 Sequence 4, Appl
28	360.5	65.2	110 1	US-10-648-816-6 Sequence 6, Appl
29	360.5	65.2	110 1	US-10-648-816-7 Sequence 7, Appl
30	360.5	65.2	110 1	US-10-648-816-8 Sequence 8, Appl
31	348.5	63.2	111 7	US-11-077-978-1 Sequence 1, Appl
32	342.5	61.9	259 1	US-10-512-184-31 Sequence 31, Appl
33	342.5	61.9	329 1	US-10-512-184-58 Sequence 29, Appl
34	340.5	61.6	263 1	US-10-512-184-69 Sequence 47, Appl
35	337.5	61.0	126 1	US-10-839-799-47 Sequence 65, Appl
36	337.5	61.0	126 1	US-10-839-799-65 Sequence 85, Appl
37	337.5	61.0	236 7	US-11-144-248-48 Sequence 48, Appl
38	336.5	60.8	126 1	US-10-839-799-85 Sequence 35, Appl
39	335.5	60.7	127 1	US-10-721-763-35 Sequence 3, Appl
40	334	60.4	106 7	US-11-174-186-3 Sequence 43, Appl
41	333.5	60.3	126 1	US-10-839-799-43 Sequence 53, Appl
42	333.5	60.3	126 7	US-10-839-799-53 Sequence 52, Appl
43	333.5	60.3	259 1	US-11-144-248-52 Sequence 33, Appl
44	333.5	60.3	329 1	US-10-512-184-33 Sequence 70, Appl
45	333.5	60.3	329 1	US-10-512-184-70 Sequence 3, Appl

## ALIGNMENTS

```

RESULT 1
US-10-512-184-36
; Sequence 36, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschafft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: seqv SS2 with
; OTHER INFORMATION: specificity against sclerotinia sclerotiorum;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-36

Query Match      80.8% Score 447; DB 1; Length 248;
Best Local Similarity 81.3% Pred. No. 8.9e-23;
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 DTELQSPALMSASGPKVKTCSASSSVYMYWYQOKGSSPRLIYDTSNLAGVPR 60
   |||||
DB 141 DTVLQSPVINSASGPKVKTCSASSSVYMYWYQOKGSSPRLIYDTSNLAGVPR 200
   |||||
QY 61 FSGSSGTSYSLTISRMEDATYTCQWSSNPLTFSGTLEIKR 107
   |||||
DB 201 FSGSSGTSYSLTISRMEDATYTCQWSSNPLTFSGTLEIKR 247
   |||||

RESULT 2
US-10-512-184-50
; Sequence 50, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschafft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184

```

/ CURRENT FILING DATE: 2004-10-22  
/ NUMBER OF SEQ ID NOS: 72  
/ SOFTWARE: Patent Ver. 2.1  
/ SEQ ID NO 50  
/ LENGTH: 615  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: fusion protein  
/ OTHER INFORMATION: comprising the leader peptide - chitinase - linker  
/ OTHER INFORMATION: - bcpv S52 - cmyc/H186.  
US-10-512-184-50

Query Match 80.8%; Score 447; DB 1; Length 615;  
Best Local Similarity 81.3%; Pred. No. 1,8e-22;  
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DTBLTQSPAIMSASPERKVTTCSSASSSVSYMYWYQOKPSSPRLIYDTSNLSAGVPVRFSG 60  
Db 482 DIVLFGSPVIMSASPERKVTTCSSASSSVSYMYWYQOKSGTSPKRWIFDTSNLSAGVPVRFSG 541  
Qy 61 SSGSGTSLTISRMEDADATYYCOQWSSNPLTFGSGTKLEIKR 107  
Db 542 SSGSGTSLTISRMEDADATYYCOQWSSNPLTFGAGTKLEIKR 588

## RESULT 3

US-11-174-186-1  
/ Sequence 1, Application US/11174186  
/ Publication No. US20050244418A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Gillies, Stephen  
/ APPLICANT: Lo, Kin-Ming  
/ APPLICANT: Qian, Xingyi  
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
/ FILE REFERENCE: LEX-019  
/ CURRENT APPLICATION NUMBER: US/11/174,186  
/ CURRENT FILING DATE: 2005-07-01  
/ PRIOR APPLICATION NUMBER: US 60/288,564  
/ PRIOR FILING DATE: 2001-05-03  
/ NUMBER OF SEQ ID NOS: 42  
/ SOFTWARE: Patent version 3.3  
/ SEQ ID NO 1  
/ LENGTH: 106  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ OTHER INFORMATION: KS VK mouse  
US-11-174-186-1

Query Match 78.7%; Score 435; DB 7; Length 106;  
Best Local Similarity 83.5%; Pred. No. 2,6e-22;  
Matches 86; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 4 LTQSPAIMSASPERKVTTCSSASSSVSYMYWYQOKPSSPRLIYDTSNLSAGVPVRFSG 63  
Db 4 LTQSPAIMSASPERKVTTCSSASSSVSYMYWYQOKPSSPRLIYDTSNLSAGVPVRFSG 63  
Qy 64 SSGGTSLTISRMEDADATYYCOQWSSNPLTFGSGTKLEIK 106  
Db 64 SSGGTSLTISRMEDADATYYCHORSQGYPTFGGKTLEIK 106

## RESULT 4

US-11-174-186-8  
/ Sequence 8, Application US/11174186  
/ Publication No. US20050244418A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Gillies, Stephen  
/ APPLICANT: Lo, Kin-Ming  
/ APPLICANT: Qian, Xingyi  
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
/ FILE REFERENCE: LEX-019

/ CURRENT APPLICATION NUMBER: US/11/174,186  
/ CURRENT FILING DATE: 2005-07-01  
/ PRIOR APPLICATION NUMBER: US 60/288,564  
/ PRIOR FILING DATE: 2001-05-03  
/ NUMBER OF SEQ ID NOS: 42  
/ SOFTWARE: Patent version 3.3  
/ SEQ ID NO 8  
/ LENGTH: 106  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ OTHER INFORMATION: VK7 light chain  
US-11-174-186-8

Query Match 77.2%; Score 427; DB 7; Length 106;  
Best Local Similarity 81.6%; Pred. No. 8e-22;  
Matches 84; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Qy 4 LTQSPAIMSASPERKVTTCSSASSSVSYMYWYQOKPSSPRLIYDTSNLSAGVPVRFSG 63  
Db 4 LTQSPAIMSASPERKVTTCSSASSSVSYMYWYQOKPSSPRLIYDTSNLSAGVPVRFSG 63  
Qy 64 SSGGTSLTISRMEDADATYYCOQWSSNPLTFGSGTKLEIK 106  
Db 64 SSGGTSLTISRMEDADATYYCHORSQGYPTFGGKTLEIK 106

## RESULT 5

US-11-172-320-4  
/ Sequence 4, Application US/11172320  
/ Publication No. US20050244413A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Adolf, Guenther  
/ APPLICANT: Baum, Anke  
/ APPLICANT: Heider, Karl-Heinz  
/ TITLE OF INVENTION: Compositions and Methods for Treating Cancer using  
/ TITLE OF INVENTION: Cytotoxic CD4 Antibody Immunocjugates and  
/ FILE REFERENCE: 1/1383  
/ CURRENT APPLICATION NUMBER: US/11/172,320  
/ CURRENT FILING DATE: 2005-06-30  
/ PRIOR APPLICATION NUMBER: US/10/645,215  
/ PRIOR FILING DATE: 2003-08-21  
/ PRIOR APPLICATION NUMBER: EP 02 018 686.2  
/ PRIOR FILING DATE: August 21, 2002  
/ PRIOR APPLICATION NUMBER: US 60/405,956  
/ PRIOR FILING DATE: August 26, 2002  
/ NUMBER OF SEQ ID NOS: 9  
/ SOFTWARE: Patent Ver. 2.1  
/ SEQ ID NO 4  
/ LENGTH: 213  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain  
US-11-172-320-4

Query Match 77.0%; Score 426; DB 7; Length 213;  
Best Local Similarity 75.0%; Pred. No. 1,6e-21;  
Matches 78; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

Qy 4 LTQSPAIMSASPERKVTTCSSASSSVSYMYWYQOKPSSPRLIYDTSNLSAGVPVRFSG 63  
Db 4 LTQSPAIMSASPERKVTTCSSASSSVSYMYWYQOKPSSPRLIYDTSNLSAGVPVRFSG 63  
Qy 64 SSGGTSLTISRMEDADATYYCOQWSSNPLTFGSGTKLEIKR 107  
Db 64 SSGGTSLTISRMEDADATYYCOQWSSNPLTFGSGTKLEIKR 107

## RESULT 6

US-11-174-186-42  
/ Sequence 42, Application US/11174186

```
/ Publication No. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xingyi
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ PRIOR FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 42
/ LENGTH: 213
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: light chain
US-11-174-186-42
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Query Match 76.7%; Score 424; DB 7; Length 213;
Best Local Similarity 79.8%; Pred. No. 2,1e-21;
Matches 83; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
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QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPRFSG 63
DB 4 LTQSPATISLSPGRVITLTCSASSSVSYMLWYQOKPGSSPKWIPDTSNLSAGVPRFSG 63
```

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QY 64 SSGSTSYSLTISRMEADATYYCOQWSNPLTFGSGTKLEIKR 107
DB 64 SSGSTSYSLTISRMEADATYYCHORSGVPTFGGKLEIKR 107
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RESULT 7
US-11-174-186-9
/ Sequence 9, Application US/11/174186
/ Publication No. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xingyi
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ PRIOR FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 9
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: VK6 light chain
US-11-174-186-9
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Query Match 75.8%; Score 419; DB 7; Length 106;
Best Local Similarity 79.6%; Pred. No. 2,5e-21;
Matches 82; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
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QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPRFSG 63
DB 4 LTQSPATISLSPGRVITLTCSASSSVSYMLWYQOKPGSSPKWIPDTSNLSAGVPRFSG 63
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QY 64 SSGSTSYSLTISRMEADATYYCOQWSNPLTFGSGTKLEIKR 106
DB 64 SSGSTSYSLTISRMEADATYYCHORSGVPTFGGKLEIKR 106
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RESULT 8
US-11-172-320-8
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/ Sequence 8, Application US/11/172320
/ Publication No. US20050244413A1
/ GENERAL INFORMATION:
/ APPLICANT: Adolf, Guenther
/ APPLICANT: Baum, Anke
/ APPLICANT: Heider, Karl-Heinz
/ TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
/ TITLE OF INVENTION: Cytotoxic CD4 Antibody Immunoconjugates and
/ FILE REFERENCE: 1/1383
/ CURRENT APPLICATION NUMBER: US/11/172,320
/ PRIOR FILING DATE: 2005-06-30
/ PRIOR APPLICATION NUMBER: US/10/645,215
/ PRIOR FILING DATE: 2003-08-21
/ PRIOR APPLICATION NUMBER: EP 02 018 686.2
/ PRIOR FILING DATE: August 21, 2002
/ PRIOR APPLICATION NUMBER: US 60/405,956
/ PRIOR FILING DATE: August 26, 2002
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 213
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanised Antibody B1A 8 light chain
US-11-172-320-8
```

```
Query Match 75.2%; Score 416; DB 7; Length 213;
Best Local Similarity 73.1%; Pred. No. 4,5e-21;
Matches 76; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
```

```
QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPRFSG 63
DB 4 LTQSPATISLSPGRVITLTCSASSSVSYMLWYQOKPGAPRILYDTSNLSAGVPRFSG 63
```

```
QY 64 SSGSTSYSLTISRMEADATYYCOQWSNPLTFGSGTKLEIKR 107
DB 64 SSGSTFTLTISLPEDEFAVYCLQWSNPLTFGSGTKLEIKR 107
```

```
RESULT 9
US-11-174-186-7
/ Sequence 7, Application US/11/174186
/ Publication No. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xingyi
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ PRIOR FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 7
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: VK6 light chain
US-11-174-186-7
```

```
Query Match 74.0%; Score 409; DB 7; Length 106;
Best Local Similarity 74.8%; Pred. No. 1e-20;
Matches 77; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
```

```
QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPRFSG 63
DB 4 LTQSPATISLSPGRVITLTCSASSSVSYMLWYQOKPGAPKILIPDTSNLSAGVPRFSG 63
```

Qy 64 SSGTSYSLTISRMEADATYYCQWSSNPLTFPGSGTKLEK 106  
| | | | : | | | | | | | | | | : |  
Db 64 SSGSDTYLTLTSSLPEDPAVYYCHQRSQPYPTFGSGTKLEIK 106

```

RESULT 10
US-11-174-186-16
/ Sequence 16, Application US/11/174186
/ Publication No. US2005024418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xiang
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 16
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: KS VK mouse
US-11-174-186-16

```

[illegible]

```

RESULT 11
US-11-174-186-15
/ Sequence 15, Application US/11/174186
/ Publication NO. US2005024418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen,
/ APPLICANT: Lo, Kin-Ming
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ PRT REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 15
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: KS de-immunized VKS
US-11-174-186-15

```

Query Match	73.6%	Score 407,	DB 7,	Length 106;
Best Local Similarity	74.8%	Pred. Mism. 1.4e-20;		
Matches	77;	Conservative 16;	Indels 0;	Gaps 0;
Qy	4	LTGSPALMSASGPEKVTTCSSASSSVSYMYVYQKPGSSPLLTYDTSTNLASGVVPRSG	63	
Qb	4	LTGSPALMSASGPEKVTTCSSASSSVSYMYVYQKPGSSPLLTYDTSTNLASGVVPRSG	63	

```
QY      64 SGGSTSYLTISRMEABDAATYYQQWSSNPLTFGSGTKLELK 106
        |||||::|||:||||| | | | | | | | :|
Db      64 SGGSTSYLTINSLEABDAATYYCHORSGYPTFGGKTKEIK 106
```

```

RESULT 12
US-11-174-186-10
; Sequence 10, Application US/11/174186
; Publication NO. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial1
; FEATURE:
; OTHER INFORMATION: KS VK veneered
US-11-174-186-10

```

	Query Match	Similarity	Score	IDB	Length
Best Local	71.8%	Pred. 8.75-20.			
Matches	74	Conservative 11	Mismatches 18	Indels 0	Gaps 0
QY	4	LTGSPALMASPGKAVTTTCASSSVSYMYTQKPGSSPLLHYDYSNLASGVPRVRS	63		
DB	4	LTGSPALMASPGKAVTTTCASSSVSYMYTQKPGSSPLLHYDYSNLASGVPRVRS	63		
QY	64	SGSGTSTYLLTIRMEADDAATYYCQWSSNPLTFGSGTKLEK	106		
DB	64	SGSGTSTYLLTIRMEADDAATYYCQWSSNPLTFGSGTKLEK	106		

```

RESULT 13
US-11-174-186-14
Sequence 14, Application US/11/174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gilless, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xiang
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
PTE REFERENCE: lex-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 14
LENGTH: 106
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VK4
US-11-174-186-14

```

Query Match 71.2%; Score 394; DB 7; Length 106;  
Best Local Similarity 71.8%; Pred. No. 8.7e-20;  
Matches 74; Conservative 11; Mismatches 18; Gaps 0;

OY 4 LTGSPAIMSASPGKAVTTTCASSSVSTIMVYQOKPSSPLLIDYSINLSAGVPVRISG 63  
|||:::|||||:::|||||:::|||||:::|||||



Db 4 LTGSPALAVSPGQRATITCSASSSVSYMLTYQKPGQPKPWIFDTSNLASGPFARFSG 63  
QY 64 SSGSTSYSLTISRMEADATYTCQOWSNPLTFGSGTKLEK 106  
Db 64 SSGSTSYTLTINSLEADATYTCQOWSNPLTFGSGTKLEK 106

RESULT 14  
US-11-174-186-12  
; Sequence 12, Application US/11174186  
; Publication No. US20050244418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Xiang  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR FILING DATE: 2005-07-01  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 12  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: KS de-immunized VK2  
US-11-174-186-12

Query Match 70.9%; Score 392; DB 7; Length 106;  
Best Local Similarity 71.8%; Pred. No. 1.2e-19;  
Matches 74; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 4 LTGSPALAVSPGQRATITCSASSSVSYMLTYQKPGQPKPWIFDTSNLASGPFARFSG 63  
Db 4 LTGSPALAVSPGQRATITCSASSSVSYMLTYQKPGQPKPWIFDTSNLASGPFARFSG 63  
QY 64 SSGSTSYSLTISRMEADATYTCQOWSNPLTFGSGTKLEK 106  
Db 64 SSGSTSYTLTINSLEADATYTCQOWSNPLTFGSGTKLEK 106

RESULT 15  
US-11-174-186-13  
; Sequence 13, Application US/11174186  
; Publication No. US20050244418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Xiang  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR FILING DATE: 2005-07-01  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: KS-deimmunized VK3  
US-11-174-186-13

Query Match 70.9%; Score 392; DB 7; Length 106;  
Best Local Similarity 71.8%; Pred. No. 1.2e-19;  
Matches 74; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 4 LTGSPALAVSPGQRATITCSASSSVSYMLTYQKPGQPKPWIFDTSNLASGPFARFSG 63

Db 4 LTGSPALAVSPGQRATITCSASSSVSYMLTYQKPGQPKPWIFDTSNLASGPFARFSG 63  
QY 64 SSGSTSYSLTISRMEADATYTCQOWSNPLTFGSGTKLEK 106  
Db 64 SSGSTSYTLTINSLEADATYTCQOWSNPLTFGSGTKLEK 106

Search completed: November 21, 2005, 12:33:50  
Job time : 2.05971 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:32 / Search time 145.932 Seconds  
(without alignments)  
328.182 Million cell updates/sec

Title: US-10-632-706-88  
Perfect score: 559  
Sequence: 1 DIETQSPALMSAPGKVT.....QWSSNPLTFGSGTKELKR 109

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_21:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	559	100.0	109	8	ADR38686	Adt38686 Mouse Ilg
2	518	92.7	107	8	ADR38685	Adt38685 Mouse Ilg
3	492	88.0	107	8	ADR38673	Adt38673 Mouse Ilg
4	491	87.8	107	9	ADM86126	Adw86126 Novel cyt
5	491	87.8	210	8	ADU86565	Adu86565 Immunoglo
6	491	87.8	210	8	ADU86571	Adu86571 Immunoglo
7	490	87.7	110	2	AAR21305	Aar21305 Murine VL
8	489	87.5	129	5	ABR75616	Abt75616 Anti-RANK
9	486	86.9	107	8	ADR38670	Adt38670 Mouse Ilg
10	482	86.2	244	2	AAR79867	Aar79867 Anti-EGFR
11	481	86.0	108	8	ADT74993	Adt74993 Light cha
12	481	86.0	109	8	ADR38691	Adt38691 Mouse Ilg
13	481	86.0	242	2	AAR79870	Aar79870 Anti-EGFR
14	481	86.0	242	2	AAR79871	Aar79871 Anti-EGFR
15	479	85.7	110	2	AAR21306	Aar21306 Murine VL
16	478	85.5	122	2	AAR25958	Aar25958 ICAM-1 in
17	477	85.3	110	2	AAR21304	Aar21304 Murine VL
18	476	85.2	106	4	AAB69673	Aab69673 Murine ml
19	476	85.2	106	8	ADO47720	Ado47720 Mouse mlk
20	476	85.2	110	2	AAR21287	Aar21287 Murine VL
21	476	85.2	128	4	AAB69655	Aab69655 Murine ml
22	476	85.2	128	8	ADO47747	Ado47747 Mouse mlk
23	475	85.0	106	5	ABG32682	Abg32682 Murine an
24	475	85.0	106	5	AAE27810	AAe27810 Mouse 425

25	475	85.0	128	2	AAR27050	Aar27050 VL425 ant
26	475	85.0	242	2	AAR79872	Aar79872 Anti-EGFR
27	473	84.6	106	5	AAU72834	Aau72834 Anti-NG2
28	473	84.6	107	4	ADM80852	Adm80852 Anti-CD3
29	472	84.4	246	2	AAR79869	Aar79869 Anti-EGFR
30	471.5	84.3	108	9	ADM86127	Adm86127 Novel cyt
31	471.5	84.3	214	8	ADU86519	Adu86519 Immunoglo
32	471	84.3	108	2	AAR21293	Aar21293 Murine VL
33	471	84.3	110	2	ADT75125	Adt75125 Light cha
34	471	84.3	110	8	ADT75054	Adt75054 Light cha
35	471	84.3	110	8	ADT75053	Adt75053 Light cha
36	470	84.1	106	8	ADOL6878	Adol6878 Murine an
37	470	84.1	109	8	ADH59707	Adh59707 ChimERIC
38	470	84.1	109	8	ADH59707	Adh59707 ChimERIC
39	469	83.9	106	9	ADV66151	Adv66151 CD3-speci
40	469	83.9	106	9	ADZ64982	Adz64982 Non-deimm
41	469	83.9	106	9	ADZ83490	Adz83490 Non-deimm
42	469	83.9	106	5	AAE22196	Aae22196 CD3-speci
43	469	83.9	110	2	AAR21307	Aar21307 Murine VL
44	469	83.9	128	4	AAE65521	Aae65521 Mouse ant
45	469	83.9	240	9	ADV14577	Adv14577 VL(CD3)-V

## ALIGNMENTS

RESULT 1  
ID ADR38686 standard; peptide; 109 AA.

AC ADR38686;

DT 02-DEC-2004 (first entry)

DE Mouse light chain variable region scFv seqid 88.

KM antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;

KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;

KM light chain variable region; single chain antibody; scFv.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC ) UNIV CALIFORNIA.

XX Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

PS Example 1; SEQ ID NO 88; 110pp; English.

The invention describes an isolated antibody (I) that specifically binds

to an epitope specifically bound by an antibody expressed by a specific

clone where (I) binds to and neutralises botulinum neurotoxin type A

(BoNT/A). An isolated antibody (I) that specifically binds to an epitope

specifically bound by an antibody expressed by a clone chosen from clone

S25, C35, C39, 1C6, 3D12, B4, 1F3, huc25, At1, Ar2, WRI (V), WRI (V), 3-1,

3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum

neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)

comprising BoNT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I) and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of a mouse light chain variable fragment anti-botulinum toxin  
CC scFv.  
XX  
CC Sequence 109 AA;  
SQ  
Query Match 100.0%; Score 559; DB 8; Length 109;  
Best Local Similarity 100.0%; Pred. No. 1e-34;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DIELTQSPAIMSAPGKRVTTTCRASSSVSSSYLGWYQKQKSSPRLIYDTSNLASGVP 60  
1 DIELTQSPAIMSAPGKRVTTTCRASSSVSSSYLGWYQKQKSSPRLIYDTSNLASGVP 60  
DB 61 VRFGSGSGTSGYSLTISRMEADATYYCQWGSNPLTFGSGTKLEIKR 109  
61 VRFGSGSGTSGYSLTISRMEADATYYCQWGSNPLTFGSGTKLEIKR 109  
Db 61 VRFGSGSGTSGYSLTISRMEADATYYCQWGSNPLTFGSGTKLEIKR 109  
RESULT 2  
ADR38685  
ID ADR38685 standard; peptide; 107 AA.  
XX  
AC ADR38685;  
XX  
DT 02-DEC-2004 (first entry)  
DE Mouse light chain variable region scFv seqid 87.  
XX  
XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
KM light chain variable region; single chain antibody; scFv.  
XX  
OS Mus sp.  
XX  
PN US2004175385-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 01-AUG-2003; 2003US-00632706.  
XX  
PR 31-AUG-1998; 98US-00144886.  
PR 01-AUG-2002; 2002US-0400721P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Marks JD, Ameredorfer P;  
XX  
DR WPI; 2004-652009/63.  
XX  
PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
XX  
XX Example 1; SEQ ID NO 87; 110pp; English.  
XX  
CC The invention describes an isolated antibody (I) that specifically binds  
CC to an epitope specifically bound by an antibody expressed by a specific

CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone  
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
CC 3-8, 3-10 and INGI, where (I) binds to and neutralises botulinum  
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
CC comprising BoNT/A neutralising epitope having an epitope that is  
CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I) and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of a mouse light chain variable fragment anti-botulinum toxin  
CC scFv.  
XX  
CC Sequence 107 AA;  
SQ  
Query Match 92.7%; Score 518; DB 8; Length 107;  
Best Local Similarity 94.5%; Pred. No. 1.2e-31;  
Matches 103; Conservative 1; Mismatches 3; Indels 2; Gaps 1;  
QY 1 DIELTQSPAIMSAPGKRVTTTCRASSSVSSSYLGWYQKQKSSPRLIYDTSNLASGVP 60  
1 DIELTQSPAIMSAPGKRVTTTCRASSSV--SYMYQKQKSSPRLIYDTSNLASGVP 58  
DB 61 VRFGSGSGTSGYSLTISRMEADATYYCQWGSNPLTFGSGTKLEIKR 109  
61 VRFGSGSGTSGYSLTISRMEADATYYCQWGSNPLTFGSGTKLEIKR 109  
Db 59 VRFGSGSGTSGYSLTISRMEADATYYCQWGSNPLTFGSGTKLEIKR 107  
RESULT 3  
ADR38673  
ID ADR38673 standard; peptide; 107 AA.  
XX  
AC ADR38673;  
XX  
DT 02-DEC-2004 (first entry)  
DE Mouse light chain variable region scFv seqid 75.  
XX  
XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
KM light chain variable region; single chain antibody; scFv.  
XX  
OS Mus sp.  
XX  
PN US2004175385-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 01-AUG-2003; 2003US-00632706.  
XX  
PR 31-AUG-1998; 98US-00144886.  
PR 01-AUG-2002; 2002US-0400721P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Marks JD, Ameredorfer P;  
XX  
DR WPI; 2004-652009/63.  
XX  
PT New isolated antibody that neutralizes botulinum neurotoxin type A,

PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.

PS Example 1; SEQ ID NO 75; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralizes botulinum neurotoxin type A  
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and IN61, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC , producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contracting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of a mouse light chain variable fragment anti-botulinum toxin  
 CC scFv.

XX Sequence 107 AA;

Query Match 88.0%; Score 492; DB 8; Length 107;  
 Best Local Similarity 90.8%; Pred. No. 1.1e-29;  
 Matches 99; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DIELTQSPAINASPGKVTTCRASSSVSSTYLGWYQOKPGSSPRLLIYDTSNLSAGVP 60  
 DB 1 DIELTQSPAINASPGKVTTCRASSSVSSTYLGWYQOKPGSSPRLLIYDTSNLSAGVP 58  
 QY 61 VRFSGSGSGTSTSLTISRMEADATYYCQGNSSNPITFGSGTKLELR 109  
 DB 59 VRFSGSGSGTSTSLTISRMEADATYYCQGNSSNPITFGSGTKLELR 107

RESULT 4

ID ADM86126  
 ID ADM86126 standard; protein; 107 AA.

AC ADM86126;

DT 21-APR-2005 (first entry)

DE Novel cytotoxic conjugate-related mouse aY1 protein region SeqID46.

XX cytotoxic; immunosuppressive; cytostatic; immunosuppressive; virucide;  
 KW apoptotic stimulation; cancer; ovary tumor; uterine cervix tumor;  
 KW endometrial carcinoma; breast tumor; pancreas tumor; CA6 glycoprotein;  
 KW autoimmune disease; graft rejection; viral infection; DS6;  
 KW antibody engineering; aY1.

OS Mus musculus.

XX WO2005009369-A2.

XX 03-FEB-2005.

XX 21-JUL-2004; 2004WO-US023340.

XX 21-JUL-2003; 2003US-0488447P.

PA (IMMU-) IMMUNOGEN INC.

PI Payne G, Chun P, Tavares DJ;

DR WPI; 2005-142544/15.

PT Cytotoxic conjugate useful for treating cancer, autoimmune diseases, and  
 PT graft rejections or viral infections, comprises cell binding agent and  
 PT cytotoxic agent.

PS Example 12; SEQ ID NO 46; 179pp; English.

XX This invention relates to a novel cytotoxic conjugate which comprises a  
 CC cell binding agent and a cytotoxic agent, where the cell binding agent  
 CC binds to CA6 glycoprotein. Preferably, the cell binding agent is the murine  
 CC anti-CA6 monoclonal antibody DS6 or their epitope-binding fragments or a  
 CC humanized version of the same. The cytotoxic agent is chosen from  
 CC maytansinoid compounds, taxoid compounds, CC-1065 compounds, dolastatin  
 CC compounds, daunorubicin compounds or doxorubicin compounds. The invention  
 CC may be useful for the production of compounds with a cytostatic,  
 CC immunosuppressive or virucide activity acting as stimulators of  
 CC apoptosis. The invention is useful for inhibiting growth of a cell  
 CC expressing CA6 glycoprotein and may be used for treating a subject having a  
 CC cancer (for example serous ovarian carcinoma, endometrial ovarian  
 CC carcinoma, neoplasm of the uterine cervix, neoplasm of the endometrium,  
 CC neoplasm of the vulva, breast carcinoma, pancreatic tumor or tumor of the  
 CC urothelium), in which CA6 glycoprotein is expressed or overexpressed. In  
 CC addition, the invention may be useful for treating autoimmune diseases,  
 CC graft rejections or viral infections. The present sequence is that of a  
 CC region of the mouse aY1 protein which was used to demonstrate homology  
 CC with a region of the mouse DS6 antibody light chain protein during the  
 CC exemplification of the invention.

XX Sequence 107 AA;

Query Match 87.8%; Score 491; DB 9; Length 107;  
 Best Local Similarity 88.1%; Pred. No. 1.3e-29;  
 Matches 96; Conservative 7; Mismatches 4; Indels 2; Gaps 1;

QY 1 DIELTQSPAINASPGKVTTCRASSSVSSTYLGWYQOKPGSSPRLLIYDTSNLSAGVP 60  
 DB 1 DIELTQSPAINASPGKVTTCRASSSVSSTYLGWYQOKPGSSPRLLIYDTSNLSAGVP 58  
 QY 61 VRFSGSGSGTSTSLTISRMEADATYYCQGNSSNPITFGSGTKLELR 109  
 DB 59 VRFSGSGSGTSTSLTISRMEADATYYCQGNSSNPITFGSGTKLELR 107

RESULT 5

ID ADU86565  
 ID ADU86565 standard; protein; 210 AA.

AC ADU86565;

DT 10-FEB-2005 (first entry)

DE Immunoglobulin variable domain protein SeqID 54.

XX antiinflammatory; antibacterial; virucide; cytostatic; antiproliferative;  
 KW antidiabetic; vasotropic; vaccine; protein purification; protein folding;  
 KW diagnosis; inflammation; immune disorder; allergic hypersensitivity;  
 KW infection; autoimmune disease; asthma; psoriasis;  
 KW insulin dependent diabetes; multiple sclerosis; rheumatoid arthritis;  
 KW systemic lupus erythematosus; myasthenia gravis; hematological disease;  
 KW neoplasm; immunoglobulin; variable region.

XX Homo sapiens.

XX WO2004101790-A1.

XX 25-NOV-2004.

XX 14-MAY-2004; 2004WO-GB002102.

```

XX 14-MAY-2003; 2003US-0470340P.
PR 17-MAR-2004; 2004US-0554021P.
XX (DOMA-) DOMANTIS LTD.
XX Jespers LS, Jones PC, Famm KHJ, Winter GP,
XX WPI, 2004-821888/81.
DR
XX
XX Recovering a polypeptide that unfolds reversibly from a repertoire of
PT polypeptides for treating e.g., cancer, by unfolding a portion of the
PT displayed polypeptides and refolding a portion of the unfolded
PT polypeptides.
XX
XX Disclosure; SEQ ID NO 54; 222pp; English.
XX
XX The invention describes a method of recovering a polypeptide that unfolds
CC reversibly from a repertoire of polypeptides that distinguishes folded
CC has a common selectable characteristic that distinguishes folded
CC polypeptides from unfolded or misfolded polypeptides. The method
CC comprises: providing a polypeptide display system comprising the
CC repertoire of displayed polypeptides; unfolding at least a portion of the
CC displayed polypeptides; refolding at least one polypeptide that unfolds
CC polypeptides; and recovering at least one polypeptide that unfolds
CC reversibly and has the selectable characteristic from the refolded
CC portion. The method is useful in recovering a polypeptide that unfolds
CC reversibly from a repertoire of polypeptides that unfolds reversibly. The
CC library or repertoire is useful for selecting a polypeptide comprising an
CC antibody variable domain that unfolds reversibly or a polypeptide that
CC is useful in the manufacture of a medicament for diagnosing, treating or
CC preventing a disease or medical condition mediated by a cytokine,
CC cytokine receptor, enzyme, enzyme co-factor or DNA binding protein, such
CC as an inflammatory state, allergic hypersensitivity, cancer, bacterial or
CC viral infection or an autoimmune disorder, e.g., asthma, psoriasis, Type
CC I diabetes, multiple sclerosis, rheumatoid arthritis, systemic lupus
CC erythematosus, Crohn's disease, myasthenia gravis, leukemia or solid
CC tumor. This is the amino acid sequence of an immunoglobulin variable
CC region associated with the protein purification method of the invention.
XX
XX Sequence 210 AA;
SQ
Query Match 87.8%; Score 491; DB 8; Length 210;
Best Local Similarity 88.1%; Pred. No. 2; e-29;
Matches 96; Conservative 7; Mismatches 4; Indels 2; Gaps 1;
QY 1 DIELTOSPAIMASAPGKVTTCRASSVS8SYLGMVQOKRSGSPRLIYDTSNLAGVP 60
1 DIELTOSPAIMASAPGKVTTCRASSVS--SYMYVQOKRSGSPRLIYDTSNLAGVP 58
Db 1 DIELTOSPAIMASAPGKVTTCRASSVS--SYMYVQOKRSGSPRLIYDTSNLAGVP 58
QY 61 VRFGSGSGTSGSYSLTISRMEADAAATYYCOQMSNPITFGSGTKLEIKR 109
59 VRFGSGSGTSGSYSLTISRMEADAAATYYCOQMSNPITFGSGTKLEIKR 107
Db 59 VRFGSGSGTSGSYSLTISRMEADAAATYYCOQMSNPITFGSGTKLEIKR 107
RESULT 6
ADU86571 standard; protein; 210 AA.
ADU86571;
XX
XX 10-FEB-2005 (first entry)
XX
XX Immunoglobulin variable domain protein seqid 60.
XX
XX antiinflammatory; antibacterial; virucide; cytosstatic; antiparasitic;
XX antidiabetic; vasotrophic; vaccine; protein purification; protein folding;
XX diagnosis; inflammation; immune disorder; allergic hypersensitivity;
XX infection; autoimmune disease; asthma; psoriasis;
XX insulin dependent diabetes; multiple sclerosis; rheumatoid arthritis;
XX systemic lupus erythematosus; myasthenia gravis; hematological disease;
XX neoplasm; immunoglobulin; variable region.

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XX
XX Homo sapiens.
OS
XX MO2004101790-A1.
EN
XX 25-NOV-2004.
PD
XX
XX 14-MAY-2004; 2004MO-GB002102.
PF
XX
XX 14-MAY-2003; 2003US-0470340P.
PR 17-MAR-2004; 2004US-0554021P.
XX (DOMA-) DOMANTIS LTD.
XX
XX Jespers LS, Jones PC, Famm KHJ, Winter GP;
XX WPI, 2004-821888/81.
DR
XX
XX Recovering a polypeptide that unfolds reversibly from a repertoire of
PT polypeptides for treating e.g., cancer, by unfolding a portion of the
PT displayed polypeptides and refolding a portion of the unfolded
PT polypeptides.
XX
XX Disclosure; SEQ ID NO 60; 222pp; English.
XX
XX The invention describes a method of recovering a polypeptide that unfolds
CC reversibly from a repertoire of polypeptides that distinguishes folded
CC has a common selectable characteristic that distinguishes folded
CC polypeptides from unfolded or misfolded polypeptides. The method
CC comprises: providing a polypeptide display system comprising the
CC repertoire of displayed polypeptides; unfolding at least a portion of the
CC displayed polypeptides; refolding at least a portion of the unfolded
CC polypeptides; and recovering at least one polypeptide that unfolds
CC reversibly and has the selectable characteristic from the refolded
CC portion. The method is useful in recovering a polypeptide that unfolds
CC reversibly from a repertoire of polypeptides that unfolds reversibly. The
CC library or repertoire is useful for selecting a polypeptide comprising an
CC antibody variable domain that unfolds reversibly or a polypeptide that
CC refolds reversibly and comprising an antibody format. The polypeptide is
CC useful in the manufacture of a medicament for diagnosing, treating or
CC preventing a disease or medical condition mediated by a cytokine,
CC cytokine receptor, enzyme, enzyme co-factor or DNA binding protein, such
CC as an inflammatory state, allergic hypersensitivity, cancer, bacterial or
CC viral infection or an autoimmune disorder, e.g., asthma, psoriasis, Type
CC I diabetes, multiple sclerosis, rheumatoid arthritis, systemic lupus
CC erythematosus, Crohn's disease, myasthenia gravis, leukemia or solid
CC tumor. This is the amino acid sequence of an immunoglobulin variable
CC region associated with the protein purification method of the invention.
XX
XX Sequence 210 AA;
SQ
Query Match 87.8%; Score 491; DB 8; Length 210;
Best Local Similarity 88.1%; Pred. No. 2; e-29;
Matches 96; Conservative 7; Mismatches 4; Indels 2; Gaps 1;
QY 1 DIELTOSPAIMASAPGKVTTCRASSVS8SYLGMVQOKRSGSPRLIYDTSNLAGVP 60
1 DIELTOSPAIMASAPGKVTTCRASSVS--SYMYVQOKRSGSPRLIYDTSNLAGVP 58
Db 1 DIELTOSPAIMASAPGKVTTCRASSVS--SYMYVQOKRSGSPRLIYDTSNLAGVP 58
QY 61 VRFGSGSGTSGSYSLTISRMEADAAATYYCOQMSNPITFGSGTKLEIKR 109
59 VRFGSGSGTSGSYSLTISRMEADAAATYYCOQMSNPITFGSGTKLEIKR 107
Db 59 VRFGSGSGTSGSYSLTISRMEADAAATYYCOQMSNPITFGSGTKLEIKR 107
RESULT 7
AAR21305 standard; protein; 110 AA.
AAR21305;
XX
XX 21-MAY-1992 (first entry)
XX
XX Murine VL kappa group IV/VI chain c specific for phox.

```

XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;  
KW g3p; binding; adsorption; gene VIII; diverse repertoire;  
KM specific binding pairs; replicable genetic display package.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Binding-site 24..35  
FT /label= CDR1  
FT Binding-site 51..57  
FT /label= CDR2  
FT Binding-site 90..98  
FT /label= CDR3  
FT /note= "D-X-G-X-X motif"  
XX  
PN WO9201047-A.  
XX  
PD 23-JAN-1992.  
XX  
PF 10-JUL-1990; 90GB-00015198.  
XX  
PR 10-JUL-1990; 90GB-00015198.  
PR 19-OCT-1990; 90GB-00022845.  
PR 12-NOV-1990; 90GB-00024503.  
PR 06-MAR-1991; 91GB-00004744.  
PR 15-MAY-1991; 91GB-00010549.  
XX  
PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
PA (MSDI-) MED RES COUNCIL.  
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;  
PI Jackson RH, Holliger KP, Marks JD;  
XX WPI: 1992-056862/07.  
XX  
PT Producing members of specific binding pairs - by expression in  
PT recombinant host cells with a secreting replicable genetic display  
PT package.  
XX  
PS Example 22; Fig 24; 209pp; English.  
XX  
CC The VK sequence is one of 23 (AAR21286-308) expressed from a single chain  
CC Fv library. The library produces a diverse repertoire of antibody  
CC fragments specific for 2-phenyl-5-oxazolone (phox). It was prepd. using  
CC cDNA generated from mRNA from mice immunised with phox coupled to chicked  
CC serum albumin. The VH and VL kappa sequences were separately amplified by  
CC PCR (AAQ23474-84) and ligated into fdCAT2 (AAQ23463) for expression on  
CC the phage surface as fusions with gene III. The resulting library of  
CC clones was diverse; 23 hapten binding clones were sequenced revealing 8  
CC VH genes (A-H; AAR21264-71) in a variety of pairings with 7 VK genes (a-g  
CC ; AAR21286-92). Most clones were VH-B combinations so a further  
CC hierarchical library was prepd. by "crossing" VH-B with the VK  
CC repertoire. The resulting library was screened for hapten binding and 24  
CC clones sequenced. 14 new partners (AAR21293-308) for VH-B were  
CC identified. Nearly all the VK genes were "ox-like", only f, (from the  
CC original library) and h, p, q, and r (from the hierarchical library) were  
CC V-kol type genes. Of the 24 hierarchical clones, only one was of type  
CC "v". The Ka of VH-B/VK-d for phox-GABA was 10 nM, one of the highest  
CC values found. This suggests that phage bearing scFv fragments having weak  
CC affinity-ies can be selected with antigen, probably due to the avidity of  
CC the multiple antibody heads on the phage. The different combinations  
CC could also be isolated on a basis of antigen affinity. See also AAR21260-  
CC 307, 309-311; AAR22450, 565-581  
XX  
SQ Sequence 110 AA;  
Query Match 87.7%; Score 490; DB 2; Length 110;  
Best Local Similarity 89.0%; Pred. No. 1.6e-29;  
Matches 97; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

DB 1 DIELTOSPAIMASPRBKVTTCRASSSVS\$SYLNMWYQKSGAPKLMISTNSLASGVP 60  
QY 61 VRPSGSGSGTSYSTLTISRMEADATYTCQWMSNPITPSSGTYLAKR 109  
DB 61 ARFSGSGSGTSYSTLTISRMEADATYTCQWMSNPITPFGAGTYLAKR 109  
RESULT 8  
ABB75616  
ID ABB75616 standard; protein; 129 AA.  
XX  
AC ABB75616;  
XX  
DT 10-JUN-2002 (first entry)  
XX  
DE Anti-RANK ligand mAb 19H22 light chain variable region.  
XX  
KW RANK ligand; RANK-L; monoclonal antibody; mAb; 19H22; antibody;  
KW complementarity determining region; CDR; rheumatoid arthritis;  
KW osteoporosis; bone cancer; metastasis; osteolysis; osteoarthritis;  
KW psoriasis; inflammatory bowel disease; multiple sclerosis; diabetes;  
KW cytostatic; antiarthritic; antiinflammatory; osteopathic; antidiabetic;  
KW antineumatic; immunosuppressive; antiporiatic; neuroprotective;  
KW light chain; VL; mouse.  
XX  
OS Mus musculous.  
XX  
FH Key Location/Qualifiers  
FT Region 24..33  
FT /label= CDR1  
FT /note= "complementarity determining region 1"  
FT Region 49..55  
FT /label= CDR2  
FT /note= "complementarity determining region 2"  
FT Region 88..96  
FT /label= CDR3  
FT /note= "complementarity determining region 3"  
XX  
PN WO200215846-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 21-AUG-2001; 2001WO-US026161.  
XX  
PR 21-AUG-2000; 2000US-0226524P.  
PR 07-SEP-2000; 2000US-0230639P.  
XX  
PA (SMK ) SMITHKLINE BEECHAM CORP.  
PA (SMK ) SMITHKLINE BEECHAM PLC.  
PI Sweet RW, Tornetta MA, Truneh A, Watam TA;  
PI WPI: 2002-242022/29.  
DR N-PSDB; ABL53530.  
XX  
CC A mouse monoclonal antibody 19H22 for treating or preventing osteopenic  
CC disease including rheumatoid arthritis and osteoporosis.  
XX  
PS Claim 6; Page 7; 45pp; English.  
XX  
CC The present sequence is that of the light chain variable region of  
CC claimed anti-human RANK ligand (RANK-L) murine monoclonal antibody (mAb)  
CC 19H22 (isotype IgG2b/kappa). The mAb is produced by hybridoma cells  
CC obtained by immunising CB6 f1 mice with human RANK-L protein, and fusing  
CC spleen cells with X63-Ag8.653 myeloma cells. 19H22 mAb is specific for  
CC human RANK-L, having a binding affinity characterised by a dissociation  
CC constant of about 10 power -10 M. RANK-L is a member of the tumour  
CC necrosis factor family of proteins and a key regulator of the immune  
CC system, bone development and homeostasis. The invention provides altered,  
CC chimeric and humanised 19H22 antibodies, including Fab or Fab'1/2  
CC fragments, antibodies comprising the light and heavy chain variable  
CC regions of 19H22, and antibodies comprising the complementarity  
CC determining regions of 19H22. These are used in methods for the

CC diagnosis, treatment and prevention of osteopenic diseases, including  
 CC rheumatoid arthritis, osteoporosis, metastatic and primary bone cancer,  
 CC wear debris induced osteolysis or osteoarthritis, and immune diseases  
 CC including psoriasis, insulin dependent diabetes, inflammatory bowel  
 CC disease or multiple sclerosis. Methods are also provided for the  
 CC recombinant production of the antibodies, using isolated nucleic acids  
 CC and transfected host (preferably mammalian) host cells, and a method of  
 CC diagnosing conditions associated with Th1 T-cell activity or osteoclast  
 CC development and activation, in particular those listed above

XX Sequence 129 AA;  
 SQ

Query Match 87.5%; Score 489; DB 5; Length 129;  
 Best Local Similarity 90.7%; Pred. No. 2,2e-29;  
 Matches 98; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 2 IELTQSPAIMSASPEKRYTTTCRASSSVSSYLGMVQOKPGSSPRLIYDTSNLASGVPV 61  
 DB 2 IVLTOSPAIMSASPEKRYTTTCRASSSVSSYLGMVQOKPGSSPRLIYDTSNLASGVPV 59  
 62 RFSGSGSGTSTSLTISRMEADATYTCQOWSNPLTFSGTKLELKR 109  
 DB 60 RFSGSGSGTSTSLTISRMEADATYTCQOWSNPLTFAGTKLELKR 107

RESULT 9  
 ADR38670  
 ID ADR38670 standard; peptide; 107 AA.  
 AC ADR38670;  
 DT 02-DEC-2004 (first entry)  
 DE Mouse light chain variable region scFv seqid 72.

XX antidiabetic; antibody; botulinum neurotoxin type A; BONT/A;  
 XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 XX light chain variable region; single chain antibody; scFv.

OS Mus sp.  
 XX US2004175385-A1.  
 PN 09-SEP-2004.  
 PD 01-AUG-2003; 2003US-00632706.  
 PF 31-AUG-1998; 98US-00144886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA Marke JD, Amerdortfer P;  
 PI WPI; 2004-652009/63.  
 DR New isolated antibody that neutralizes botulinum neurotoxin type A,  
 XX useful for diagnosing botulism or for treating pathologies associated  
 XX with botulinum neurotoxin poisoning.  
 PT Example 1; SEQ ID NO 72; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and 1NG1, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
 CC comprising BONT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)

CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplis. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplis, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplis. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of a mouse light chain variable fragment anti-botulinum toxin  
 CC scFv.

XX Sequence 107 AA;  
 SQ

Query Match 86.9%; Score 486; DB 8; Length 107;  
 Best Local Similarity 89.0%; Pred. No. 3.1e-29;  
 Matches 97; Conservative 2; Mismatches 8; Indels 2; Gaps 1;

QY 1 DIELTQSPAIMSASPEKRYTTTCRASSSVSSYLGMVQOKPGSSPRLIYDTSNLASGVP 60  
 DB 1 DIELTQSPAIMSASPEKRYTTTCRASSSVSSYLGMVQOKPGSSPRLIYDTSNLASGVP 58  
 61 VRFGSGSGTSTSLTISRMEADATYTCQOWSNPLTFSGTKLELKR 109  
 DB 59 IRFGSGSGTSTSLTISRMEADATYTCQOWSNPLTFSGTKLELKR 107

RESULT 10  
 AAR79867  
 ID AAR79867 standard; protein; 244 AA.  
 XX AAR79867;  
 AC AAR79867;  
 DT 02-JUL-1996 (first entry)  
 DE Anti-EGFR single chain antibody (Clone 1b D 2).

XX Single chain antibody; antibody; epidermal growth factor receptor; EGFR;  
 XX tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;  
 XX phage antibody library.

OS Mus musculus.  
 XX WO9525167-A1.  
 PN 21-SEP-1995.  
 PD 16-MAR-1995; 95WO-EP000978.  
 PF 17-MAR-1994; 94EP-00104160.  
 PR 02-DEC-1994; 94EP-00118970.  
 XX (MERE ) MERCK PATENT GMBH.  
 PA Kettleborough AC, Bendig MM, Ansell KH, Guesow D, Adan J;  
 PI Mcljans F, Rosell E, Blasco F, Plutats J;  
 DR WPI; 1995-336972/43.  
 DR N-PSDB; AAT04020.  
 XX Anti-EGFR antibodies and single chain Fv antibody fragments - obtained  
 PT from phage-antibody libraries, useful for diagnosis and therapy of  
 PT tumours.  
 XX Claim 4; Page 60-61; 93pp; English.  
 PS Anti-epidermal growth factor receptor (EGFR) single chain antibodies and  
 CC antibodies constructed from anti-EGFR antibody fragments can be used for



diagnosis of tumours and assessment of tumour growth in vitro and in vivo. They may also be used in a pharmaceutical composition for the therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and fragments are derived from mice but are humanised so as to cause minimum reaction against them. They are produced using the phage antibody library. They are produced using the phage antibody library. (see AA104011-704026 and AA179858-R79873)

Sequence 244 AA:

Query Match 86.2%; Score 482; DB 2; Length 244;  
 Best Local Similarity 89.1%; Pred. No. 1.3e-26;  
 Matches 98; Conservative 2; Mismatches 6; Indels 4; Gaps 2;

QY 1 DIETQSPAIMSAPGKQVTTTCRASSSVSSYLGMVQOKPGSSPRLLIYDTSNLAGV 60  
 DB 137 DIETQSPAIMSAPGKQVTTTCRASSSV--SYMYWQOKPGSSPRLLIYDTSNLAGV 194  
 QY 61 VRFSGSGSTSYSLTIISMEAEADATYYCQWSSNP--LTFGSGTKLELK 108  
 DB 195 VRFSGSGSTSYSLTIISMEAEADATYYCQWSSYPPMYTFGGGTLEIK 244

RESULT 11  
 ADR74993  
 ID ADR74993 standard; protein; 108 AA.  
 AC ADR74993;  
 XX  
 DT 13-JAN-2005 (first entry)  
 XX  
 DE Light chain murine anti-hL-SIGN scFv antibody protein A2UC Seq 39.  
 XX  
 KM autoimmune disease; antibody; antigen presenting cell; APC;  
 KM diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive;  
 KM vaccine; hL-SIGN.  
 XX  
 OS Mus sp.  
 XX  
 PM WO2004091543-A2.  
 PD 28-OCT-2004.  
 PF 04-MAR-2004; 2004WO-US006570.  
 PR 04-MAR-2003; 2003US-0451816P.  
 PR 15-DEC-2003; 2003US-0523500P.  
 PR 28-FEB-2004; 2004US-0548385P.  
 XX  
 PA (ALEX-) ALEXION PHARM INC.  
 XX  
 PI Bowdish KS, Kretz-Rommel A, Dakeppagari N;  
 DR WPI; 2004-758274/74.  
 XX  
 PT Treating an autoimmune disease comprises providing an  
 PT antibody/antigen construct containing an autoantigen linked to an  
 PT antibody to a receptor of an antigen presenting cell and administering  
 PT the construct to a subject.  
 XX  
 PS Example 9; Fig 8; 71pp; English.  
 XX  
 CC This invention relates to the novel treatment of an autoimmune disease  
 CC that utilises an antibody/ antigen construct. Specifically, it refers  
 CC to a peptide autoantigen that is linked to an antibody raised against an  
 CC antigen presenting cell (APC) receptor. The present invention describes a  
 CC method for treating diabetes mellitus by inducing an immune tolerance to  
 CC an autoantigen, which can be chosen from glutamic acid decarboxylase  
 CC (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived  
 CC from each thereof or beta cell antigens that are linked to an APC  
 CC receptor antibody. In particular, the antibody recognises a receptor  
 CC chosen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst  
 CC others, which is expressed on the surface of the APC. The antibody/

autoantigen construct then works to interfere with the interaction  
 CC between the APC and immune cells such as autoreactive T cells, and hence  
 CC inhibits T-cell proliferation. Accordingly, such compositions exhibit  
 CC antidiabetic and immunosuppressive activities and can be used in the  
 CC development of vaccines. Note that the single chain antibodies (scFvs)  
 CC used in this specification contain both variable light and heavy chain  
 CC regions connected by a linker, their short length makes these antibody  
 CC fragments particularly suitable for antigen linkage, and the capacity for  
 CC binding to the receptor is preserved. This polypeptide sequence is a  
 CC light chain murine anti-human L-SIGN (hL-SIGN) antibody protein of the  
 CC invention.

Sequence 108 AA:

Query Match 86.0%; Score 481; DB 8; Length 108;  
 Best Local Similarity 90.6%; Pred. No. 7.4e-23;  
 Matches 96; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 4 LTQSPAIMSAPGKQVTTTCRASSSVSSYLGMVQOKPGSSPRLLIYDTSNLAGV 63  
 DB 4 LTQSPAIMSAPGKQVTTTCRASSSV--SYMYWQOKPGSSPRLLIYDTSNLAGV 107  
 QY 64 SSGSGSTSYSLTIISMEAEADATYYCQWSSNP-LTFGSGTKLEIK 109  
 DB 62 SSGSGSTSYSLTIISMEAEADATYYCQWSSYPPMYTFGGGTLEIK 107

RESULT 12  
 ADR38691  
 ID ADR38691 standard; peptide; 109 AA.  
 AC ADR38691;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Mouse light chain variable region scFv seqid 93.  
 XX  
 KM antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
 KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 KM light chain variable region; single chain antibody; scFv.  
 XX  
 OS Mus sp.  
 XX  
 PM US2004175385-A1.  
 PD 09-SEP-2004.  
 PF 01-AUG-2003; 2003US-00632706.  
 PR 01-AUG-1998; 98US-00144886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Marks JD, Amersdorfer P;  
 DR WPI; 2004-652009/63.  
 XX  
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 XX  
 PS Example 1; SEQ ID NO 93; 110pp; English.  
 XX  
 CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), 3-1,  
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)



```

XX SQ Sequence 242 AA;
Query Match 86.0%; Score 481; DB 2; Length 242;
Best Local Similarity 86.9%; Pred. No. 1.6e-28;
Matches 96; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

OY 1 DIELTOSPAIMWASPGKVTTCRASSSVSSSYLGWYQOKGSSPRLIYDTSNLAGVP 60
DB 137 DIELTOSPAIMWASPGKVTTCRASSSVSSSYLGWYQOKGSSPRLIYDTSNLAGVP 194
OY 61 VRFSGSGGTSYSLTISRMEADATYYCQOWSSNPITFGSGTKLEIK 108
DB 195 VRFSGSGGTSYSLTISRMEADATYYCQOWSSNPITFGSGTKLEIK 242

RESULT 15
AAR21306
ID AAR21306 standard; protein; 110 AA.
XX AC AAR21306;
XX DT 21-MAY-1992 (first entry)
XX DB Murine VL kappa group IV/VI chain u specific for phox.
XX FD; bacteriophage; gene III; filamentous; phagemid; capsid; coat; plus;
XX KM g3p; binding; adsorption; gene VIII; diverse repertoire;
XX KW specific binding pairs; replicable genetic display package.
XX OS Synthetic.
XX RH Key Location/Qualifiers
FT Binding-site 24..35
FT Binding-site /label= CDR1
FT Binding-site 51..57
FT Binding-site /label= CDR2
FT Binding-site 90..98
FT Binding-site /label= CDR3
FT /note= "D-X-G-X-X motif"

XX PN WO9201047-A.
XX PD 23-JAN-1992.
XX PF 10-JUL-1990; 90GB-00015198.
XX PR 10-JUL-1990; 90GB-00015198.
XX PR 19-OCT-1990; 90GB-00022845.
XX PR 12-NOV-1990; 90GB-00024503.
XX PR 06-MAR-1991; 91GB-00004744.
XX PR 15-MAY-1991; 91GB-00010549.
XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PA (MEDI-) MED RES COUNCIL.
XX PI McCaferly J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
XX PI Jackson RH, Holliger KP, Marks JD;
XX DR WPI; 1992-056862/07.
XX PT Producing members of specific binding pairs - by expression in
XX PT recombinant host cells with a secreting replicable genetic display
XX PT package.
XX PS Example 22; Fig 24; 209pp; English.
XX CC The VK sequence is one of 23 (AAR21286-308) expressed from a single chain
XX CC Fv library. The library produces a diverse repertoire of antibody
XX CC fragments specific for 2-phenyl-5-oxazolone (phox). It was prepd. using
XX CC cDNA generated from mRNA from mice immunised with phox coupled to chicked
XX CC serum albumin. The VH and VL kappa sequences were separately amplified by
XX CC PCR (AA023474-84) and ligated into fdCAT2 (AA023463) for expression on

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CC the phage surface as fusions with gene III. The resulting library of
CC clones was diverse; 23 hapten binding clones were sequenced revealing 8
CC VH genes (A-H; AAR21264-71) in a variety of pairings with 7 VK genes (a-g
CC ; AAR21286-92). Most clones were VH-B combinations so a further
CC hierarchical library was prepd. by "crossing" VH-B with the VK
CC repertoire. The resulting library was screened for hapten binding and 24
CC clones sequenced. 14 new partners (AAR21293-308) for VH-B were
CC identified. Nearly all the VK genes were "ox-like"; only f (from the
CC original library) and h, p, q, and r (from the hierarchical library) were
CC Vko1 type genes. Of the 24 hierarchical clones, only one was of type
CC "u". The Kd of VH-B/VK-d for phox-GABA was 10 nM, one of the highest
CC values found. This suggests that phage bearing scfv fragments having weak
CC affinity-ies can be selected with antigen, probably due to the avidity of
CC the multiple antibody heads on the phage. The different combinations
CC could also be isolated on a basis of antigen affinity. See also AAR21260-
CC 307, 309-311; AAR22450, 565-581
XX SQ Sequence 110 AA;
Query Match 85.7%; Score 479; DB 2; Length 110;
Best Local Similarity 86.2%; Pred. No. 1.1e-28;
Matches 94; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 1 DIELTOSPAIMWASPGKVTTCRASSSVSSSYLGWYQOKGSSPRLIYDTSNLAGVP 60
DB 1 DIELTOSPAIMWASPGKVTTCRASSSVSSSYLGWYQOKGAPKLMYDTSNLAGVP 60
OY 61 VRFSGSGGTSYSLTISRMEADATYYCQOWSSNPITFGSGTKLEIKR 109
DB 61 ARFSGSGGTSYSLTISRMEADATYYCQOWSGVPLTFGAGTKLEIKR 109

```

Search completed: November 21, 2005, 12:19:56  
 Job time : 146.932 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 ; Search time 26.5513 Seconds  
(without alignments)  
394.995 Million cell updates/sec

Title: US-10-632-706-88

Perfect score: 559  
Sequence: 1 DIETLOSPAIMSASPGKRVK.....QWSSNPLTFGGSTKLELR 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	463	82.8	107 2	PC4405 Ig kappa chain V r
2	462	82.6	130 2	A32513 Ig kappa chain pre
3	456	81.6	107 2	A42848 Ig light chain V r
4	455	81.4	120 2	S66536 Ig light chain V r
5	455	81.4	130 2	B32456 Ig kappa chain pre
6	453	81.0	130 2	S04573 Ig kappa chain pre
7	452	80.9	107 2	A30562 Ig kappa chain V r
8	452	80.9	113 2	S03410 Ig kappa chain pre
9	451	80.7	107 2	B30562 Ig kappa chain V r
10	450	80.5	130 1	JI0079 Ig kappa chain pre
11	450	80.5	235 1	S25058 Ig kappa chain - m
12	446	79.8	103 2	S29591 Ig kappa chain V r
13	446	79.8	123 2	S05269 Ig kappa chain pre
14	445	79.6	108 2	S29581 Ig kappa chain V r
15	444.5	79.5	108 2	S38720 Ig light chain V r
16	444	79.4	106 2	PS0071 Ig kappa chain V r
17	443	79.2	108 2	PS0069 Ig kappa chain V r
18	442	79.1	104 2	B49049 Ig kappa chain V r
19	441	78.9	107 2	PD0011 Ig kappa chain V r
20	441	78.9	140 2	PD0013 Ig kappa chain pre
21	440	78.7	109 2	PT0405 Ig light chain V r
22	439.5	78.6	108 2	G30560 Ig kappa chain V r
23	439	78.5	108 2	PL0278 Ig kappa chain V r
24	438	78.4	124 2	S05267 Ig kappa chain pre
25	436	78.0	107 2	S11119 Ig kappa chain V r
26	435	77.8	106 2	PL0082 Ig kappa chain V r
27	435	77.8	106 2	B54378 Ig light chain V r
28	435	77.8	108 2	PL0277 Ig kappa chain V r
29	435	77.8	108 2	PL0276 Ig kappa chain V r

30	435	77.8	109 2	S13699 Ig kappa chain V r
31	435	77.8	109 2	PT0404 Ig light chain V r
32	434	77.6	107 2	S11118 Ig kappa chain V r
33	428	76.6	107 2	S11121 Ig kappa chain V r
34	426	76.2	107 2	PT0406 Ig kappa chain V r
35	426	76.2	108 2	S11125 Ig kappa chain V r
36	424	75.8	132 2	S05268 Ig kappa chain pre
37	422	75.5	106 2	PS0070 Ig kappa chain V r
38	422	75.5	106 2	G27867 Ig kappa chain V r
39	421	75.3	105 2	S26338 Ig kappa chain V r
40	421	75.3	106 2	S29583 Ig kappa chain V r
41	421	75.3	107 2	S11117 Ig kappa chain V r
42	420	75.1	100 2	S29590 Ig kappa chain V r
43	420	75.1	129 1	KVMS7B Ig kappa chain pre
44	418	74.8	97 2	S26341 Ig light chain V r
45	418	74.8	102 2	S29582 Ig kappa chain V r

#### ALIGNMENTS

##### RESULT 1

PC4405 Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 10-Nov-1997 #sequence\_revision 23-Jan-1998 #text\_change 09-Jul-2004

C/Accession: PC4405

R/Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.

Chinese Biochem. J. 12, 648-653, 1996

A/Title: Generation of a phage display library of the immunoglobulin repertoire from hum

A/Reference number: PC4405

A/Accession: PC4405

A/Molecule type: mRNA

A/Residues: 1-107 <DEN>

A/Cross-references: UNIPROT:Q8K1F0; UNIPARC:UPI000017677B

A/Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 463; DB 2; Length 107;

Best Local Similarity 82.6%; Pred. No. 3.4e-32;

Matches 90; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

QY 1 DIETLOSPAIMSASPGKRVKTTTCASSVSISYICWYQKSGSRLLIYDTSNLSAGVP 60  
DB 1 DIETLOSPAIMSASPGKRVKTTTCASSSI--SYHWYQKSGSRKVIYDTSKLASVP 58

QY 61 VRFSGSGSTSYSLTIISMEADATYYCQWSSNPLTFGGSTKLELR 109  
DB 59 ARFGSGSGSTSYSLTIISMEADATYYCQWRDNPFTFGGKLELR 107

##### RESULT 2

A32513 Ig kappa chain precursor V region (MRL22) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000

R/Koffler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.R.; Noonan, D.J.; Duchosal, M.A.; I

U. Clin. Invest. 82, 852-860, 1988

A/Title: Immunoglobulin kappa light chain variable region gene complex organization and i

A/Reference number: A94689; MUID:88331394; PMID:3138286

A/Accession: A32513

A/Molecule type: DNA

A/Cross-references: UNIPARC:UPI0000114D9C; GB:M20834; NID:9196943; PID:AAA3846.1; PID:6

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 82.6%; Score 462; DB 2; Length 130;  
Best Local Similarity 85.0%; Pred. No. 5.1e-32;  
Matches 91; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Oy 2 ELTQSPAIMSAPGKRYTTTCRASSSVSSSYLGMVYQKPPSSPRLLIYDTSNLASGV 61  
 Db 24 IVLQSPAIMSAPGKRYTTTCRASSSVSSSYLGMVYQKPPSSPRLLIYDTSNLASGV 83  
 Oy 62 RFGSGSGSTSYSLTISRMEADATYYCCQMSNPDPFGSGTKLEK 108  
 Db 84 RFGSGSGSTSYSLTISRMEADATYYCCQMSNPDPFGSGTKLEK 130  
 RESULT 3  
 A42848  
 Ig light chain V region - mouse (fragment)  
 N:Alternate names: I6 anti-tumor antibody  
 C:Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: A42848, S33502  
 R:Feil, H.P.; Gayle, M.A.; Yelton, D.; Lipetch, L.; Schieven, G.L.; Marken, J.S.; Aruffa  
 J. Biol. Chem. 267, 1552-1558, 1992  
 A:Title: Chimeric I6 anti-tumor antibody. Genomic construction, expression, and character  
 A:Reference number: A42848, MUID:92348410, PMID:1639794  
 A:Accession: A42848  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residue: 1-107 <FEU>  
 A:Cross-references: UNIPARC:UPI000011534; EMBL:M90690  
 A:Note: sequence extracted from NCBI backbone (NCBI:109958, NCBI:P:109959)  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: Immunoglobulin  
 F:16-89/Domain: Immunoglobulin homology <IMM>  
 Query Match 81.6%; Score 456; DB 2; Length 107;  
 Best Local Similarity 83.3%; Pred. No. 1,3e-31;  
 Matches 90; Conservative 8; Mismatches 8; Indels 2; Gaps 1;  
 Oy 2 IELTQSPAIMSAPGKRYTTTCRASSSVSSSYLGMVYQKPPSSPRLLIYDTSNLASGV 61  
 Db 2 IVLQSPAIMSAPGKRYTTTCRASSSV--SFMMVYQKPPSSPRPWYATSNLASGV 59  
 Oy 62 RFGSGSGSTSYSLTISRMEADATYYCCQMSNPDPFGSGTKLEK 109  
 Db 60 RFGSGSGSTSYSLTISRMEADATYYCCQMSNPDPFGSGTKLEK 107  
 RESULT 4  
 866536  
 Ig light chain V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
 C:Accession: S66536  
 R:Stoltz, G.; Haase, W.; Engel, A.; Michel, H.  
 Eur. J. Biochem. 231, 823-830, 1995  
 A:Title: Isolation and structural characterization of trimeric cyanobacterial photosyste  
 A:Reference number: S66536, MUID:95377318, PMID:7649183  
 A:Accession: S66536  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-120 <TSA>  
 A:Cross-references: UNIPARC:UPI0000113780; EMBL:X88903; NID:9895870; PIDD:CAA61365.1; P  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 F:16-91/Domain: Immunoglobulin homology <IMM>  
 Query Match 81.4%; Score 455; DB 2; Length 120;  
 Best Local Similarity 80.7%; Pred. No. 1.1e-31;  
 Matches 88; Conservative 6; Mismatches 15; Indels 0; Gaps 0;  
 Oy 1 DIELTQSPAIMSAPGKRYTTTCRASSSVSSSYLGMVYQKPPSSPRLLIYDTSNLASGV 60  
 Db 1 DIELTQSPAIMSAPGKRYTTTCRASSSVSSSYLGMVYQKPPSSPRLLIYDTSNLASGV 60  
 Oy 61 VRFGSGSGSTSYSLTISRMEADATYYCCQMSNPDPFGSGTKLEK 109  
 Db 61 VRFGSGSGSTSYSLTISRMEADATYYCCQMSNPDPFGSGTKLEK 109

RESULT 5

Ig kappa chain precursor V region - mouse

B32456

CISpecies: Mus musculus (house mouse)

CIDate: 26-Oct-1989 #sequence revision 26-Oct-1989 #text\_change 21-Jan-2000

CAccession: B32456

R.Dombrik-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedayk, W.D.; Vose Jr., E.W.

J. Biol. Chem. 264, 4513-4522, 1989

Article: Variable region primary structures of a high affinity anti-fluorescein immunoglobulin

A.Reference number: A32456; MUID:89174706; PMID:2494173

A.Accession: B32456

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-130 <DOM>

A.Cross-references: UNIPARC:UPI0000114899; GB:J04610; NID:9556313; PIDN:AAA50296.1; PID:9556313

C.Keywords: heterotetramer; immunoglobulin

F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 453; DB 2; Length 130;

Best local similarity 84.8%; Pred. No. 2e-31;

Matches 89; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

RESULT 6

S04573

Ig kappa chain precursor V region (MRL-histone 7L) - mouse (fragment)

CISpecies: Mus musculus (house mouse)

CIDate: 04-Dec-1992 #sequence revision 04-Dec-1992 #text\_change 21-Jan-2000

CAccession: S04573

R.Kotler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Theodorsson, E.

Article: Molecular analysis of the murine lupus-associated anti-self response: involvement of a

A.Reference number: S04573; MUID:87133856; PMID:3102255

A.Accession: S04573

A.Molecule type: mRNA

A.Residues: 1-130 <KOP>

A.Cross-references: UNIPARC:UPI0000115DFE; EMBL:X14620; NID:952031; PIDN:CAA32773.1; PID:952031

A.Note: the authors translated the codon AGC for residue 47 as Asn

C.Keywords: immunoglobulin V region; immunoglobulin homology

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-130/Product: Ig kappa chain V region (fragment) #status predicted <MAT>

F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 453; DB 2; Length 130;

Best local similarity 83.2%; Pred. No. 2.9e-31;

Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

RESULT 7

A30562

Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse

CISpecies: Mus musculus (house mouse)

CIDate: 23-Mar-1989 #sequence revision 23-Mar-1989 #text\_change 21-Jan-2000

2 IELTSPAIMSASPEKVTTCRASSSVSSSYIGYQKPGSSPRLLIYTSNLASGVPA 61

Db 24 IVLTPSPAIMSASPEKVTTCRASSSVSSSYIGYQKPGSSPRLLIYTSNLASGVPA 83

QY 62 RFSGGSGTSTSLTISRMBAEDATYTCQOWSSNPITFGSGTGLTEIK 108

Db 84 RFSGGSGTSTSLTISRVBAEDATYTCQOWSSNPITFGSGTGLTEIK 130

J. Siskander, S.K.; Borden, P.; Grunezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.  
J. Immunol. 142, 888-893, 1989  
A>Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site  
A/Reference number: A30562; MUID:89110066; PMID:2464031  
A/Accession: A30562  
A>Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-107 <SIK>  
A/Cross-references: UNIPARC:DPI00001767B0  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:16-89/Domain: immunoglobulin homology <IMV>

Query Match 80.9%; Score 452; DB 2; Length 107;  
Best Local Similarity 83.3%; Pred. No. 2.9e-31;  
Matches 90; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

2 IELTSPALMSAPGGRKVTTTCRASSSVSSSYLGWYOOKPPSGPRLITYDTSNLASGVV 61  
|||||  
2 IVLTSPALMSAPGGRKVTTCSASSV--SYMHWYOKSGTSPRWIYDTSKLASGVA 59  
|||||

62 RPSGGSGGTSTSTISRMEDATATYYCCQWSSNPITFGSGTKLELR 109  
60 RPSSGSGGTSTSTISMEDATATYYCCQWSSNPITFGSGTKLEIKR 107  
|||||

RESULT 8  
S03410  
Ig kappa chain precursor V region (ABE8) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C/Accession: S03410  
R/Selning, E.; Vosr, J.; Storb, U.  
Nucleic Acids Res. 12, 4229-4246, 1984  
A>Title: Immunoglobulin gene 'remnant' DNA - implications for antibody gene recombination  
A/Reference number: S03410; MUID:84221356; PMID:6328416  
A/Accession: S03410  
A/Molecule type: DNA  
A/Residues: 1-113 <SEL>  
A/Cross-references: UNIPARC:UPI00001767BE; EMBL:X00651  
A/Note: this sequence was determined from the nonfunctional differentiated gene C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F:1-6/Domain: signal sequence (fragment) #status predicted <SIG>  
F:7-113/Product: Ig kappa chain V region ABE8 #status predicted <MAT>  
F:22-97/Domain: immunoglobulin homology <IMV>

Query Match 80.9%; Score 452; DB 2; Length 113;  
Best Local Similarity 83.5%; Pred. No. 3e-31;  
Matches 91; Conservative 6; Mismatches 10; Indels 2; Gaps 1;

1 DIELTSPALMSAPGGRKVTTTCRASSSVSSSYLGWYOOKPPSGPRLITYDTSNLASGVV 60  
|||||  
7 EIVLTSPALMSAPGGRKVTTCSASSSVSSSYLTWYOOKSGSPRLMYSINLASGVV 66  
|||||

61 VRFSGSGGTSTSTISRMEDATATYYCCQWSSNPITFGSGTKLELR 109  
67 ARFSGSGGTSTSTISMEDATATYYCCQWST--LTFGAQTKELEKR 113  
|||||

RESULT 9  
B30562  
Ig kappa chain V region (27.10.2) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
C/Accession: B30562  
R/Siskander, S.K.; Borden, P.; Grunezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.  
J. Immunol. 142, 888-893, 1989  
A>Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site  
A/Reference number: A30562; MUID:89110066; PMID:2464031  
A/Accession: B30562  
A>Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-107 <SIK>  
A:Cross-references: UNIPARC:UPI00001767BA  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match      80.7%; Score 451; DB 2; Length 107;  
Best Local Similarity    82.4%; Pred. No. 3,5e-31;  
Matches    89; Conservative    5; Mismatches    12; Indels    2; Gaps    1;

OY      2 IELTSPAIMSAPGEKVTTTCGRASSVSSTYLGMVQOKRGSPLLIDTSNLASGVPV 61  
         |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB    2 IVLTGPSAIMSAPGEKVTTMTCSASSV--SYWHMYQQSGKTSPKRWVDITSLASGVPT 59

OY      62 RPSGGSGSTYSLTSRMKEADPATYYCCQMSSNPFTPGSGTLDELKR 109  
         |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB    60 RPSGGSGSTYSLTSRMKEADPATYYCCQMSSNPFTPGSGTLDELKR 107

RESULT 10  
JL0079  
Ig kappa chain precursor V region (anti-phenylloxazalone 6f6) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1991 #sequence revision 09-Aug-1996 #ext\_change 16-Jul-1999  
C:Accession: JL0079; A49044; B49044  
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, J.  
MOL. Immunol. 25, 859-865, 1988  
A>Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reactive V regions  
A:Reference number: JL0076; MWID:89096973; PMID:3211160  
A:Accession: JL0079  
A:Molecule type: mRNA  
A:Residues: 1-130 <KAA>  
A:Cross-references: UNIPARC:UPI000017371F; GB:M27792; NID:9197159  
A:Experimental source: mRNA clones for anti-phenylloxazalone antibody 6f6  
A>Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10 as Leu; the codon given for 1-Met (AGT) is inconsistent with the authors' translation  
R.Milstein, C.; Ewen, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gerhardt, B.  
Eur. J. Immunol. 22, 1627-1634, 1992  
A>Title: Non-random features of the repertoire expressed by the members of one V kappa gene family  
A:Reference number: A49044; MWID:92289826; PMID:1601044  
A:Molecule type: DNA  
A:Residues: 1-25 <ML>  
A:Cross-references: UNIPARC:UPI000011760C; GB:S37663; NID:g250214; PIDN:AAB22331.1; PID:g250214  
A>Note: sequence extracted from NCBI backbone (NCBIn:106802, NCBIRP:106809)  
A:Accession: B49044  
A:Molecule type: DNA  
A:Residues: 114-116 <ML2>  
A:Cross-references: UNIPARC:UPI000011E8E5; GB:S37664; NID:g250215; PIDN:AAB22332.1; PID:g250215  
A:Experimental source: BALB/c germ-line  
A>Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 additional sequences extracted from NCBI backbone (NCBIn:106807, NCBIRP:106822)  
C:Genetics:  
A:Gene: V(kappa)Ox1  
A:introns: 17/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-130/Product: Ig kappa chain V region (6f6) #status predicted <MAT>  
F:18-111/Domains: immunoglobulin homology <IMM>  
F:45-109/Disulfide bonds: #status predicted

Query Match      80.5%; Score 450; DB 1; Length 130;  
Best Local Similarity    83.3%; Pred. No. 5.1e-31;  
Matches    90; Conservative    4; Mismatches    12; Indels    2; Gaps    1;

OY      2 IELTSPAIMSAPGEKVTTTCGRASSVSSTYLGMVQOKRGSPLLIDTSNLASGVPV 61  
         |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
DB    2 IVLTGPSAIMSAPGEKVTTTCGRASSV--SYWHMYQQSGKTSPKRWVDITSLASGVPA 81



Qy 62 RFGSGSGTSTSLTISRMEADATYTCQWSSNPLTFGSGTKLELR 109  
 Db 82 RFGSGSGTSTSLTISRMEADATYTCQWSSNPLTFGSGTKLELR 129

## RESULT 11

S25058

Ig kappa chain - mouse

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000

C/Accession: S25058

R/Fischer, R.; Voss, A.; Nierbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.

Submitted to the EMBL Data Library, July 1992

A/Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m

A/Reference number: S25057

A/Accession: S25058

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-235 &lt;F18&gt;

A/Cross-references: UNIPARC:UPI0000116096; EMBL:X67211; NID:G54828; PIDN:CAA47650.1; PII

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/38-111/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 80.5%; Score 450; DB 2; Length 235;  
 Best Local Similarity 84.3%; Pred. No. 9.2e-31;  
 Matches 91; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

Qy 2 IELTOSPAIMASGKVTTCRASVSYSYLGMVQOKPGSSPRLIYDTSNLASGVP 61  
 Db 24 IVLQSPAIMASGKVTTCRASVSYSK--KMWYQOKSGTSPKRWIYDTSNLASGVP 81  
 Qy 62 RFGSGSGTSTSLTISRMEADATYTCQWSSNPLTFGSGTKLELR 109  
 Db 82 RFGSGSGTSTSLTISRMEADATYTCQWSSNPLTFGSGTKLELR 129

## RESULT 12

S29591

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C/Accession: S29591

R/Kavaler, J.

Submitted to the EMBL Data Library, April 1991

A/Reference number: S26459

A/Accession: S29591

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-103 &lt;KAV&gt;

A/Cross-references: UNIPARC:UPI0000115F57; EMBL:X59094; NID:G52227; PIDN:CAA41820.1; PII

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-88/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 79.8%; Score 446; DB 2; Length 103;  
 Best Local Similarity 84.8%; Pred. No. 8.8e-31;  
 Matches 89; Conservative 4; Mismatches 10; Indels 2; Gaps 1;

Qy 2 IELTOSPAIMASGKVTTCRASVSYSYLGMVQOKPGSSPRLIYDTSNLASGVP 61  
 Db 1 IVLQSPAIMASGKVTTCRASVSYSV--SYMWYQOKSGTSPKRWIYDTSNLASGVP 58  
 Qy 62 RFGSGSGTSTSLTISRMEADATYTCQWSSNPLTFGSGTKLELR 106  
 Db 59 RFGSGSGTSTSLTISRMEADATYTCQWSSNPLTFGSGTKLELR 103

## RESULT 13

S05269

Ig kappa chain precursor V-J region (38C13-V4) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Jan-2000

C/Accession: S05269; JI0064; S03847

R/Levy, S.  
 Submitted to the EMBL Data Library, February 1989

A/Reference number: S05267

A/Accession: S05269

A/Molecule type: mRNA

A/Residues: 1-123 &lt;LEV&gt;

A/Cross-references: UNIPARC:UPI0000115D8D; EMBL:X14099; NID:G52568; PIDN:CAA32261.1; PID:

J. Exp. Med. 168, 1607-1620, 1988

A/Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An explanat

A/Reference number: JI0061; NID:89035985; PMID:3141553

A/Accession: JI0064

A/Molecule type: mRNA

A/Residues: 1-121 &lt;CAR&gt;

A/Cross-references: UNIPARC:UPI0000176799; EMBL:X14099

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-13/Domain: signal sequence (fragment) #status predicted &lt;SID&gt;

F/14-123/Product: Ig kappa chain (fragment) #status predicted &lt;MAT&gt;

F/14-107/Domain: V region (V-kappa-4) &lt;VRE&gt;

F/29-104/Domain: immunoglobulin homology &lt;IMM&gt;

F/108-123/Domain: J region (J-kappa-4) (fragment) &lt;JRE&gt;

Query Match 79.8%; Score 446; DB 2; Length 123;  
 Best Local Similarity 79.8%; Pred. No. 1e-30;  
 Matches 87; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DIELTOSPAIMASGKVTTCRASVSYSYLGMVQOKPGSSPRLIYDTSNLASGVP 60  
 Db 14 IELTOSPAIMASGKVTTCRASVSYSNPLMHWYQOKPGSPRLIYDTSNLASGVP 73  
 Qy 61 VRFSGSGGTSTSLTISRMEADATYTCQWSSNPLTFGSGTKLELR 109  
 Db 74 ARFSGSGGTSTSLTISRMEADATYTCQWSSNPLTFGSGTKLELR 122

## RESULT 14

S29581

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C/Accession: S29581; S26477; S29589; B33730; S26476

R/Kavaler, J.

Submitted to the EMBL Data Library, April 1991

A/Reference number: S26459

A/Accession: S29581

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-108 &lt;KAV&gt;

A/Cross-references: UNIPARC:UPI00001150BD; EMBL:X59096; NID:G52199; PIDN:CAA41822.1; PID:

A/Accession: S26477

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-106 &lt;KA2&gt;

A/Cross-references: UNIPARC:UPI0000115F5D; EMBL:X59103; NID:G52213; PIDN:CAA41829.1; PID:

A/Accession: S29589

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 2-104 &lt;KA3&gt;

A/Cross-references: UNIPARC:UPI0000115F55; EMBL:X59092; NID:G52223; PIDN:CAA41818.1; PID:

R/Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Geathart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989

A/Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unij

A/Reference number: A33730; NID:89367325; PMID:2505260

A/Accession: B33730

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-96 &lt;LAW&gt;

A/Cross-references: UNIPARC:UPI0000114B56; GB:M25998; NID:G197113; PIDN:AAA3913.1; PID:

C/Note: the authors translated the codon ATT for residue 2 as Ala

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-91/Domain: immunoglobulin homology &lt;IMM&gt;





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55 ; Search time 161.304 Seconds  
(without alignments)  
476.756 Million cell updates/sec

Title: US-10-632-706-88  
Perfect score: 559  
Sequence: 1 DIELOSPAINASPGKRYT.....QQSSNPITFGSGTKLEIKR 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	474	84.8	106	Q9U410_MOUSE
2	468	83.7	114	Q8K1F1_MOUSE
3	463.5	82.9	131	Q811C3_MOUSE
4	461	82.5	108	KV6K_MOUSE
5	461	82.5	112	Q8K1F2_MOUSE
6	450	80.5	235	Q58BV6_MOUSE
7	447	80.0	235	Q5XYF8_MOUSE
8	445	79.6	107	KV6F_MOUSE
9	440	78.7	107	KV6I_MOUSE
10	439	78.5	107	KV6H_MOUSE
11	439	78.5	112	Q8K1F3_MOUSE
12	438	78.4	107	KV6G_MOUSE
13	438	78.4	107	KV6J_MOUSE
14	438	78.4	237	Q569Y8_MOUSE
15	433	77.5	112	Q8K1F0_MOUSE
16	431	77.1	134	Q8VDD0_MOUSE
17	420	75.1	129	KV4A_MOUSE
18	408	73.0	109	Q9UL78_HUMAN
19	401.5	71.8	97	Q9UL76_MOUSE
20	399.5	71.5	101	Q9UL78_MOUSE
21	397	71.0	129	KV3I_HUMAN
22	395	70.7	107	KV6B_MOUSE
23	394	70.5	107	KV6C_MOUSE
24	394	70.5	129	KV3K_HUMAN
25	393	70.3	109	KV3D_HUMAN
26	391	69.9	107	KV6D_MOUSE
27	390	69.8	107	KV6E_MOUSE
28	389	69.8	109	KV3B_HUMAN
29	389	69.8	109	KV3E_HUMAN
30	387	69.2	107	KV6A_MOUSE
31	383.5	68.6	236	Q6P1I8_HUMAN

32	382.5	68.4	235	2	Q6P1I7_HUMAN	Q6P1I7_homo sapien
33	380	68.0	235	2	Q6GMV9_HUMAN	Q6GMV9_homo sapien
34	379	67.8	109	2	Q9UL86_HUMAN	Q9UL86_homo sapien
35	376	67.3	109	1	KV3F_HUMAN	P01624_homo sapien
36	375	67.1	235	2	Q6PJF2_HUMAN	Q6PJF2_homo sapien
37	373	66.7	107	2	Q66SA9_HUMAN	Q66SA9_homo sapien
38	371.5	66.5	108	2	Q9UL77_HUMAN	Q9UL77_homo sapien
39	371.5	66.5	244	2	Q65ZC8_HUMAN	Q65ZC8_homo sapien
40	370.5	66.3	108	2	Q9UL70_HUMAN	Q9UL70_homo sapien
41	369.5	66.1	236	2	Q6P1T5_HUMAN	Q6P1T5_homo sapien
42	368.5	65.9	128	1	KV3A_HUMAN	P06311_homo sapien
43	368	65.8	108	1	KV3A_HUMAN	P01594_homo sapien
44	367.5	65.7	108	1	KV3B_HUMAN	P01594_homo sapien
45	367.5	65.7	108	2	Q9UL79_HUMAN	Q9UL79_homo sapien

## ALIGNMENTS

```

RESULT 1
Q9U410_MOUSE                                PRT; 106 AA.
ID Q9U410_MOUSE PRELIMINARY;
AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30
DE immunoglobulin light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12567627;
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Yu X.C., Xiong Y., Yin C.C.,
RA Huang H.L., Guan X.H.;
RT "Cloning and sequence analysis of the light chain variable region
RT gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma
RT japonicum.";
RL Zhongguo Ji Sheng Chong Xue Yu Ji Sheng Chong Bing Za Zhi
RL 18:257-259(2000).
RL EMBL: AF207620; AAF19434.1; -, Genomic DNA.
DR HSSP; P01679; 2FBJ.
DR SMR; Q9U410; 4-106.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER
FT 106
SQ SEQUENCE 106 AA; 11478 MW; F20F5444jBAE63B CRC64;

Query Match      84.8%; Score 474; DB 2; Length 106;
Best Local Similarity 90.5%; Pred. No. 1.1e-38;
Matches 95; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 4 LQSPAINASPGKRYTTCRASVSYSYLCMYOQKPPSSPRLLIYDTSNLASGVPRF 63
DB 4 LQSPAINASPGKRYTTCRASVSYSYLCMYOQKPPSSPRLLIYDTSNLASGVPRF 61
QY 64 SSGSGGTSYSLTISRMEADAATYYCOQNSNPITFGSGTKLEIK 108
DB 62 SSGSGGTSYSLTISRMEADAATYYCOQNTYPTFGSGTKLEIK 106

RESULT 2
Q8K1F1_MOUSE                                PRT; 114 AA.
ID Q8K1F1_MOUSE PRELIMINARY;
AC Q8K1F1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Act1-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Plaque S., Kari S., Nishiyama Y., Paul S.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Terrynek T., Avrameas S.;
RT "Two murine natural polyclonal autoantibodies are encoded by
RT nonmutated germ-line genes."
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
RA Tilieman D.M., Jon N.T., Hill R.J., Marion T.N.;
RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
RT selective B cell stimulation in (NZB x NZW)F1 mice."
RL J. Exp. Med. 176:761-779(1992).
DR EMBL; AF516284; AAM64202.1; -; Genomic_DNA.
DR PIR; A33933; A33933.
DR PIR; PH1058; PH1058.
DR HSBP; P01837; 25C8.
DR SMR; Q8K1F1; 2-114.
DR Ensembl; ENSMUSG0000058986; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT SEQUENCE 114 AA; 12163 MW; 8BD9833DBF3BFD1 CRC64;
SQ
Query Match 83.7%; Score 468; DB 2; Length 114;
Best Local Similarity 85.3%; Pred. No. 4.8e-38;
Matches 93; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
QY 1 DIELTOSPAIMASPGKRVTTTCRASSSVSSSYLGWYQOKGSSPRLIYDTSNLASGVP 60
DB 1 DIELTOSPAIMASPGKRVTTTCRASSSVSSSYLGWYQOKGSSPRLIYDTSNLASGVP 60
QY 61 VRFGSGSGTSYSLTISRMEABDAATYYCQWMSNP-LTFSGGTLELKR 109
DB 61 ARFSGSGSGTSYSLTISRMEABDAATYYCQWMSNP-LTFSGGTLELKR 109

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RL Mol. Immunol. 30:177-182(1993).
DR EMBL; D14629; BAA03482.1; -; mRNA.
DR HSBP; P01679; 2FBJ.
DR SMR; Q81C3; 23-131.
DR Ensembl; ENSMUSG0000058987; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Signal.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 >131 Immunoglobulin gamma-3 kappa chain.
FT NON TER 131
FT SEQUENCE 131 AA; 14083 MW; 5E83659546682E CRC64;
SQ
Query Match 82.9%; Score 463.5; DB 2; Length 131;
Best Local Similarity 86.1%; Pred. No. 1.6e-37;
Matches 93; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
QY 2 IELTOSPAIMASPGKRVTTTCRASSSVSSSYLGWYQOKGSSPRLIYDTSNLASGVP 61
DB 2 IELTOSPAIMASPGKRVTTTCRASSSVSSSYLGWYQOKGSSPRLIYDTSNLASGVP 61
QY 62 RFSGSGSGTSYSLTISRMEABDAATYYCQWMSNP-LTFSGGTLELKR 108
DB 84 RFSGSGSGTSYSLTISRMEABDAATYYCQWMSNP-LTFSGGTLELKR 131

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RESULT 4
KV6K MOUSE STANDARD; PRT; 108 AA.
ID KV6K MOUSE STANDARD; PRT; 108 AA.
AC P04945;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-JI region NQ2-6.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=687733;
RA Kaartinen M., Griffiths G.M., Martham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazoline and its early diversification."
RL Nature 304:320-324(1983).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X00746; AAA38691.1; -; mRNA.
DR HSBP; O91W12; 1AY1.
DR SMR; P04945; 1-108.
DR Ensembl; ENSMUSG0000062686; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 98 Complementarity-determining-3.
FT REGION 99 108 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON TER 108 108

```

SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;  
 Query Match 82.5%; Score 461; DB 1; Length 108;  
 Best Local Similarity 86.2%; Pred. No. 2.2e-37;  
 Matches 94; Conservative 5; Mismatches 6; Indels 4; Gaps 2;

QY 2 IELTQSPAIMSAPPEKVTTCRASSSVSSYLGMVQKPGSSPRLIYDTSNLSAGVPV 61  
 DB 2 ILLTQSPAIMSAPPGKVTMTCSASSV--SYMHWYQKPGSSPRLIYDTSNLSAGVPV 59

QY 62 RPSGSGSGTSYSLTISRMEADDAATYYCOQWSSNP--LTSPSGTLEIK 108  
 DB 60 RPSGSGSGTSYSLTISRMEADDAATYYCOQWSSNPPLTFAGTKLEIK 108

RESULT 5  
 Q8K1P2\_MOUSE PRELIMINARY; PRT; 112 AA.  
 ID Q8K1P2\_MOUSE PRELIMINARY; PRT; 112 AA.  
 AC Q8K1P2;  
 DT 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Antl-VI phase light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RX PubMed=2499887;  
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;  
 RA Zhou Y.-X., Teguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
 RA Submitted (May-2002) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BAUB/c; TISSUE=Hypermunized spleen;  
 RL Submitted (May-2002) to the EMBL/Genbank/DBJ databases.

QY 1 DIELTQSPAIMSAPPEKVTTCRASSSVSSYLGMVQKPGSSPRLIYDTSNLSAGVP 60  
 DB 1 ILLTQSPAIMSAPPGKVTMTCSASSV--SYMHWYQKPGSSPRLIYDTSNLSAGVP 58

QY 61 VPPSGSGSGTSYSLTISRMEADDAATYYCOQWSSNPPLTFAGTKLEIKR 109  
 DB 59 RPPSGSGSGTSYSLTISRMEADDAATYYCOQWSSNPPLTFAGTKLEIKR 107

RESULT 6  
 Q58EV6\_MOUSE PRELIMINARY; PRT; 235 AA.  
 ID Q58EV6\_MOUSE PRELIMINARY; PRT; 235 AA.  
 AC Q58EV6;  
 DT 10-MAY-2005 (Tremblrel. 30, Created)  
 DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)  
 DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)

DE Igk-C protein.  
 GN Name=Igk-C;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uadiri T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Boeak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalski M., Smallos D.B.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RG NIH MGC Project;  
 RL Submitted (Mar-2005) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BC091738; AAH91738.1; -, mRNA.  
 DR SMR; Q58EV6; 23-235.  
 DR GO; GO:0003823; F:antigen binding; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF07654; C1-sec; 1.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 SQ SEQUENCE 235 AA; 25719 MW; BEA84ABD2576252 CRC64;  
 Query Match 80.5%; Score 450; DB 2; Length 235;  
 Best Local Similarity 82.4%; Pred. No. 6.7e-36;  
 Matches 89; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

QY 2 IELTQSPAIMSAPPEKVTTCRASSSVSSYLGMVQKPGSSPRLIYDTSNLSAGVP 61  
 DB 24 ILLTQSPAIMSAPPGKVTMTCSAGV--SYMHWYQKPGSGSPKRWIYDTSNLSAGVP 81

QY 62 RPSGSGSGTSYSLTISRMEADDAATYYCOQWSSNPPLTFAGTKLEIKR 109  
 DB 82 RPSGSGSGTSYSLTISRMEADDAATYYCOQWSSNPPLTFAGTKLEIKR 129

RESULT 7  
 Q5XFY8\_MOUSE PRELIMINARY; PRT; 235 AA.  
 ID Q5XFY8\_MOUSE PRELIMINARY; PRT; 235 AA.  
 AC Q5XFY8;  
 DT 25-OCT-2004 (Tremblrel. 28, Created)  
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
 DE Hypothetical protein.

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OC NCBI_taxid=10090;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klusner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dichterman L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelman M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedlin T.B., Tothlynti S., Carrinot P., Prange C.,
RA Rata S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Valley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Bickelley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalske U., Smallus D.B.,
RA Schnerch A., Schein J.R., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Director MGC Project;
RA Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC084663; AA84663.1; -; mRNA.
RA SMR; Q5XY8; 23-235.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-sec; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25835 MW; 828E9ED277FDC667 CRC64;

Query Match 80.0%; Score 447; DB 2; Length 235;
Best Local Similarity 81.5%; Pred. No. 1,3e-35;
Matches 88; Conservative 8; Mismatches 10; Indels 2; Gaps 1;

QY 2 IELTQSPAINASASGKAVTTTCRASSSVSSSYLGWYQOKPSPRLIYDTSNLASGVV 61
DB 24 IVLSQSPAILSLGFGKAVTTCRASSSV--NYMNYQOKPSSSKPMYATSKLASGVV 81

QY 62 RFSGSGGTSYSLTISRMEADAAATYTCQWBSNPLTFGSGTKLELR 109
DB 82 RFSGSGGTSYSLTISRMEADAAATYTCQWBSNPLTFGAGTKLELR 129

RESULT 8
KV6F MOUSE STANDARD; PRT; 107 AA.
AC P04940;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DS Ig kappa chain V-VI region NQ2-17.4.1.
OS Mus musculus (Mouse).

```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OC NCBI_taxid=10090;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=63271467; PubMed=6877353;
RA Karcinen M., Griffiths G.M., Markham A.F., Milstien C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification."
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; K00735; AAA3680.1; -; mRNA.
CC HSSP; P01679; 2PBJ.
DR SMR; P04940; 1-107.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hydrionema; Immunoglobulin domain; Immunoglobulin V region.
RN
RP REGION 1 23
FT REGION 1 23 Complementarity-determining-1.
FT REGION 2 33 Complementarity-determining-1.
FT REGION 3 48 Framework-2.
FT REGION 4 55 Complementarity-determining-2.
FT REGION 5 87 Framework-3.
FT REGION 6 88 Framework-4.
FT REGION 7 96 Complementarity-determining-3.
FT REGION 8 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11561 MW; 6F694284BCFA8E6 CRC64;

Query Match 79.6%; Score 445; DB 1; Length 107;
Best Local Similarity 81.5%; Pred. No. 8e-36;
Matches 88; Conservative 7; Mismatches 11; Indels 2; Gaps 1;

QY 2 IELTQSPAINASASGKAVTTTCRASSSVSSSYLGWYQOKPSPRLIYDTSNLASGVV 61
DB 2 IVLTQSPAILSLGFGKAVTTCRASSSV--SYMNYQOKSGTSKPMYATSKLASGVV 59

QY 62 RFSGSGGTSYSLTISRMEADAAATYTCQWBSNPLTFGSGTKLELR 109
DB 60 RFSGSGGTSYSLTISRMEADAAATYTCQWBSNPLTFGAGTKLELR 107

RESULT 9
KV6I MOUSE STANDARD; PRT; 107 AA.
AC P04943;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DS Ig kappa chain V-VI region NQ6-8.3.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OC NCBI_taxid=10090;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=63271467; PubMed=6877353;
RA Karcinen M., Griffiths G.M., Markham A.F., Milstien C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification."
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.

```

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 CC removed.  
 -----

DR EMBL, K00740, AAA38685.1; -, mRNA.

DR HSSP, P01679, 2FBJ.

DR SMR, P04943, 1-107.

DR Ensembl, ENSMUSG00000062047, Mus musculus.

DR InterPro, IPR007110, Ig-like.

DR SMART, SM00406, IGV, 1.

DR PROSITE, PS50835, IG\_LIKE, 1.

KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.

FT REGION 1 23 Framework-1.

FT REGION 24 33 Complementarity-determining-1.

FT REGION 34 48 Framework-2.

FT REGION 49 55 Complementarity-determining-2.

FT REGION 56 87 Framework-3.

FT REGION 88 96 Complementarity-determining-3.

FT REGION 97 106 Framework-4.

FT DISULFID 23 87 By similarity.

FT NON TER 107 107

FT SEQUENCE 107 AA; 11573 MW; 6F694824ECFC8E6 CRC64;

Query Match 78.7%; Score 440; DB 1; Length 107;

Best Local Similarity 80.6%; Pred. No. 2.5e-35;

Matches 87; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 2 IELTSPAIMSASPEKVTTCRASSSVSSYLGWYQOKPSSPRLIYDTSNLASGVPV 61

DB 2 IVLTPSPAIMSASPEKVTTCRASSSVSSYLGWYQOKPSSPRLIYDTSNLASGVPV 59

QY 62 RPSGSGSGTYSILTSRMEADATYYCOQSSNPLTFGAGTKLEIKR 109

DB 60 RPSGSGSATYSILTSRMEADATYYCOQSSNPLTFGAGTKLEIKR 107

RESULT 10

ID KV6H MOUSE STANDARD; PRT; 107 AA.

AC P04942;

DT 13-AUG-1987 (rel. 05, Created)

DT 13-AUG-1987 (rel. 05, Last sequence update)

DT 10-MAY-2005 (rel. 47, Last annotation update)

DE Ig kappa chain V-VI region NQ5-61.1.2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

NP NUCLEOTIDE SEQUENCE.

RA MEDLINE=83271467; PubMed=6877353;

RT Kaartman M., Griffiths G.M., Markham A.F., Mjellein C.;

RT "mRNA sequences define an unusually restricted Igg response to 2-

RT phenylloxazolone and its early diversification.";

RT Nature 304:320-324(1993).

CC 1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.

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CC removed.

CC EMBL, K00739, AAA38684.1; -, mRNA.

DR HSSP, P01679, 2FBJ.

DR SMR, P04942, 1-107.

DR Ensembl, ENSMUSG00000062047, Mus musculus.

DR InterPro, IPR007110, Ig-like.

DR InterPro, IPR003596, Ig\_V.

DR SMART, SM00406, IGV, 1.

DR PROSITE, PS50835, IG\_LIKE, 1.

KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.

FT REGION 1 23 Framework-1.

FT REGION 24 33 Complementarity-determining-1.

FT REGION 34 48 Framework-2.

FT REGION 49 55 Complementarity-determining-2.

FT REGION 56 87 Framework-3.

FT REGION 88 96 Complementarity-determining-3.

FT DISULFID 23 87 Framework-4.

FT NON TER 107 107 By similarity.

FT SEQUENCE 107 AA; 11605 MW; C46C4284ECFC8550 CRC64;

Query Match 78.5%; Score 439; DB 1; Length 107;

Best Local Similarity 80.6%; Pred. No. 3.1e-35;

Matches 87; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 2 IELTSPAIMSASPEKVTTCRASSSVSSYLGWYQOKPSSPRLIYDTSNLASGVPV 61

DB 2 IVLTPSPAIMSASPEKVTTCRASSSVSSYLGWYQOKPSSPRLIYDTSNLASGVPV 59

QY 62 RPSGSGSGTYSILTSRMEADATYYCOQSSNPLTFGAGTKLEIKR 109

DB 60 RPSGSGSATYSILTSRMEADATYYCOQSSNPLTFGAGTKLEIKR 107

RESULT 11

ID O8KIF3 MOUSE PRELIMINARY; PRT; 112 AA.

AC O8KIF3;

DT 01-OCT-2002 (TRENBLREL. 22, Created)

DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)

DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)

DE Anti-Vipase light chain variable region (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

NP NUCLEOTIDE SEQUENCE.

RA STRAIN=BA6/c; TISSUE=Hypertrophied spleen;

RT Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;

RT "Two murine natural polyreactive autoantibodies are encoded by

RT nonmutated germ-line genes.";

RT Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).

CC 13

CC NUCLEOTIDE SEQUENCE.

RA MEDLINE=92381444; PubMed=1512540; DOI=10.1004/jem.176.3.761;

RT Tjilman D.M., Jou N.T., Hill R.J., Marion T.N.;

RT "Both Igm and Igg anti-DNA antibodies are the products of clonally

RT selective B cell stimulation in (NZB x NZM)F1 mice.";

RT J. Exp. Med. 176:761-779(1992).

CC EMBL, AF516282; AF516282.1; -, Genomic DNA.

DR PIR, A33933; A33933.

DR PIR, P01085; P01085.

DR HSSP, P01837, 25C8.

DR SMR, O8KIF3, 2-112.

DR Ensembl, ENSMUSG00000063156, Mus musculus.

DR InterPro, IPR007110, Ig-like.

DR SMART, SM00406, IGV, 1.

DR PROSITE, PS50835, IG\_LIKE, 1.

FT NON TER 1 1

FT SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

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Query Match      78.5%; Score 439; DB 2; Length 112;
Best Local Similarity 81.7%; Pred. No. 3.3e-35;
Matches 89; Conservative 5; Mismatches 13; Indels 2; Gaps 1;

Qy 1 DIELTOSPAIMASPGKVTTCRASSSVSSYLGMVYQOKPGSSPRLIYDTSNLASGVP 60
Db 1 DVLTLQSPAIMASPGKVTTCRASSSVSSYLGMVYQOKPGSSPRLIYDTSNLASGVP 58
Qy 61 VRFSGSGGTSTSLTISRMEADATYYCOQMSNPFLFGSGTKLEKR 109
Db 59 ARFGSGSGTSTSLTISRMEADATYYCOQMSNPFLFGSGTKLEKR 107

RESULT 12
KV6G_MOUSE STANDARD; PRT; 107 AA.
ID KV6G_MOUSE
AC P04941;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NQ2-48.2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
CC -----
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CC removed.
CC -----
DR EMBL; K00737; AAA38682.1; -; mRNA.
DR HSBP; Q91W12; IAY1.
DR SMR; P04941; 1-103.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hydrion; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11557 MW; 72488DA9EF354934 CRC64;

Query Match      78.4%; Score 438; DB 1; Length 107;
Best Local Similarity 80.6%; Pred. No. 3.9e-35;
Matches 87; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

Qy 2 IELTOSPAIMASPGKVTTCRASSSVSSYLGMVYQOKPGSSPRLIYDTSNLASGVP 61
Db 2 ILTLQSPAIMASPGKVTTCRASSSVSSYLGMVYQOKPGSSPRLIYDTSNLASGVP 59
Qy 62 RFGSGSGTSTSLTISRMEADATYYCOQMSNPFLFGSGTKLEKR 109
Db 60 RFGSGSGTSTSLTISRMEADATYYCOQMSNPFLFGSGTKLEKR 107
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RESULT 13
KV6J_MOUSE STANDARD; PRT; 107 AA.
ID KV6J_MOUSE
AC P04944;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NQ5-78.2.6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
CC -----
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CC removed.
CC -----
DR EMBL; K00744; AAA38689.1; -; mRNA.
DR HSBP; Q91W12; IAY1.
DR SMR; P04944; 1-106.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hydrion; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11613 MW; A38290781F3C30D3 CRC64;

Query Match      78.4%; Score 438; DB 1; Length 107;
Best Local Similarity 80.6%; Pred. No. 3.9e-35;
Matches 87; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

Qy 2 IELTOSPAIMASPGKVTTCRASSSVSSYLGMVYQOKPGSSPRLIYDTSNLASGVP 61
Db 2 ILTLQSPAIMASPGKVTTCRASSSVSSYLGMVYQOKPGSSPRLIYDTSNLASGVP 59
Qy 62 RFGSGSGTSTSLTISRMEADATYYCOQMSNPFLFGSGTKLEKR 109
Db 60 RFGSGSGTSTSLTISRMEADATYYCOQMSNPFLFGSGTKLEKR 107

RESULT 14
Q569Y8_MOUSE PRELIMINARY; PRT; 237 AA.
ID Q569Y8_MOUSE
AC Q569Y8;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
```



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 [1]  
 RP NCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klusner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carroll P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.T., Skalska U., Smalins D.B.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Kidney;  
 RL NIH MGC Project;  
 RL Submitted (Apr-2005) to the EMBL/Genbank/DBJ databases.  
 DR EMBL, BC092251; AA92251.1; -, mRNA.  
 DR SMR, Q66978; 23-337.  
 DR InterPro: IPR003597; IG.  
 DR InterPro: IPR007110; IG-1like.  
 DR InterPro: IPR003597; IG-1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam, PF07654; CI-sect; 1.  
 DR SMART, SM00409; IG; 2.  
 DR SMART, SM00407; IG1; 1.  
 DR SMART, SM00406; IG; 1.  
 DR PROSITE, PS50835; IG LIKE; 2.  
 DR PROSITE, PS00290; IG\_MHC; UNKNOWN 1.  
 SQ SEQUENCE 237 AA; 25978 MW; A85596AA47FBB932 CRC64;

Query Match 78.4%; Score 438; DB 2; Length 237;  
 Best Local Similarity 78.0%; Pred. No. 1e-34;  
 Matches 85; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

OY 1 DIELTGSPAINASPGKVTTCRASSSVSSSYLGWYQKQKSSPRLLIYDTSNLASGVP 60  
 DB 23 BVLTLGSPALMAASPGKVTTCRASSSVSSSIDSSNLHMYQKQKSPKAWIYDTSNLASGVP 82  
 OY 61 VRFSGSGSTSYSLTISRMEADATYYCCQWSNPLTFGSGTKLEIKR 109  
 DB 83 RRFSGSGSTSYSLTISRMEADATYYCCQWSNPLTFGSGTKLEIKR 131

RESULT 15  
 OKLIFO\_MOUSE PRELIMINARY; PRT; 112 AA.

AC OKLIFO\_MOUSE  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Anti-Virapase 11ght chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NCLEOTIDE SEQUENCE.  
 RC STRAIN=BLB/c; TISSUE=Hyperimmunized spleen;  
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
 RL Submitted (May-2002) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP NCLEOTIDE SEQUENCE.  
 RC PubMed=2499887;  
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;  
 RT "Two murine natural polyreactive autoantibodies are encoded by  
 RT nonmutated germ-line genes."  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).  
 DR EMBL, AF516285; AA064203.1; -, Genomic DNA.  
 DR PIR, A33933; A33933.  
 DR PIR, PC4405; PC4405.  
 DR HSSP, P01837; 10R0.  
 DR SMR, OKLIFO; 3-112.  
 DR EMBL, ENSMUSG0000062047; Mus musculus.  
 DR InterPro: IPR007110; IG-1like.  
 DR InterPro: IPR003596; IG\_V.  
 DR SMART, SM00406; IG; 1.  
 DR PROSITE, PS50835; IG LIKE; 1.  
 FT NON\_TER 1  
 FT 112  
 SQ SEQUENCE 112 AA; 11901 MW; F6644663201AA239 CRC64;

Query Match 77.5%; Score 433; DB 2; Length 112;  
 Best Local Similarity 81.1%; Pred. No. 1.3e-34;  
 Matches 86; Conservative 4; Mismatches 14; Indels 2; Gaps 1;

OY 4 LTGSPAINASPGKVTTCRASSSVSSSYLGWYQKQKSSPRLLIYDTSNLASGVP 63  
 DB 4 LTGSPAINASPGKVTTCRASSSV--SYHMYQKQKSGTSPKAWIYDTSNLASGVP 61  
 OY 64 SGSGSGSTSYSLTISRMEADATYYCCQWSNPLTFGSGTKLEIKR 109  
 DB 62 SGSGSGSTSYSLTISRMEADATYYCCQWSNPLTFGSGTKLEIKR 107

Search completed: November 21, 2005, 12:04:06  
 Job time : 162.304 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:31 ; Search time 41.1245 Seconds  
(without alignments)  
219.131 Million cell updates/sec

Title: US-10-632-706-88

Perfect score: 559  
Sequence: 1 DIELTQSPAIMSASPEKVT.....QQMSNPFTFGSGTKELIKR 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: /cgnt2\_6/ptodata/1/1aa/5\_COMB.pep:\*  
2: /cgnt2\_6/ptodata/1/1aa/6\_COMB.pep:\*  
3: /cgnt2\_6/ptodata/1/1aa/7\_COMB.pep:\*  
4: /cgnt2\_6/ptodata/1/1aa/8\_COMB.pep:\*  
5: /cgnt2\_6/ptodata/1/1aa/9\_COMB.pep:\*  
6: /cgnt2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	86.6	110	2	US-09-126-219A-237
2	484	86.6	110	2	US-09-196-522-237
3	482	86.2	244	1	US-08-553-497A-20
4	481	86.0	110	2	US-09-126-219A-255
5	481	86.0	110	2	US-09-196-522-255
6	481	86.0	242	1	US-08-553-497A-26
7	481	86.0	242	1	US-08-553-497A-28
8	476	85.2	106	1	US-07-634-278-58
9	476	85.2	106	1	US-08-474-040-58
10	476	85.2	106	1	US-08-474-040-58
11	476	85.2	106	1	US-08-487-200-58
12	476	85.2	106	2	US-08-484-537-58
13	476	85.2	128	1	US-07-634-278-31
14	476	85.2	128	1	US-08-477-728-31
15	476	85.2	128	1	US-08-474-040-31
16	476	85.2	128	1	US-08-487-200-31
17	476	85.2	128	2	US-08-484-537-31
18	475	85.0	128	1	US-07-946-421-26
19	472	84.4	246	1	US-08-553-497A-24
20	471	84.3	108	2	US-09-126-219A-243
21	471	84.3	108	2	US-09-196-522-243
22	470	84.1	110	2	US-09-126-219A-256
23	470	84.1	110	2	US-09-196-522-256
24	469	83.9	108	2	US-09-948-004-28
25	469	83.9	107	2	US-09-948-004-18
26	468	83.7	107	1	US-08-211-202-3
27	468	83.7	110	2	US-09-126-219A-254

28	468	83.7	110	2	US-09-196-522-254	Sequence 254, App
29	468	83.7	246	1	US-08-469-486-57	Sequence 57, App1
30	468	83.7	246	1	US-08-469-658-57	Sequence 57, App1
31	467	83.5	108	2	US-09-126-219A-251	Sequence 251, App
32	467	83.5	108	2	US-09-196-522-251	Sequence 251, App
33	466	83.4	110	2	US-09-126-219A-250	Sequence 250, App
34	466	83.4	110	2	US-09-196-522-250	Sequence 250, App
35	464	83.0	244	1	US-08-553-497A-22	Sequence 22, App1
36	463.5	82.9	108	2	US-09-232-290-2	Sequence 2, App1
37	463	82.8	255	2	US-09-553-498-8	Sequence 8, App1
38	463	82.8	255	2	US-09-618-869-8	Sequence 8, App1
39	462	82.6	215	6	5455030-3	Sequence 9, App1
40	461	82.5	108	2	US-09-171-945-9	Sequence 9, App1
41	461	82.5	108	2	US-09-910-059-9	Sequence 9, App1
42	460	82.3	105	2	US-09-091-071-1	Sequence 1, App1
43	460	82.3	108	2	US-09-126-219A-253	Sequence 253, App
44	460	82.3	108	2	US-09-196-522-253	Sequence 253, App
45	460	82.3	110	2	US-09-126-219A-257	Sequence 257, App

#### ALIGNMENTS

RESULT 1  
US-09-126-219A-237  
Sequence 237, Application US/09726219A  
Patent No. 6806079  
GENERAL INFORMATION:  
APPLICANT: Cambridge Antibody Technology  
APPLICANT: Medical Research Council  
APPLICANT: McAfferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Johnson, Kevin  
APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew  
APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kasper  
APPLICANT: Marks, James  
APPLICANT: Jackson, Timothy  
APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory  
APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
FILE REFERENCE: 213839-00013  
CURRENT FILING DATE: 2000-11-28  
CURRENT APPLICATION NUMBER: US/09726,219A  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1990-11-12  
PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 237  
LENGTH: 110  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone

US-09-726-219A-237

Query Match 86.6%; Score 484; DB 2; Length 110;  
Best Local Similarity 86.2%; Pred. No. 7,36-39;  
Matches 94; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIELTOSPAIMASGPKKVTTCRASSSVSSYLGMVQOKPGSPRLLIYDTSNLASGVP 60  
DB 1 DIELTOSPAIMASGPKKVTTCRASSSVSSYLGMVQOKPGSPRLLIYDTSNLASGVP 60

QY 61 VRFGSGSGTSYSLTISRMEADATYYCCQWSSNPLTFSGTLEIKR 109  
DB 61 ARFGSGSGTSYSLTISRMEADATYYCCQYSGVPLTFGAGTLEIKR 109

RESULT 2  
US-09-196-522-237  
Sequence 237, Application US/09196522  
Patent No. 6916605

GENERAL INFORMATION:  
APPLICANT: Cambridge Antibody Technology  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Johnson, Kevin  
APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Giffiths, Andrew  
APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kasper  
APPLICANT: Marks, James  
APPLICANT: Clackson, Timothy  
APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory  
APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
FILE REFERENCE: 213839-0004  
CURRENT APPLICATION NUMBER: US/09/196,522  
CURRENT FILING DATE: 1998-11-28  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1990-11-12  
PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 237  
LENGTH: 110  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone  
US-09-196-522-237

Query Match 86.6%; Score 484; DB 2; Length 110;  
Best Local Similarity 86.2%; Pred. No. 7,36-39;  
Matches 94; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIELTOSPAIMASGPKKVTTCRASSSVSSYLGMVQOKPGSPRLLIYDTSNLASGVP 60  
DB 1 DIELTOSPAIMASGPKKVTTCRASSSVSSYLGMVQOKPGSPRLLIYDTSNLASGVP 60

DB 1 DIELTOSPAIMASGPKKVTTCRASSSVSSYLGMVQOKPGSPRLLIYDTSNLASGVP 60

QY 61 VRFGSGSGTSYSLTISRMEADATYYCCQWSSNPLTFSGTLEIKR 109  
DB 61 ARFGSGSGTSYSLTISRMEADATYYCCQYSGVPLTFGAGTLEIKR 109

RESULT 3  
US-08-553-497A-20  
Sequence 20, Application US/08553497A  
Patent No. 5844093

GENERAL INFORMATION:  
APPLICANT: KETTERBROUGH, C. A.  
APPLICANT: BRIDIG, MARY M.  
APPLICANT: ANSEL, KEITH H.  
APPLICANT: GUSOW, DETLEF  
APPLICANT: ADAM, JADME  
APPLICANT: MITJANS, FRANCESCA  
APPLICANT: ROSELI, ELISABET  
APPLICANT: BLASCO, FRANCESC  
APPLICANT: PILATS, JADME  
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZEILAND & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD, SUITE 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,497A  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/00978  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94104160.0  
FILING DATE: 17-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94118970.6  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1726  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-553-497A-20

Query Match 86.2%; Score 482; DB 1; Length 244;  
Best Local Similarity 89.1%; Pred. No. 2,86-38;  
Matches 98; Conservative 2; Mismatches 6; Indels 4; Gaps 2;

QY 1 DIELTOSPAIMASGPKKVTTCRASSSVSSYLGMVQOKPGSPRLLIYDTSNLASGVP 60  
DB 137 DIELTOSPAIMASGPKKVTTCRASSSV--SYMVYQOKPGSPRLLIYDTSNLASGVP 194  
QY 61 VRFGSGSGTSYSLTISRMEADATYYCCQWSSNPLTFSGTLEIKR 108

Db 195 VRFGSGSGTSTLTISRMEADATYYCQQRSSYPPLTFGAGTKLEIK 244

## RESULT 4

US-09-726-219A-255  
Sequence 255, Application US/09726219A  
Patent No. 6806079  
GENERAL INFORMATION:  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew  
APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kasper  
APPLICANT: Marks, James  
APPLICANT: Clackson, Timothy  
APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory  
APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
FILE REFERENCE: 213839-00013  
CURRENT APPLICATION NUMBER: US/09/726,219A  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1990-11-12  
PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 255  
LENGTH: 110  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone  
US-09-726-219A-255

Query Match 86.0%; Score 481; DB 2; Length 110;  
Best Local Similarity 87.2%; Pred. No. 1,4e-38;  
Matches 95; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTTCRASSSVSSYLGWYQOKPGSPRLIYDTISNLASGP 60  
DB 1 DIELTQSPAIMSASPGKVTTCRASSSVSSYLGWYQOKPGSPRLIYDTISNLASGP 60  
QY 61 VRFGSGSGTSTLTISRMEADATYYCQQRSSYPPLTFGAGTKLEIK 109  
DB 61 VRFGSGSGTSTLTISRMEADATYYCQQRSSYPPLTFGAGTKLEIK 109

## RESULT 5

US-09-196-522-255  
Sequence 255, Application US/09196522  
Patent No. 6916605

## GENERAL INFORMATION:

APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew  
APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kasper  
APPLICANT: Marks, James  
APPLICANT: Clackson, Timothy  
APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory  
APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
FILE REFERENCE: 213839-00004  
CURRENT APPLICATION NUMBER: US/09/196,522  
CURRENT FILING DATE: 1998-11-28  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 255  
LENGTH: 110  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone  
US-09-196-522-255

Query Match 86.0%; Score 481; DB 2; Length 110;  
Best Local Similarity 87.2%; Pred. No. 1,4e-38;  
Matches 95; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTTCRASSSVSSYLGWYQOKPGSPRLIYDTISNLASGP 60  
DB 1 DIELTQSPAIMSASPGKVTTCRASSSVSSYLGWYQOKPGSPRLIYDTISNLASGP 60  
QY 61 VRFGSGSGTSTLTISRMEADATYYCQQRSSYPPLTFGAGTKLEIK 109  
DB 61 VRFGSGSGTSTLTISRMEADATYYCQQRSSYPPLTFGAGTKLEIK 109

## RESULT 6

US-08-553-497A-26  
Sequence 26, Application US/08553497A  
Patent No. 5844093

## GENERAL INFORMATION:

APPLICANT: KETTERBOROUGH, C. A.  
APPLICANT: BENDIG, MARY M.  
APPLICANT: ANSELL, KEITH H.  
APPLICANT: GUSLOW, DETLEF  
APPLICANT: ADAM, JAUME  
APPLICANT: MITTANS, FRANSISC  
APPLICANT: ROSELL, ELISABET

```

/ APPLICANT: BLASCO, FRANCESC
/ APPLICANT: PIVATS, JAUME
/ TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
/ TITLES OF INVENTION: ANTIBODIES
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MILLEN, WHITE, ZEILANO & BRANIGAN, P.C.
/ STREET: 2200 CLARENDON BLVD, SUITE 1400
/ CITY: ARLINGTON
/ STATE: VA
/ COUNTRY: US
/ ZIP: 22201
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/553,497A
/ FILING DATE: 17-NOV-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/EP95/00978
/ FILING DATE: 16-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 94104160.0
/ FILING DATE: 17-MAR-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 94118970.6
/ FILING DATE: 02-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: HAMLET-KING, DIANA
/ REGISTRATION NUMBER: 33,302
/ REFERENCE/DOCKET NUMBER: MERCK 1726
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-243-6333
/ TELEFAX: 703-243-6410
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 242 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-553-497A-26

Query Match      86.0%; Score 481; DB 1; Length 242;
Best Local Similarity 88.9%; Pred. No. 3.5e-38;
Matches 96; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 1 DIETOSPAIMASPEKVTTCRASSSVSSSYLGWYQOKRGSSPRLIYDTSNLASGVP 60
DB 137 DIETOSPTIMASPGKVTMTCSDDSSVBTY--WYQOKTGSSPRLIYDTSNLASGVP 194

QY 61 VRFSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 108
DB 195 VRFSGSGSGTSTSLTISRMEADATYYCOQWSSYPLTFGAGTKLEIK 242

RESULT 7
US-08-553-497A-28
/ Sequence 28, Application US/08553497A
/ Patent No. 5844093
/ GENERAL INFORMATION:
/ APPLICANT: KETTLERBROUGH, C. A.
/ APPLICANT: BENDIG, MARY M.
/ APPLICANT: ANSELL, KEITH H.
/ APPLICANT: GUSOW, DETLEF
/ APPLICANT: ADAM, JAUME
/ APPLICANT: MITIANS, FRANCESC
/ APPLICANT: ROSELL, ELISABET
/ APPLICANT: BLASCO, FRANCESC
/ APPLICANT: PIVATS, JAUME
/ TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
```

```

/ TITLE OF INVENTION: ANTIBODIES
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MILLEN, WHITE, ZEILANO & BRANIGAN, P.C.
/ STREET: 2200 CLARENDON BLVD, SUITE 1400
/ CITY: ARLINGTON
/ STATE: VA
/ COUNTRY: US
/ ZIP: 22201
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/553,497A
/ FILING DATE: 17-NOV-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/EP95/00978
/ FILING DATE: 16-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 94104160.0
/ FILING DATE: 17-MAR-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 94118970.6
/ FILING DATE: 02-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: HAMLET-KING, DIANA
/ REGISTRATION NUMBER: 33,302
/ REFERENCE/DOCKET NUMBER: MERCK 1726
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-243-6333
/ TELEFAX: 703-243-6410
/ INFORMATION FOR SEQ ID NO: 28:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 242 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-553-497A-28

Query Match      86.0%; Score 481; DB 1; Length 242;
Best Local Similarity 88.9%; Pred. No. 3.5e-38;
Matches 96; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 1 DIETOSPAIMASPEKVTTCRASSSVSSSYLGWYQOKRGSSPRLIYDTSNLASGVP 60
DB 137 DIETOSPTIMASPGKVTMTCSDDSSV--BYWYQOKTGSSPRLIYDTSNLASGVP 194

QY 61 VRFSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 108
DB 195 VRFSGSGSGTSTSLTISRMEADATYYCOQWSSYPLTFGAGTKLEIK 242

RESULT 8
US-07-634-278-58
/ Sequence 58, Application US/07634278
/ Patent No. 5530101
/ GENERAL INFORMATION:
/ APPLICANT: QUEEN, Cary L.
/ APPLICANT: SCHREIBER, William P.
/ APPLICANT: LANDOLFI, Nicholas F.
/ APPLICANT: COSLING, Kathleen L.
/ APPLICANT: SELICK, Harold B.
/ TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
/ NUMBER OF SEQUENCES: 113
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourile and Crew
/ STREET: 379 Lytton Avenue
/ CITY: Palo Alto
/ STATE: California
```



APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-474-040-58

Query Match 85.2%; Score 476; DB 1; Length 106;  
Best Local Similarity 88.8%; Pred. No. 48-38; Indels 2; Gaps 1;  
Matches 95; Conservative 3; Mismatches 7;

QY 2 IELTQSPAINASAPGKVTTCRASSSVSSSYLGWYQKFGSSPRLIYDTSNLAGVPV 61  
DB 2 IVLTQSPAINASAPGKVTTCRASSSVSSSYLGWYQKFGSSPRLIYDTSNLAGVPV 59  
QY 62 RFGSGSGSYSLTISRMEADAATYYCQWMSNPITFGSGTLELK 108  
DB 60 RFGSGSGSYSLTISRMEADAATYYCQWMSNPITFGSGTLELK 106

RESULT 11  
US-08-487-200-58  
Sequence 58, Application US/08487200  
Patent No. 5693762  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,200  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-487-200-58

Query Match 85.2%; Score 476; DB 1; Length 106;  
Best Local Similarity 88.8%; Pred. No. 48-38; Indels 2; Gaps 1;  
Matches 95; Conservative 3; Mismatches 7;

QY 2 IELTQSPAINASAPGKVTTCRASSSVSSSYLGWYQKFGSSPRLIYDTSNLAGVPV 61  
DB 2 IVLTQSPAINASAPGKVTTCRASSSVSSSYLGWYQKFGSSPRLIYDTSNLAGVPV 59  
QY 62 RFGSGSGSYSLTISRMEADAATYYCQWMSNPITFGSGTLELK 108  
DB 60 RFGSGSGSYSLTISRMEADAATYYCQWMSNPITFGSGTLELK 106

RESULT 12  
US-08-484-537-58  
Sequence 58, Application US/08484537  
Patent No. 6180370  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Knoutie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,537  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-537-58

Query Match 85.2%; Score 476; DB 2; Length 106;  
Best Local Similarity 88.8%; Pred. No. 4e-38;  
Matches 95; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 2 IELTOSPAIMASPGKVTTCRASSVSSYLGMYYOQKPGSSPRLIYDTSNLASGVFV 61  
Db 2 IELTOSPAIMASPGKVTTCRASSVSSYLGMYYOQKPGSSPRLIYDTSNLASGVFV 59

Qy 62 RFGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLEK 108  
Db 60 RFGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGAGTKLEK 106

RESULT 13  
US-07-634-278-31  
Sequence 31, Application US/07634278  
Patent No. 5530101  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas P.  
APPLICANT: SELICK, Harold E.  
APPLICANT: COBLENZ, Kathleen L.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend Kourile and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-634-278-31

Query Match 85.2%; Score 476; DB 1; Length 128;  
Best Local Similarity 88.8%; Pred. No. 5e-38;  
Matches 95; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 2 IELTOSPAIMASPGKVTTCRASSVSSYLGMYYOQKPGSSPRLIYDTSNLASGVFV 61  
Db 24 IELTOSPAIMASPGKVTTCRASSVSSYLGMYYOQKPGSSPRLIYDTSNLASGVFV 81

Qy 62 RFGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLEK 108  
Db 82 RFGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGAGTKLEK 128

RESULT 14  
US-08-477-728-31  
Sequence 31, Application US/08477728  
Patent No. 5585089  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th floor  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,728  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 128 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-040-31

Query Match 85.2%; Score 476; DB 1; Length 128;  
Best Local Similarity 88.8%; Pred. No. 58-38;  
Matches 95; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 2 IELTOSPAIMASAPGKVTTCRASSSVSSYLGMVQKRPSSPRLLIYDTSNLASGVPV 61  
DB 24 IYLTOSPAIMASAPGKVTTCRASSSVSSYLGMVQKRPSSPRLLIYDTSNLASGVPV 81

QY 62 RFSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFSGSTKLELK 108  
DB 82 RFSGSGSGTSTSLTISRMEADATYYCOQWSTYPLTFGAGTKLELK 128

## RESULT 15

US-08-474-040-31  
Sequence 31, Application US/08474040  
Patent No. 5693761

## GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US

ZIP: 94301

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,040  
FILING DATE: 07-JUN-1995

## CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988

## ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2422  
FAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 31:

## SEQUENCE CHARACTERISTICS:

LENGTH: 128 amino acids  
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-474-040-31

Query Match 85.2%; Score 476; DB 1; Length 128;  
Best Local Similarity 88.8%; Pred. No. 58-38;  
Matches 95; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 2 IELTOSPAIMASAPGKVTTCRASSSVSSYLGMVQKRPSSPRLLIYDTSNLASGVPV 61  
DB 24 IYLTOSPAIMASAPGKVTTCRASSSVSSYLGMVQKRPSSPRLLIYDTSNLASGVPV 81

QY 62 RFSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFSGSTKLELK 108  
DB 82 RFSGSGSGTSTSLTISRMEADATYYCOQWSTYPLTFGAGTKLELK 128

Search completed: November 21, 2005, 12:07:36  
Job time : 41.1245 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: November 21, 2005, 11:50:51 / Search time 134.952 Seconds  
(without alignments)  
337.478 Million cell updates/sec

Title: US-10-632-706-88  
Perfect score: 559  
Sequence: 1 DIETQSPAINASGPKRVT.....QQWSSNPLTFGSGTKLELR 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues  
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559	100.0	109	4	US-10-632-706-88 Sequence 88, App1
2	518	92.7	107	4	US-10-632-706-87 Sequence 87, App1
3	518	92.7	109	3	US-09-144-886-91 Sequence 91, App1
4	500	89.4	107	3	US-09-144-886-78 Sequence 78, App1
5	494	88.4	107	3	US-09-144-886-75 Sequence 75, App1
6	492	88.0	107	4	US-10-632-706-75 Sequence 75, App1
7	491	87.8	107	5	US-10-895-135-46 Sequence 46, App1
8	489	87.5	129	4	US-10-344-779-2 Sequence 2, App1
9	489	87.5	129	4	US-10-738-809-2 Sequence 2, App1
10	486	86.9	107	4	US-09-144-886-90 Sequence 90, App1
11	485	86.9	107	3	US-09-144-886-90 Sequence 90, App1
12	484	86.6	110	4	US-10-803-653-237 Sequence 237, App
13	484	86.6	110	4	US-10-803-653-237 Sequence 237, App
14	481	86.0	109	3	US-09-144-886-96 Sequence 96, App1
15	481	86.0	109	4	US-10-632-706-93 Sequence 93, App1
16	481	86.0	110	4	US-10-803-622-255 Sequence 255, App
17	481	86.0	110	4	US-10-803-653-255 Sequence 255, App
18	476	85.2	106	4	US-10-389-155-17 Sequence 17, App1
19	476	85.2	106	4	US-10-389-155-17 Sequence 17, App1
20	476	85.2	106	4	US-10-452-357-58 Sequence 58, App1
21	476	85.2	128	4	US-10-452-357-31 Sequence 51, App1
22	475	85.0	106	4	US-10-468-370-643 Sequence 643, App1
23	475	85.0	106	4	US-10-468-370-643 Sequence 643, App1
24	473	84.6	106	4	US-10-239-656-18 Sequence 18, App1
25	471.5	84.3	108	5	US-10-895-135-47 Sequence 47, App1
26	471	84.3	108	4	US-10-803-622-243 Sequence 243, App
27	471	84.3	108	4	US-10-803-653-243 Sequence 243, App

28	470	84.1	109	4	US-10-461-878-12 Sequence 12, App1
29	470	84.1	109	5	US-10-461-878-12 Sequence 12, App1
30	470	84.1	110	4	US-10-803-622-256 Sequence 256, App
31	470	84.1	110	4	US-10-803-693-256 Sequence 256, App
32	470	84.1	128	4	US-10-389-195-44 Sequence 44, App1
33	470	84.1	128	4	US-10-389-195-44 Sequence 44, App1
34	469	83.9	105	5	US-10-966-406-72 Sequence 72, App1
35	469	83.9	108	3	US-09-948-004-28 Sequence 28, App1
36	469	83.9	108	3	US-10-672-932-28 Sequence 28, App1
37	469	83.9	128	3	US-09-772-103-6 Sequence 6, App1
38	469	83.9	243	5	US-10-966-406-2 Sequence 2, App1
39	469	83.9	409	4	US-10-362-591-2 Sequence 59, App1
40	469	83.9	492	4	US-10-682-845-59 Sequence 61, App1
41	469	83.9	492	4	US-10-682-845-59 Sequence 61, App1
42	469	83.9	492	4	US-10-682-845-59 Sequence 63, App1
43	469	83.9	492	4	US-10-682-845-59 Sequence 65, App1
44	469	83.9	492	4	US-10-682-845-59 Sequence 67, App1
45	469	83.9	492	4	US-10-682-845-59 Sequence 69, App1

ALIGNMENTS

RESULT 1  
US-10-632-706-88  
Sequence 88, Application US/10632706  
Publication No. US20040175385A1  
GENERAL INFORMATION:  
APPLICANT: AMERSDORFER, PETER  
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
FILE REFERENCE: 407T-895120US  
CURRENT FILING DATE: 2003-08-01  
PRIOR FILING DATE: 2002-08-01  
PRIOR APPLICATION NUMBER: US 09/144,806  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 278  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 88  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: single chain antibody  
US-10-632-706-88  
Query Match 100.0%; Score 559 / DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 3.5e-40;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DIETQSPAINASGPKRVTTCRASSVS6YLGMVQCKPSSPRLIYDTSNLASGVP 60  
DB 1 DIETQSPAINASGPKRVTTCRASSVS6YLGMVQCKPSSPRLIYDTSNLASGVP 60  
QY 61 VRFSGSGGTSTLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 109  
DB 61 VRFSGSGGTSTLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 109  
RESULT 2  
US-10-632-706-87  
Sequence 87, Application US/10632706  
Publication No. US20040175385A1  
GENERAL INFORMATION:  
APPLICANT: MARKS, JAMES D.  
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
FILE REFERENCE: 407T-895120US  
CURRENT FILING DATE: 2003-08-01  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 278  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 87  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: single chain antibody  
US-10-632-706-87

```
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-87
```

```
Query Match      92.7%; Score 518; DB 4; Length 107;
Best Local Similarity 94.5%; Pred. No. 1,1e-36;
Matches 103; Conservative 1; Mismatches 3; Indels 2; Gaps 1;
```

```
QY 1 DIELTOSPAIMASAPGKVTTCRASSSVSSSYLGWYQOKPGSPRLIYDTSNLSAGVP 60
DB 1 DIELTOSPAIMASAPGKVTTCRASSSV--SYMYTQOKPGSPRLIYDTSNLSAGVP 58
```

```
QY 61 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPFLTFGSGTKLEIKR 109
DB 59 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPFLTFGSGTKLEIKR 107
```

```
RESULT 3
US-09-144-886-91
; Sequence 91, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: 3H4 region VL epitope 2
US-09-144-886-91
```

```
Query Match      92.7%; Score 518; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 1,1e-36;
Matches 102; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 DIELTOSPAIMASAPGKVTTCRASSSVSSSYLGWYQOKPGSPRLIYDTSNLSAGVP 60
DB 1 DIELTOSPAIMASAPGKVTTCRASSSVSSSYLGWYQOKPGSPRLIYDTSNLSAGVP 60
```

```
QY 61 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPFLTFGSGTKLEIKR 109
DB 61 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPFLTFGSGTKLEIKR 109
```

```
RESULT 4
US-09-144-886-78
; Sequence 78, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: Botulinum Neurotoxins
```

```
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C1 region VL epitope 1
US-09-144-886-78
```

```
Query Match      89.4%; Score 500; DB 3; Length 107;
Best Local Similarity 91.7%; Pred. No. 3,7e-35;
Matches 100; Conservative 2; Mismatches 5; Indels 2; Gaps 1;
```

```
QY 1 DIELTOSPAIMASAPGKVTTCRASSSVSSSYLGWYQOKPGSPRLIYDTSNLSAGVP 60
DB 1 DIELTOSPAIMASAPGKVTTCRASSSV--SYMYTQOKPGSPRLIYDTSNLSAGVP 58
```

```
QY 61 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPFLTFGSGTKLEIKR 109
DB 59 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPFLTFGSGTKLEIKR 107
```

```
RESULT 5
US-09-144-886-75
; Sequence 75, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C15 region VL epitope 1
US-09-144-886-75
```

```
Query Match      88.4%; Score 494; DB 3; Length 107;
Best Local Similarity 89.9%; Pred. No. 1,2e-34;
Matches 98; Conservative 2; Mismatches 7; Indels 2; Gaps 1;
```

```
QY 1 DIELTOSPAIMASAPGKVTTCRASSSVSSSYLGWYQOKPGSPRLIYDTSNLSAGVP 60
DB 1 DIELTOSPAIMASAPGKVTTCRASSSVSSSYLGWYQOKPGSPRLIYDTSNLSAGVP 58
```

```
QY 61 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPFLTFGSGTKLEIKR 109
DB 59 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPFLTFGSGTKLEIKR 107
```

```
RESULT 6
US-10-632-706-75
; Sequence 75, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
```

CURRENT APPLICATION NUMBER: US/10/632.706  
 CURRENT FILING DATE: 2003-08-01  
 PRIOR APPLICATION NUMBER: US 60/400,721  
 PRIOR FILING DATE: 2002-08-01  
 PRIOR APPLICATION NUMBER: US 09/144,806  
 PRIOR FILING DATE: 1998-08-31  
 NUMBER OF SEQ ID NOS: 278  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 75  
 LENGTH: 107  
 TYPE: PRT  
 ORGANISM: Artificial  
 FEATURE:  
 OTHER INFORMATION: single chain antibody  
 US-10-632-706-75

Query Match 88.0%; Score 492; DB 4; Length 107;  
 Best Local Similarity 90.8%; Pred. No. 1.8e-34;  
 Matches 99; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Qy 1 DIELTQSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPSSPRLIYDTSNLSAGVP 60  
 Db 1 DIELTQSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPSSPRLIYDTSNLSAGVP 58

Qy 61 VRFSGSGGTSTSLTISRMEADATYYCOQWNSNPLTFGSGTKLELR 109  
 Db 59 VRFSGSGGTSTSLTISRMEADATYYCOQWNSYPLTFGAGTKLELR 107

RESULT 7  
 US-10-895-135-46  
 Sequence 46, Application US/10895135  
 Publication No. US20050123549A1

GENERAL INFORMATION:  
 APPLICANT: Immunogen, Inc.  
 APPLICANT: PAYNE, Gillian  
 APPLICANT: CHUN, Philip  
 APPLICANT: TAVARES, Daniel  
 TITLE OF INVENTION: A CA6 ANTIGEN-SPECIFIC CYTOTOXIC CONJUGATE AND METHODS OF USING  
 TITLE OF INVENTION: THE SAME  
 FILE REFERENCE: A8621  
 CURRENT APPLICATION NUMBER: US/10/895,135  
 CURRENT FILING DATE: 2004-07-21  
 PRIOR APPLICATION NUMBER: 60/488,447  
 PRIOR FILING DATE: 2003-07-21  
 NUMBER OF SEQ ID NOS: 63  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 46  
 LENGTH: 107  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-10-895-135-46

Query Match 87.8%; Score 491; DB 5; Length 107;  
 Best Local Similarity 88.1%; Pred. No. 2.1e-34;  
 Matches 96; Conservative 7; Mismatches 4; Indels 2; Gaps 1;

Qy 1 DIELTQSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPSSPRLIYDTSNLSAGVP 60  
 Db 1 DIELTQSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPSSPRLIYDTSNLSAGVP 58

Qy 61 VRFSGSGGTSTSLTISRMEADATYYCOQWNSNPLTFGSGTKLELR 109  
 Db 59 VRFSGSGGTSTSLTISRMEADATYYCOQWNSYPLTFGAGTKLELR 107

RESULT 8  
 US-10-344-779-2  
 Sequence 2, Application US/10344779  
 Publication No. US20030211106A1  
 GENERAL INFORMATION:  
 APPLICANT: SWEET, RAYMOND W.  
 APPLICANT: TORNETTA, MARK A.

APPLICANT: TRUNEH, ALEMESEGED  
 APPLICANT: WATTAM, TREVOR A.  
 TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES  
 TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS  
 FILE REFERENCE: GP50033  
 CURRENT APPLICATION NUMBER: US/10/344,779  
 CURRENT FILING DATE: 2003-02-17  
 PRIOR APPLICATION NUMBER: PCT/US01/26161  
 PRIOR FILING DATE: 2001-08-21  
 PRIOR APPLICATION NUMBER: US 60/226,524  
 PRIOR FILING DATE: 2000-08-21  
 PRIOR APPLICATION NUMBER: US 60/230,639  
 PRIOR FILING DATE: 2000-09-07  
 NUMBER OF SEQ ID NOS: 18  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 2  
 LENGTH: 129  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-10-344-779-2

Query Match 87.5%; Score 489; DB 4; Length 129;  
 Best Local Similarity 90.7%; Pred. No. 3.8e-34;  
 Matches 98; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 2 IELTQSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPSSPRLIYDTSNLSAGVP 61  
 Db 2 IELTQSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPSSPRLIYDTSNLSAGVP 59

Qy 62 RPSGSGGTSTSLTISRMEADATYYCOQWNSNPLTFGSGTKLELR 109  
 Db 60 RPSGSGGTSTSLTISRMEADATYYCOQWNSYPLTFGAGTKLELR 107

RESULT 9  
 US-10-738-809-2  
 Sequence 2, Application US/10738809  
 Publication No. US2004017117A1  
 GENERAL INFORMATION:  
 APPLICANT: SWEET, RAYMOND W.  
 APPLICANT: TORNETTA, MARK A.  
 APPLICANT: TRUNEH, ALEMESEGED  
 APPLICANT: WATTAM, TREVOR A.  
 TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES  
 TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS  
 FILE REFERENCE: GP50033  
 CURRENT APPLICATION NUMBER: US/10/738,809  
 CURRENT FILING DATE: 2003-12-17  
 PRIOR APPLICATION NUMBER: US/10/344,779  
 PRIOR FILING DATE: 2003-02-19  
 PRIOR APPLICATION NUMBER: PCT/US01/26161  
 PRIOR FILING DATE: 2001-08-21  
 PRIOR APPLICATION NUMBER: US 60/226,524  
 PRIOR FILING DATE: 2000-08-21  
 PRIOR APPLICATION NUMBER: US 60/230,639  
 PRIOR FILING DATE: 2000-09-07  
 NUMBER OF SEQ ID NOS: 18  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 2  
 LENGTH: 129  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-10-738-809-2

Query Match 87.5%; Score 489; DB 4; Length 129;  
 Best Local Similarity 90.7%; Pred. No. 3.8e-34;  
 Matches 98; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 2 IELTQSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPSSPRLIYDTSNLSAGVP 61  
 Db 2 IELTQSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPSSPRLIYDTSNLSAGVP 59

Qy 62 RPSGSGGTSTSLTISRMEADATYYCOQWNSNPLTFGSGTKLELR 109  
 Db 60 RPSGSGGTSTSLTISRMEADATYYCOQWNSYPLTFGAGTKLELR 107

```

Db
60 RFGSGSGTSLTISRMEADATYYCQMSNPLTFQAGTKLELR 107

```

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1      RESULT 10
2      US-10-632-706-72
3      / Sequence 72, Application US/10632706
4      / Publication No. US20040175385A1
5      / GENERAL INFORMATION:
6      / APPLICANT: MARKS, JAMES D.
7      / APPLICANT: AMERSOORER, PETER
8      / TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
9      / TITLE OF INVENTION: NEUROTOXINS
10     / FILE REFERENCE: 407T-895120US
11     / CURRENT APPLICATION NUMBER: US/10/632,706
12     / CURRENT FILING DATE: 2003-08-01
13     / PRIOR APPLICATION NUMBER: US 60/400,721
14     / PRIOR FILING DATE: 2002-08-01
15     / PRIOR APPLICATION NUMBER: US 09/144,806
16     / PRIOR FILING DATE: 1998-08-31
17     / NUMBER OF SEQ ID NOS: 278
18     / SOFTWARE: PatentIn version 3.2
19     / SEQ ID NO 72
20     / LENGTH: 107
21     / TYPE: PRT
22     / ORGANISM: Artificial
23     / FEATURE:
24     / OTHER INFORMATION: single chain antibody
25     / US-10-632-706-72

```

Query Match	86.9%	Score 486	DB 4	Length 107
Best Local Similarity	89.0%	Pred. No. 5	7e-34	
Matches	97	Conservative	2	Mismatches 8, Indels 2, Gaps 1

  

QY	1	DILTQSGALINSAPGKENTTTTCRASSVSASSYLCAWYQKQKSGSRLLIYDTSNLASGVP	60
	1	DIETQSGALINSAPGKENTTTTCRASSVSASSYLCAWYQKQKSGSRLLIYDTSNLASGVP	58
Db	1	DILTQSGALINSAPGKENTTTTCRASSVSASSYLCAWYQKQKSGSRLLIYDTSNLASGVP	58
QY	61	VRFGSGSGGTYSYLTITSMEDADATYYCCQWSSNPILTFGSGTKLELR	109
	61	VRFGSGSGGTYSYLTITSMEDADATYYCCQWSSNPILTFGSGTKLELR	107
Db	59	IRFGSGSGGTYSYLTITSMEDADATYYCCQWSSNPILTFGSGTKLELR	107

```

RESULT 11
US-09-144-886-90
/ Sequence 90, Application US/09144886
/ Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
/ TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144, 886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 90
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
/ OTHER INFORMATION: 3F4 region VL epitope 2
US-09-144-886-90

```

Query Match Similarity 86.8%; Score 485; DB 3; Length 107;  
Best Local Similarity 89.0%; Pred.No.6.9e-34;  
Matches 977 Conservative 2; Mismatched 8; Indels 2; Gaps 1;

Cy 1 DILTOSPAINSAAPGEKVTYTCRASSSVSSAYLAWYOOKQSSPRLLIYYTSNIASGVP 60  
|||||  
|||.....  
Db 1 DTETLOSAPAISAPGEEKVTCASASSVV--SYMMYVOOKQSSPRLRIYYTSNIASGVP 58  
|||||

**Qy** 61 VRFGSGSGTSYSLTISRMEADATYYCQOMSSNPLTFGSGTKLEIKR 109  
		:		
**Db** 59 VRFGSGSGTSYSLTISRMEADATYYCQOMSSYPPTFGGKTGLEIKR 107

```

1 RESULT 12
2 US-10-803-622-237
3 Sequence 237, Application US/10803622
4 Publication No. US2004015721A1
5 GENERAL INFORMATION:
6 APPLICANT: Cambridge Antibody Technology
7 APPLICANT: Cambridge Antibody Technology Limited
8 APPLICANT: Medical Research Council
9 APPLICANT: McCafferty, John
10 APPLICANT: Pope, Anthony
11 APPLICANT: Johnson, Kevin
12 APPLICANT: Hoogenboom, Hendricus
13 APPLICANT: Griffiths, Andrew
14 APPLICANT: Jackson, Ronald
15 APPLICANT: Holliger, Kasper
16 APPLICANT: Marks, James
17 APPLICANT: Clarkson, Timothy
18 APPLICANT: Chiswell, David
19 APPLICANT: Winter, Gregory
20 APPLICANT: Bonett, Timothy
21 TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
22 FILE REFERENCE: 13839-00013
23 CURRENT APPLICATION NUMBER: US/10/803,622
24 CURRENT FILING DATE: 2004-03-18
25 PRIOR APPLICATION NUMBER: GB 9015198.6
26 PRIOR FILING DATE: 1990-07-10
27 PRIOR APPLICATION NUMBER: GB 9022845.3
28 PRIOR FILING DATE: 1990-10-19
29 PRIOR APPLICATION NUMBER: GB 9022845.3
30 PRIOR FILING DATE: 1990-10-19
31 PRIOR APPLICATION NUMBER: GB 9024503.6
32 PRIOR FILING DATE: 1990-11-12
33 PRIOR APPLICATION NUMBER: GB 9104744.9
34 PRIOR FILING DATE: 1991-03-06
35 PRIOR APPLICATION NUMBER: GB 9110549.4
36 PRIOR FILING DATE: 1991-05-15
37 PRIOR APPLICATION NUMBER: PCT/GB91/01134
38 PRIOR FILING DATE: 1991-07-10
39 PRIOR APPLICATION NUMBER: US 07/971,857
40 PRIOR FILING DATE: 1993-01-08
41 PRIOR APPLICATION NUMBER: US 08/484,893
42 PRIOR FILING DATE: 1995-06-07
43 NUMBER OF SEQ ID NOS: 272
44 SOFTWARE: PatentIn version 3.1
45 SEQ ID NO 237
46 LENGTH: 110
47 TYPE: PRT
48 ORGANISM: Artificial Sequence
49 FEATURE:
50 OTHER INFORMATION: VL of scFv from mouse 1immunized with 2-phenyl-5-oxazolone
51 US-10-803-622-237

```

Query Match	86.6%	Score 484;	DB 4;	Length 110;
Best Local Similarity	86.2%	Pred. No. 8.7e-34;		
Matches 94; Conservative	7;	Mismatches 8;	Indels 0;	Gaps 0;

[illegible]

RESULT 13  
US-10-803-653-237

```
Sequence 237, Application US/10803653
Publication No. US20040157215A1
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Grifflths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 13839-00013
CURRENT APPLICATION NUMBER: US/10/803,653
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: Patent version 3.1
SEQ ID NO 237
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL of scfv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-237

Query Match      86.6%; Score 484; DB 4; Length 110;
Best Local Similarity 86.2%; Pred. No. 8.7e-34;
Matches 94; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIELTOSPAIMASPEKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 60
DB 1 DIELTOSPAIMASPEKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 60

QY 61 VRFSGSGGTSTSLTISRMEADDAATYYCOQWSSNPITFGSGTKLELR 109
DB 61 AAFSGSGGTSTSLTISRMEADDAATYYCOQWSSNPITFGSGTKLELR 109

RESULT 14
US-09-144-886-96
Sequence 96, Application US/09144886
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
FILE REFERENCE: 2500.117USO
```

```
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 96
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
OTHER INFORMATION: 1H6 region VL epitope 3
US-09-144-886-96

Query Match      86.0%; Score 481; DB 3; Length 109;
Best Local Similarity 86.2%; Pred. No. 1.6e-33;
Matches 94; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIELTOSPAIMASPEKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 60
DB 1 DIELTOSPAIMASPEKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 60

QY 61 VRFSGSGGTSTSLTISRMEADDAATYYCOQWSSNPITFGSGTKLELR 109
DB 61 VRFSGSGGTSTSLTISRMEADDAATYYCOQWSSNPITFGSGTKLELR 109

RESULT 15
US-10-632-706-93
Sequence 93, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: Patent version 3.2
SEQ ID NO 93
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody
US-10-632-706-93

Query Match      86.0%; Score 481; DB 4; Length 109;
Best Local Similarity 86.2%; Pred. No. 1.6e-33;
Matches 94; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIELTOSPAIMASPEKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 60
DB 1 DIELTOSPAIMASPEKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 60

QY 61 VRFSGSGGTSTSLTISRMEADDAATYYCOQWSSNPITFGSGTKLELR 109
DB 61 VRFSGSGGTSTSLTISRMEADDAATYYCOQWSSNPITFGSGTKLELR 109

Search completed: November 21, 2005, 12:33:34
Job time : 134.952 secs
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; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker
; OTHER INFORMATION: - scfv SS2 - cmyc/H186.
US-10-512-184-50
```

Query Match 76.4%; Score 427; DB 1; Length 615;  
Best Local Similarity 78.9%; Pred. No. 4,6e-19;

Matches 86; Conservative 7; Mismatches 14; Indels 2; Gaps 1;

```
QY 1 IEILTPAIVMSASPGKVTTCRASSSVSSYLGMVQOKPGSPRLIYDTSNLAGVPV 60
DB 482 DIVLFGSPVIMASPGKVTTCRASSSV--NYLWYQMKSGTSPKWIPTDTSNLAGVP 539
QY 61 VRFGSGSGTSTSLTISMEADATYYCCQWSSNPLTFGSGTKLEIKR 109
DB 540 VRFGSGSGTSTSLTISMEADATYYCCQWSSNPLTFGAGTKLEIKR 588
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## RESULT 3

```

US-11-174-186-1
; Sequence 1, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gilless, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: KS VK mouse
US-11-174-186-1
```

Query Match 74.1%; Score 414; DB 7; Length 106;  
Best Local Similarity 79.4%; Pred. No. 7,4e-19;

Matches 85; Conservative 4; Mismatches 16; Indels 2; Gaps 1;

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QY 2 IEILTPAIVMSASPGKVTTCRASSSVSSYLGMVQOKPGSPRLIYDTSNLAGVPV 61
DB 2 IEILTPAIVMSASPGKVTTCRASSSV--SYMLWYQMKSGTSPKWIPTDTSNLAGVP 59
QY 62 VRFGSGSGTSTSLTISMEADATYYCCQWSSNPLTFGSGTKLEIKR 108
DB 60 VRFGSGSGTSTSLTISMEADATYYCHQSGVPTFGGTKLEIKR 106
```

## RESULT 4

```

US-11-174-186-8
; Sequence 8, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gilless, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
```

```

; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: VK7 light chain
US-11-174-186-8
```

Query Match 72.6%; Score 406; DB 7; Length 106;  
Best Local Similarity 77.6%; Pred. No. 2,1e-18;

Matches 83; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

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QY 2 IEILTPAIVMSASPGKVTTCRASSSVSSYLGMVQOKPGSPRLIYDTSNLAGVPV 61
DB 2 IEILTPAIVMSASPGKVTTCRASSSV--SYMLWYQMKSGTSPKWIPTDTSNLAGVP 59
QY 62 VRFGSGSGTSTSLTISMEADATYYCCQWSSNPLTFGSGTKLEIKR 108
DB 60 VRFGSGSGTSTSLTISMEADATYYCHQSGVPTFGGTKLEIKR 106
```

## RESULT 5

```

US-11-174-186-42
; Sequence 42, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gilless, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: light chain
US-11-174-186-42
```

Query Match 72.6%; Score 406; DB 7; Length 213;  
Best Local Similarity 75.2%; Pred. No. 3,3e-18;

Matches 82; Conservative 7; Mismatches 18; Indels 2; Gaps 1;

```
QY 1 IEILTPAIVMSASPGKVTTCRASSSVSSYLGMVQOKPGSPRLIYDTSNLAGVPV 60
DB 1 IEILTPAIVMSASPGKVTTCRASSSV--SYMLWYQMKSGTSPKWIPTDTSNLAGVP 59
QY 61 VRFGSGSGTSTSLTISMEADATYYCCQWSSNPLTFGSGTKLEIKR 109
DB 59 VRFGSGSGTSTSLTISMEADATYYCHQSGVPTFGGTKLEIKR 107
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## RESULT 6

```

US-11-172-320-4
; Sequence 4, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Helmut
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
```

```
;; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
;; FILE REFERENCE: 1/1383
;; CURRENT APPLICATION NUMBER: US/11/172,320
;; PRIOR FILING DATE: 2005-06-30
;; PRIOR APPLICATION NUMBER: US/10/645,215
;; PRIOR FILING DATE: 2003-08-21
;; PRIOR APPLICATION NUMBER: EP 02 018 686.2
;; PRIOR FILING DATE: August 21, 2002
;; PRIOR APPLICATION NUMBER: US 60/405,956
;; PRIOR FILING DATE: August 26, 2002
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 213
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; OTHER INFORMATION: Humanised Murine Antibody Biwa 4 Light Chain
US-11-172-320-4
```

```
Query Match 72.5%; Score 405; DB 7; Length 213;
Best Local Similarity 70.6%; Pred. No. 3.8e-18;
Matches 77; Conservative 13; Mismatches 17; Indels 2; Gaps 1;
```

```
Qy 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
Db 1 EIVLTQSPATLSLSPGERATLSCASASSI--NYIYVQOKPGQAPRLIYDTSNLASGVP 58
```

```
Qy 61 VRFGSGSGTSTSLTISRMEDADATYYCOQWSSNPLTFGGGTKLEIKR 109
Db 59 ARFSGSGGTDFTLTISLSEPEDFAVYYCQWSSNPLTFGGGTKLEIKR 107
```

```
RESULT 7
US-11-174-186-9
;; Sequence 9, Application US/11174186
;; Publication No. US20050244418A1
;; GENERAL INFORMATION:
;; APPLICANT: Gillies, Stephen
;; APPLICANT: Lo, Kin-Ming
;; APPLICANT: Qian, Xiang
;; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
;; FILE REFERENCE: LEX-019
;; CURRENT APPLICATION NUMBER: US/11/174,186
;; CURRENT FILING DATE: 2005-07-01
;; PRIOR APPLICATION NUMBER: US 60/288,564
;; PRIOR FILING DATE: 2001-05-03
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 9
;; LENGTH: 106
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: VK8 light chain
US-11-174-186-9
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```
Query Match 71.7%; Score 401; DB 7; Length 106;
Best Local Similarity 75.0%; Pred. No. 4e-18;
Matches 81; Conservative 7; Mismatches 18; Indels 2; Gaps 1;
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```
Qy 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
Db 1 EIVLTQSPATLSLSPGERATLSCASASSI--SYMILYQOKPGSSPRLIYDTSNLASGVP 58
```

```
Qy 61 VRFGSGSGTSTSLTISRMEDADATYYCOQWSSNPLTFGGGTKLEIKR 108
Db 59 ARFSGSGGTDFTLTISLSEPEDFAVYYCQWSSNPLTFGGGTKLEIKR 106
```

```
RESULT 8
US-10-721-763-27
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```
;; Sequence 27, Application US/10721763
;; Publication No. US20050249729A1
;; GENERAL INFORMATION:
;; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
;; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
;; FILE REFERENCE: PH-1573-PCT
;; CURRENT APPLICATION NUMBER: US/10/721,763
;; PRIOR FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: JP2001-150213
;; PRIOR FILING DATE: 2001-05-18
;; PRIOR APPLICATION NUMBER: JP2001-243040
;; PRIOR FILING DATE: 2001-08-09
;; PRIOR APPLICATION NUMBER: JP2001-314489
;; PRIOR FILING DATE: 2001-10-11
;; NUMBER OF SEQ ID NOS: 45
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 27
;; LENGTH: 131
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-721-763-27
```

```
Query Match 71.3%; Score 398.5; DB 1; Length 131;
Best Local Similarity 69.1%; Pred. No. 6.3e-18;
Matches 76; Conservative 14; Mismatches 19; Indels 1; Gaps 1;
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```
Qy 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
Db 21 EIVLTQSPATLSLSPGERATLSCASQSV--SYLAWYQOKPGQAPRLIYDTSNLASGVP 80
```

```
Qy 61 VRFGSGSGTSTSLTISRMEDADATYYCOQWSSNPLTFGGGTKLEIKR 109
Db 81 DRFSGSGGTDFTLTISLSEPEDFAVYYCQWSSNPLTFGGGTKLEIKR 130
```

```
RESULT 9
US-10-721-763-31
;; Sequence 31, Application US/10721763
;; Publication No. US20050249729A1
;; GENERAL INFORMATION:
;; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
;; APPLICANT: KIRIN BEER TRAIL-R ANTIBODY
;; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
;; FILE REFERENCE: PH-1573-PCT
;; CURRENT APPLICATION NUMBER: US/10/721,763
;; CURRENT FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: JP2001-150213
;; PRIOR FILING DATE: 2001-05-18
;; PRIOR APPLICATION NUMBER: JP2001-243040
;; PRIOR FILING DATE: 2001-08-09
;; PRIOR APPLICATION NUMBER: JP2001-314489
;; PRIOR FILING DATE: 2001-10-11
;; NUMBER OF SEQ ID NOS: 45
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 31
;; LENGTH: 128
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-721-763-31
```

```
Query Match 70.8%; Score 395.5; DB 1; Length 128;
Best Local Similarity 69.7%; Pred. No. 9.2e-18;
Matches 76; Conservative 13; Mismatches 19; Indels 1; Gaps 1;
```

```
Qy 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
Db 21 EIVLTQSPATLSLSPGERATLSCASQSV--SYLAWYQOKPGQAPRLIYDTSNLASGVP 79
```

```
Qy 61 VRFGSGSGTSTSLTISRMEDADATYYCOQWSSNPLTFGGGTKLEIKR 109
Db 80 ARFSGSGGTDFTLTISLSEPEDFAVYYCQWSSNPLTFGGGTKLEIKR 128
```

```
RESULT 10
```

```
US-11-172-320-8
; Sequence 8, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Antibody BIWA 8 Light Chain
US-11-172-320-8

Query Match          70.7%; Score 395; DB 7; Length 213;
Best Local Similarity 68.8%; Pred. No. 1.4e-17;
Matches 75; Conservative 14; Mismatches 18; Indels 2; Gaps 1;

QY 1 DIELTOSPAIMASAPGKRVTTTCRASSSVSSSYLGWYQOKPGSSPRLLIYDTSNLASGVP 60
DB 1 EIVLTOSPAITLSAPGRATLSCASSSI--NYLYMQKRGQAPRLIYLTSTNLASGVP 58
61 VRFGSGSGTSTSLTISRMFEADAATYYCCQWMSNPILTFSGGTLEIK 109
DB 59 ARFGSGSGTDFTLTISLEPEDPAVYYCQWMSNPILTFGGTIVKEIK 107

RESULT 11
US-11-174-186-7
; Sequence 7, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Vks 1 light chain
US-11-174-186-7

Query Match          69.9%; Score 391; DB 7; Length 106;
Best Local Similarity 70.4%; Pred. No. 1.4e-17;
Matches 76; Conservative 11; Mismatches 19; Indels 2; Gaps 1;

QY 1 DIELTOSPAIMASAPGKRVTTTCRASSSVSSSYLGWYQOKPGSSPRLLIYDTSNLASGVP 60
DB 1 EIVLTOSPAITLSAPGRVTLTCSASSV--SYMLMYQKRGQAPKLLIFDTSNLASGIP 58
```

```
QY 61 VRFGSGSGTSTSLTISRMFEADAATYYCCQWMSNPILTFSGGTLEIK 108
DB 59 ARFGSGSGTDFTLTISLEPEDPAVYYCQWMSNPILTFGGTIVKEIK 106

RESULT 12
US-11-174-186-16
; Sequence 16, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS VK mouse
US-11-174-186-16

Query Match          69.6%; Score 389; DB 7; Length 106;
Best Local Similarity 73.8%; Pred. No. 1.9e-17;
Matches 79; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

QY 2 IELTOSPAIMASAPGKRVTTTCRASSSVSSSYLGWYQOKPGSSPRLLIYDTSNLASGVP 61
DB 2 IIVTOSPAITLSAPGRVITTCASSSV--SYMLMYQKRGQSPKPIIFTSTNLASGFPs 59
62 RFSGSGSGTSTSLTISRMFEADAATYYCCQWMSNPILTFSGGTLEIK 108
DB 60 RFSGSGSGTSTSLTISLEADAATYYCHORSGPYPTFGGTLEIK 106

RESULT 13
US-10-721-763-19
; Sequence 19, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: ANTI TRAIL-R ANTIBODY
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCF
; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-19

Query Match          69.3%; Score 387.5; DB 1; Length 129;
Best Local Similarity 67.9%; Pred. No. 2.6e-17;
Matches 74; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 1 DIELTOSPAIMASAPGKRVTTTCRASSSVSSSYLGWYQOKPGSSPRLLIYDTSNLASGVP 60
DB 1 EIVLTOSPAITLSAPGRVITTCASSSV--SYMLMYQKRGQAPKLLIFDTSNLASGIP 58
```

Db 21 EIVLTQSPATLSLSPGERATLSCRAQSV-SFLAWYQKPGQAPRLIYDASNRATGIP 79  
Qy 61 VRFGSGSGTSTSYLTISRMEADATYYCOQWSSNPITFGSGTKLELR 109  
Db 80 ARFGSGSGTDFTLTISLSEPEDFAVYYCQQRSDWPLTFGGTKVDIKR 128

## RESULT 14

US-11-174-186-15  
; Sequence 15, Application US/11174186  
; Publication No. US20050244418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Xiang  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT APPLICATION NUMBER: US/11/174,186  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: US 60/288,564  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 15  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Artificial  
; PEATIRE:  
; OTHER INFORMATION: KS de-immunized VK5  
US-11-174-186-15

Query Match 69.1%; Score 386; DB 7; Length 106;  
Best Local Similarity 71.0%; Pred. No. 2,7e-17;  
Matches 76; Conservative 11; Mismatches 18; Indels 2; Gaps 1;

Qy 2 IEIITQSPAIMSASPGKVTTCRASSSVSSYIGWYQKPGSSPRLIYDTSNLSGVF 61  
Db 2 ILITQSPALAVSPGSRATITCSASSV--SYWLWYQKPGSSPKFWIYDTSNLSGVF 59  
Qy 62 RFGSGSGTSTSYLTISRMEADATYYCOQWSSNPITFGSGTKLELR 108  
Db 60 RFGSGSGTSTSYLTISRMEADATYYCHQSGYPTFGGKIVELK 106

## RESULT 15

US-10-721-763-23  
; Sequence 23, Application US/10721763  
; Publication No. US20050249729A1  
; GENERAL INFORMATION:  
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY  
; FILE REFERENCE: PH-1573-PCT  
; CURRENT APPLICATION NUMBER: US/10/721,763  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: JP2001-150213  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: JP2001-243040  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: JP2001-314489  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-721-763-23

Query Match 68.2%; Score 381.5; DB 1; Length 129;  
Best Local Similarity 67.9%; Pred. No. 5.6e-17;  
Matches 74; Conservative 13; Mismatches 21; Indels 1; Gaps 1;  
Qy 1 DIEIITQSPAIMSASPGKVTTCRASSSVSSYIGWYQKPGSSPRLIYDTSNLSGVF 60

Db 21 EIVLTQSPATLSLSPGERATLSCRAQSV-SFLAWYQKPGQAPRLIYDASNRATGSP 79  
Qy 61 VRFGSGSGTSTSYLTISRMEADATYYCOQWSSNPITFGSGTKLELR 109  
Db 80 ARFGSGSGTDFTLTISLSEPEDFAVYYCQQRSDWPLTFGGTKVDIKR 128

Search completed: November 21, 2005, 12:33:50  
Job time : 2.09634 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:32 ; Search time 145.932 Seconds  
(without alignments)  
328.182 Million cell updates/sec

Title: US-10-632-706-89

Perfect score: 563  
Sequence: 1 DSEBLQSPPTWASPGSEKIT.....QQSSIPRTFGGRTKLIRK 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: Geneseq\_21: \*  
2: geneseqp1980s: \*  
3: geneseqp1990s: \*  
4: geneseqp2000s: \*  
5: geneseqp2001s: \*  
6: geneseqp2002s: \*  
7: geneseqp2003s: \*  
8: geneseqp2004s: \*  
9: geneseqp2005s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	563	100.0	109	8	ADR38687	Adx38687 Mouse I1g
2	548	97.3	109	2	AAU79864	AAU79864 Anti-EGFR
3	541	96.1	110	2	AAU71297	AAU71297 Murine VL
4	541	96.1	315	4	AAU70843	AAU70843 SNV-env 1
5	540	95.9	110	2	AAU71299	AAU71299 Murine VL
6	537	95.4	110	2	AAU71295	AAU71295 Murine VL
7	535	95.0	110	2	AAU71288	AAU71288 Murine VL
8	532	94.5	110	2	AAU71298	AAU71298 Murine VL
9	530	94.1	297	2	AAU70533	AAU70533 HBV speci
10	528	93.8	109	2	AAU79162	AAU79162 Human IGE
11	526	93.4	256	5	AAU72866	AAU72866 PS-3 b1ng
12	525	93.4	503	5	AAU72874	AAU72874 3B10xP5-2
13	525	93.3	109	8	ADR38693	ADR38693 Mouse I1g
14	521	92.5	110	2	AAU71300	AAU71300 Murine VL
15	521	92.5	239	2	AAU71963	AAU71963 Mouse scF
16	518	92.0	110	2	AAU71289	AAU71289 Murine VL
17	518	92.0	240	8	AAU59121	AAU59121 Anti-K88
18	517	91.8	109	2	AAU72516	AAU72516 Thyroid h
19	514	91.3	137	9	AAU7084	AAU7084 Light cha
20	510	90.6	136	9	AAU7086	AAU7086 Light cha
21	508	90.2	110	2	AAU71296	AAU71296 Murine VL
22	508	90.2	136	9	AAU7090	AAU7090 Light cha
23	508	90.2	136	9	AAU7088	AAU7088 Light cha
24	508	90.2	138	9	AAU7082	AAU7082 Light cha

25	508	90.2	138	9	AAU7094	AAU7094 Light cha
26	507	90.1	245	2	AAU25783	AAU25783 Anti-T3 a
27	502	89.2	110	8	AAU25837	AAU25837 Anti-CD30
28	496	88.1	103	2	AAU705362	AAU705362 HBV speci
29	495	87.9	138	9	AAU7092	AAU7092 Light cha
30	494	87.7	109	8	AAU71908	AAU71908 Humanised
31	458	81.3	108	2	AAU70440	AAU70440 Anti-DNA
32	451	80.1	122	2	AAU25958	AAU25958 ICAW-1 in
33	450	79.9	109	8	AAU38686	AAU38686 Mouse I1g
34	446	79.2	109	6	AAU63531	AAU63531 Anti-cucu
35	445	79.0	110	2	AAU21306	AAU21306 Murine VL
36	445	79.0	110	2	AAU21305	AAU21305 Murine VL
37	444	78.9	107	8	AAU38685	AAU38685 Mouse I1g
38	444	78.9	242	6	AAU62132	AAU62132 Single ch
39	444	78.9	242	8	AAU71209	AAU71209 Single ch
40	443	78.7	108	3	AAU59306	AAU59306 DC8 Light
41	443	78.7	109	8	AAU59678	AAU59678 CPAM4 VR
42	443	78.7	109	8	AAU59707	AAU59707 Chimeric
43	443	78.7	951	3	AAU44993	AAU44993 DC8scFv-e
44	442	78.5	108	3	AAU97236	AAU97236 Variable
45	442	78.5	108	4	AAU82710	AAU82710 VEGF anta

#### ALIGNMENTS

RESULT 1  
ADR38687  
ID ADR38687 standard; peptide; 109 AA.  
XX  
AC ADR38687;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Mouse light chain variable region scFv seqid 89.  
XX  
KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
KW light chain variable region; single chain antibody; scFv.  
XX  
OS Mus sp.  
XX  
PN US2004175385-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 01-AUG-2003; 2003US-00632706.  
XX  
PR 31-AUG-1998; 98US-00144886.  
PR 01-AUG-2002; 2002US-0400721P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Marks JD, Amersdorfer P;  
XX  
XX WPI; 2004-652009/63.  
XX  
PS New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
XX  
XX Example 1; SEQ ID NO 89; 110pp; English.  
XX  
CC The invention describes an isolated antibody (I) that specifically binds  
CC to an epitope specifically bound by an antibody expressed by a specific  
CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
CC (BoNT/A). An isolated antibody (II) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone  
CC S25, C25, C39, I6, 3D12, B4, 1F3, huC25, Ar1, Ar2, W1(V), W1(T), 3-1,  
CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
CC comprising BoNT/A neutralising epitope having an epitope that is





CC The VK sequence is one of 23 (AAR21286-308) expressed from a single chain  
 CC Fv library. The library produces a diverse repertoire of antibody  
 CC fragments specific for 2-phenyl-5-oxazolone (pHox). It was prepd. using  
 CC cDNA generated from mRNA from mice immunised with pHox coupled to chick  
 CC serum albumin. The VH and VL kappa sequences were separately amplified by  
 CC PCR (AAQ23474-84) and ligated into fdCAT7 (AAQ23463) for expression on  
 CC the phage surface as fusions with gene III. The resulting library of  
 CC clones was diverse; 23 hapten binding clones were sequenced revealing 8  
 CC VH genes (A-H; AAR21264-71) in a variety of pairings with 7 VK genes (a-g  
 CC / AAR21286-92). Most clones were VH-B combinations so a further  
 CC hierarchical library was prepd. by "crossing" VH-B with the VK  
 CC repertoire. The resulting library was screened for hapten binding and 24  
 CC clones sequenced. 14 new partners (AAR21293-308) for VH-B were  
 CC identified. Nearly all the VK genes were "ox-like", only f, (from the  
 CC original library) and h, p, q, and r (from the hierarchical library) were  
 CC Vhok1 type genes. Of the 24 hierarchical clones, only one was of type  
 CC "1". The Kd of VH-B/Vk-d for pHox-GABA was 10 nM, one of the highest  
 CC values found. This suggests that phage bearing scFv fragments having weak  
 CC affinity-ies can be selected with antigen, probably due to the avidity of  
 CC the multiple antibody heads on the phage. The different combinations  
 CC could also be isolated on a basis of antigen affinity. See also AAR21260-  
 CC 307, 309-311, AAR22450, 565-581

CC Sequence 110 AA;

Query Match 96.1%; Score 541; DB 2; Length 110;  
 Best Local Similarity 96.3%; Pred. No. 5-5e-35;  
 Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DSELTQSPPTMAASPGSEKITTTCSSASSISISNYLHWYQORPGPSPKLLIYRTSNLASGVP 60  
 DB 1 DIELTQSPPTMAASPGSEKITTTCSSASSISISNYLHWYQORPGPSPKLLIYRTSNLASGVP 60

QY 61 AAFSGSGSGTYSLTITGTEADVAITYCOQSSIPYTFGGGTKEIKR 109  
 DB 61 AAFSGSGSGTYSLTITGTEADVAITYCOQSSIPYTFGGGTKEIKR 109

RESULT 4

AAB70843  
 ID AAB70843 standard; protein; 315 AA.

AC AAB70843;

DT 11-SRP-2003 (revised)  
 DT 25-JUN-2001 (first entry)

XX SNV-env leader/human 7B4-scFv fusion construct.

XX T lymphocyte; antibody; single chain variable antibody; scFv; human;  
 KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;  
 KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;  
 KW acquired immune deficiency syndrome; severe combined immune deficiency;  
 KW T cell lymphoma; fusion construct.

OS Homo sapiens.  
 OS Spleen necrosis virus.  
 OS Chimeric.

XX Key Location/Qualifiers  
 FH Protein 1..45  
 FT /label= SNV-env\_leader  
 FT 46..315  
 FT /label= 7B4-scFv

XX DE19946142-A1.

XX 29-MAR-2001.

XX 27-SRP-1999; 99DE-01046142.

XX 27-SRP-1999; 99DE-01046142.

XX

PA (BUND ) BUNDESREPUBLIK DEUT PAUL-EHRICH-INST.

XX Cichutek X, Engelstaedter M;

XX MPI; 2001-246140/26.

DR N-PSDB; AAF61512.

XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy  
 PT of e.g. acquired immune deficiency syndrome, encodes a single-chain  
 PT variable antibody fragment.

PS Claim 1; Fig 4; 18pp; German.

XX This invention describes a novel cell-targeting vector (A) containing a  
 CC DNA sequence (I) encoding a single-chain variable antibody fragment  
 CC (scFv). The products of the invention have antiviral, cytostatic and  
 CC immunostimulant activity and can be used in gene therapy, immunization  
 CC and diagnosis particularly of T cell-associated diseases, specifically  
 CC acquired immune deficiency syndrome (AIDS), severe combined immune  
 CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently  
 CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over  
 CC human B cells, and 1000 fold selectivity over other human cells. A vector  
 CC designated 7A5 encodes a 329 amino acid single-chain variable antibody  
 CC fragment, fully defined in the specification. It was used to transform  
 CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus  
 CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical  
 CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to  
 CC determine transfection. The viral titer (infectious units/ml) was over  
 CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa,  
 CC showing the high selectivity for human T cells. This sequence represents  
 CC the SNV-env leader/human 7B4-scFv fusion construct used in the  
 CC construction of novel cell targeting vectors described in the invention.  
 CC (updated on 11-SRP-2003 to standardise OS field)

SO Sequence 315 AA;

Query Match 96.1%; Score 541; DB 4; Length 315;  
 Best Local Similarity 96.3%; Pred. No. 1.6e-34;  
 Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DSELTQSPPTMAASPGSEKITTTCSSASSISISNYLHWYQORPGPSPKLLIYRTSNLASGVP 60  
 DB 184 DIELTQSPPTMAASPGSEKITTTCSSASSISISNYLHWYQORPGPSPKLLIYRTSNLASGVP 243

QY 61 AAFSGSGSGTYSLTITGTEADVAITYCOQSSIPYTFGGGTKEIKR 109  
 DB 244 AAFSGSGSGTYSLTITGTEADVAITYCOQSSIPYTFGGGTKEIKR 292

RESULT 5

AAR21299  
 ID AAR21299 standard; protein; 110 AA.

AC AAR21299;

DT 21-MAY-1992 (first entry)

XX Murine VL kappa group V chain n specifid for pHox.

KW Rd, bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;  
 KW g3p; binding; adsorption; gene VIII; diverse repertoire;  
 KW specific binding pairs; replicable genetic display package.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Binding-site 24..35  
 FT /label= CDR1  
 FT Binding-site 51..57  
 FT /label= CDR2  
 FT Binding-site 90..98  
 FT /label= CDR3  
 FT /note= "D-X-G-X-X motif "

```

XX MO9201047-A.
PN 23-JAN-1992.
XX
XX 10-JUL-1990; 90GB-00015198.
XX 10-JUL-1990; 90GB-00015198.
XX 19-OCT-1990; 90GB-00022845.
XX 12-NOV-1990; 90GB-00024503.
XX 06-MAR-1991; 91GB-00004744.
XX 15-MAY-1991; 91GB-00010549.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA (MEDI-) MED RES COUNCIL.
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD;
XX WPI; 1992-056862/07.
XX Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic display
PT package.
XX Example 22; Fig 24; 209pp; English.
XX The VK sequence is one of 23 (AA21286-308) expressed from a single chain
XX Fv library. The library produces a diverse repertoire of antibody
XX fragments specific for 2-phenyl-5-oxazolone (phox). It was prepd. using
XX cDNA generated from mRNA from mice immunised with phox coupled to chicked
XX serum albumin. The VH and VL kappa sequences were separately amplified by
XX PCR (AAQ23474-84) and ligated into fdCAT2 (AAQ23463) for expression on
XX the phage surface as fusions with gene III. The resulting library of
XX clones was diverse; 23 hapten binding clones were sequenced revealing 8
XX VH genes (A-H; AA21264-71) in a variety of pairings with 7 VK genes (a-g
XX / AA21286-92). Most clones were VH-B combinations so a further
XX hierarchical library was prepd. by "crossing" VH-B with the VK
XX repertoire. The resulting library was screened for hapten binding and 24
XX clones sequenced. 14 new partners (AA21293-308) for VH-B were
XX identified. Nearly all the VK genes were "ox-like"; only f, (from the
XX original library) and h, p, q, and r (from the hierarchical library) were
XX Vxox1 type genes. Of the 24 hierarchical clones, only one was of type
XX "n". The Kd of VH-B/VK-d for phox-GABA was 10 nM, one of the highest
XX values found. This suggests that phage bearing scfv fragments having weak
XX affinity-ies can be selected with antigen, probably due to the avidity of
XX the multiple antibody heads on the phage. The different combinations
XX could also be isolated on a basis of antigen affinity. See also AA21260-
XX 307, 309-311; AA22450, 565-581
XX
XX Sequence 110 AA;
XX
XX Query Match 95.9%; Score 540; DB 2; Length 110;
XX Best Local Similarity 96.3%; Pred. No. 6.6e-35;
XX Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 DSELTOSPTMAASGKITTTCASSSISSNYLHWYQORGFSPKLLIYRTSNLAGVP 60
XX |
XX 1 DIELTOSTTMAASGKITTTCASSSISSNYLHWYQORGFSPKLLIYRTSNLAGVP 60
XX
XX 61 ARFSGSGSGTSYSLTIGTMEADVAITYCCQGSISIPFTFGGTLEIKR 109
XX |
XX 61 ARFSGSGSGTSYSLTIGTMEADVAITYCCQGSISIPFTFGGTLEIKR 109
XX
XX RESULT 6
XX ID AA21295 standard; protein; 110 AA.
XX AC AA21295;
XX XX
XX DT 21-MAY-1992 (first entry)
XX XX

```

```

DE Murine VL kappa group V chain j specific for phox.
XX
XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
XX g3p; binding; adsorption; gene VIII; diverse repertoire;
XX specific binding pairs; replicable genetic display package.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Binding-site 24..35
XX Binding-site /label= CDR1
XX Binding-site 51..57
XX Binding-site /label= CDR2
XX Binding-site 90..98
XX /label= CDR3
XX /note= "D-X-G-X-X motif"
XX
XX MO9201047-A.
XX 23-JAN-1992.
XX
XX 10-JUL-1990; 90GB-00015198.
XX 10-JUL-1990; 90GB-00015198.
XX 19-OCT-1990; 90GB-00022845.
XX 12-NOV-1990; 90GB-00024503.
XX 06-MAR-1991; 91GB-00004744.
XX 15-MAY-1991; 91GB-00010549.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX (MEDI-) MED RES COUNCIL.
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
XX Jackson RH, Holliger KP, Marks JD;
XX WPI; 1992-056862/07.
XX Producing members of specific binding pairs - by expression in
XX recombinant host cells with a secreting replicable genetic display
XX package.
XX Example 22; Fig 24; 209pp; English.
XX The VK sequence is one of 23 (AA21286-308) expressed from a single chain
XX Fv library. The library produces a diverse repertoire of antibody
XX fragments specific for 2-phenyl-5-oxazolone (phox). It was prepd. using
XX cDNA generated from mRNA from mice immunised with phox coupled to chicked
XX serum albumin. The VH and VL kappa sequences were separately amplified by
XX PCR (AAQ23474-84) and ligated into fdCAT2 (AAQ23463) for expression on
XX the phage surface as fusions with gene III. The resulting library of
XX clones was diverse; 23 hapten binding clones were sequenced revealing 8
XX VH genes (A-H; AA21264-71) in a variety of pairings with 7 VK genes (a-g
XX / AA21286-92). Most clones were VH-B combinations so a further
XX hierarchical library was prepd. by "crossing" VH-B with the VK
XX repertoire. The resulting library was screened for hapten binding and 24
XX clones sequenced. 14 new partners (AA21293-308) for VH-B were
XX identified. Nearly all the VK genes were "ox-like"; only f, (from the
XX original library) and h, p, q, and r (from the hierarchical library) were
XX Vxox1 type genes. Of the 24 hierarchical clones, one was of type "j". The
XX Kd of VH-B/VK-d for phox-GABA was 10 nM, one of the highest values found.
XX This suggests that phage bearing scfv fragments having weak affinity-ies
XX can be selected with antigen, probably due to the avidity of the multiple
XX antibody heads on the phage. The different combinations could also be
XX isolated on a basis of antigen affinity. See also AA21260-307, 309-311;
XX AA22450, 565-581
XX
XX Sequence 110 AA;
XX
XX Query Match 95.4%; Score 537; DB 2; Length 110;
XX Best Local Similarity 95.4%; Pred. No. 1.1e-34;
XX Matches 104; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 DSELTOSPTMAASGKITTTCASSSISSNYLHWYQORGFSPKLLIYRTSNLAGVP 60
XX |

```

Db 1 |||||  
 1 DIELTOSPTTMAASPGKITTTCSSASSISNNYLMWFQOKGFSFKLITYRTSNLASGVP 60  
 QY 61 ARFSGSGSGTYSYLTIGTMEADVATYYCOQSSSIPRTFGGTYKLEIR 109  
 61 ARFSGSGSGTYSYLTIGTMEADVATYYCOQSSSIPRTFGGTYKLEIR 109

RESULT 7  
 AAR21288  
 ID AAR21288 standard; protein; 110 AA.

XX AAR21288;  
 XX  
 AC  
 XX  
 DT 21-MAY-1992 (first entry)

XX Murine VL kappa group IV chain "c", specific for phox.

XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;  
 XX g3p; binding; adsorption; gene VIII; diverse repertoire;  
 XX specific binding pairs; replicable genetic display package.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Binding-site 24..35  
 FT /label= CDR1  
 FT Binding-site 51..57  
 FT /label= CDR2  
 FT Binding-site 90..98  
 FT /label= CDR3  
 FT /note= "D-X-G-X-X motif"

XX WO9201047-A.

XX 23-JAN-1992.

XX 10-JUL-1990; 90GB-00015198.

XX 10-JUL-1990; 90GB-00015198.

XX 19-OCT-1990; 90GB-00022845.

XX 12-NOV-1990; 90GB-00024503.

XX 06-MAR-1991; 91GB-00004744.

XX 15-MAY-1991; 91GB-00010549.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX (MEDI-) MED RES COUNCIL.

XX Mccafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;  
 XX Jackson RH, Holliger KP, Marks JD;

XX WPI; 1992-056862/07.

XX Example 21; Fig 24; 209pp; English.

XX The VK sequence is one of seven (AAR21286-92) found to be expressed from  
 XX a single chain Fv library from an immunised mouse. The libra-ry produces  
 XX a diverse repertoire of antibody fragments specific for 2-phenyl-5-  
 XX oxazolon (phox). It was prep'd. using cDNA generated from mRNA from mice  
 XX immunised with phox coupled to chicked serum albumin. The VH and VL kappa  
 XX sequences were separately amplified by PCR (see AAO23474-84) and ligated  
 XX into fdCMT2 (see AAO23463) for ex-pression on the phage surface as  
 XX fusions with gene III. The result- ing library of clones was diverse.

XX Twenty three haptent binding clones were sequenced revealing eight  
 XX different VH genes (A-H) (see AAR21264-71) in a variety of pairings with  
 XX the seven different VK genes (a-g). Of the twenty three clones sequenced,  
 XX two were of type "c", and were "ox-like" genes. (See Berek et al. Nature  
 XX 316 412-418, 1985). They contain the DXGX motif in CDR3, the central Gly  
 XX of which is needed to create a cavity for phox. Most of the clones were

CC Vr-d combinations. The Kd of VH-B/Vk-b for phox-GABA was 10 uM, one of  
 CC the highest values found. This suggests that phage bearing acfv fragments  
 CC having weak affinities can be selected with antigen, probably due to the  
 CC avidity of the multiple antibody heads on the phage. See also AAR21260-  
 CC 307, 309-311; AAR22450, 565-581

XX Sequence 110 AA;

Query Match 95.0%; Score 535; DB 2; Length 110;  
 Best Local Similarity 95.4%; Pred. No. 1.66-34;  
 Matches 104; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTOSPTTMAASPGKITTTCSSASSISNNYLMWFQOKGFSFKLITYRTSNLASGVP 60  
 Db 1 DIELTOSPTTMAASPGKITTTCSSASSISNNYLMWFQOKGFSFKLITYRTSNLASGVP 60  
 QY 61 ARFSGSGSGTYSYLTIGTMEADVATYYCOQSSSIPRTFGGTYKLEIR 109  
 61 ARFSGSGSGTYSYLTIGTMEADVATYYCOQSSSIPRTFGGTYKLEIR 109

RESULT 8  
 AAR21298  
 ID AAR21298 standard; protein; 110 AA.

XX AAR21298;

XX 21-MAY-1992 (first entry)

XX Murine VL kappa group V chain m specificd for phox.

XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;  
 XX g3p; binding; adsorption; gene VIII; diverse repertoire;  
 XX specific binding pairs; replicable genetic display package.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Binding-site 24..35  
 FT /label= CDR1  
 FT Binding-site 51..57  
 FT /label= CDR2  
 FT Binding-site 90..98  
 FT /label= CDR3  
 FT /note= "D-X-G-X-X motif"

XX WO9201047-A.

XX 23-JAN-1992.

XX 10-JUL-1990; 90GB-00015198.

XX 10-JUL-1990; 90GB-00015198.

XX 19-OCT-1990; 90GB-00022845.

XX 12-NOV-1990; 90GB-00024503.

XX 06-MAR-1991; 91GB-00004744.

XX 15-MAY-1991; 91GB-00010549.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX (MEDI-) MED RES COUNCIL.

XX Mccafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;  
 XX Jackson RH, Holliger KP, Marks JD;

XX WPI; 1992-056862/07.

XX Example 22; Fig 24; 209pp; English.

XX The VK sequence is one of 23 (AAR21286-308) expressed from a single chain

Fv library. The library produces a diverse repertoire of antibody fragments specific for 2-phenyl-5-oxazolone (phOx). It was prep'd. using cDNA generated from mRNA from mice immunised with phOx coupled to chicked serum albumin. The VH and VL kappa sequences were separately amplified by PCR (AAQ2474-84) and ligated into fdCA72 (AAQ23463) for expression on the phage surface as fusions with gene III. The resulting library of clones was diverse; 23 hapten binding clones were sequenced revealing 8 VH genes (A-H; AAR21264-71) in a variety of pairings with 7 Vk genes (a-g; AAR21266-92). Most clones were VH-B combinations so a further hierarchical library was prep'd. by "crossing" VH-B with the Vk repertoire. The resulting library was screened for hapten binding and 24 clones sequenced. 14 new partners (AAR21293-308) for VH-B were identified. Nearly all the Vk genes were "ox-like", only f, (from the original library) and h, p, g, and r (from the hierarchical library) were Vkoxi type genes. Of the 24 hierarchical clones, only one was of type "m". The Kd of VH-B/Vk-d for phOx-GABA was 10 nM, one of the highest values found. This suggests that phage bearing scFv fragments having weak affinity-ies can be selected with antigen, probably due to the avidity of the multiple antibody heads on the phage. The different combinations could also be isolated on a basis of antigen affinity. See also AAR21260-307, 309-311; AAR22450, 565-581

SO Sequence 110 AA;

Query Match 94.5%; Score 532; DB 2; Length 110;  
Best Local Similarity 94.5%; Pred. No. 2.8e-34;  
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

DY 1 DSELTGPTTMAASPGKITTTCASSSSISNNYLHWYQGRGFPKLLIYRTSNLAGVP 60  
DB 1 DIELTGPPTTMAASPGKITTTCASSSSISNNLHWYQGRGFPKLLIYRTSNLAGVP 60  
DY 61 ARFSGSGSGTYSYLTIGTMEADVAITYCCQGSIPRTFGGCTKLEIKR 109  
DB 61 ARFSGSGSGTYSYLTIGTMEADVAITYCCQGSIPRTFGGCTKLEIKR 109

RESULT 9  
AA05363  
ID AA05363 standard; protein; 297 AA.

XX AAY05363;  
XX  
XX 30-JUN-1999 (first entry)  
XX  
XX HBV specific single stranded antibody.

XX Single stranded antibody; hepatitis B virus; HBV core protein;  
XX HBV infection; viral proliferation inhibitor; viral DNA synthesis;  
XX gene therapy.

XX Mus sp.

XX WO9911792-A1.

XX 11-MAR-1999.

XX 02-SEP-1998; 98WO-JP003921.

XX 02-SEP-1997; 97JP-00237054.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX (HAYA) HAYASHI N.

XX Hayashi N, Yamamoto M, Yamamoto H, Tohdoh N;

XX WPI; 1999-243623/20.

XX N-PSDB; AAX33931.

XX Single-stranded antibody against hepatitis B virus core protein,  
XX applicable as (gene) therapeutic agents for treatment of hepatitis B  
XX viral infections.

PS Claim 5; Page 55-57; 72pp; English.

XX This sequence is the single-stranded antibody of the invention, that has  
XX the capability of binding to a hepatitis B virus (HBV) core protein.  
XX Therapeutic agents can be formulated with the antibody for treatment of  
XX HBV infections by stopping proliferation of the virus through inhibition  
XX of viral DNA synthesis, and the gene encoding the antibody can be applied  
XX as an agent to gene therapy

SO Sequence 297 AA;

Query Match 94.1%; Score 530; DB 2; Length 297;  
Best Local Similarity 93.7%; Pred. No. 1.1e-33;  
Matches 104; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

DY 1 DSELTGPTTMAASPGKITTTCASSSSISNNYLHWYQGRGFPKLLIYRTSNLAGVP 60  
DB 169 DIELTGPPTTMAASPGKITTTCASSSSISNNLHWYQGRGFPKLLIYRTSNLAGVP 228

DY 61 ARFSGSGSGTYSYLTIGTMEADVAITYCCQGSIPRTFGGCTKLEIKR 109  
DB 229 ARFSGSGSGTYSYLTIGTMEADVAITYCCQGSIPRTFGGCTKLEIKR 279

RESULT 10  
AAR79162  
ID AAR79162 standard; peptide; 109 AA.

XX AAR79162;

XX 25-MAR-2003 (revised)

XX 04-MAR-1996 (first entry)

XX Human Igr receptor-binding, antibody-related peptide light chain.

XX Immunoglobulin E; antibody; receptor; monoclonal; detection;  
XX complementarity determining region.

XX Mus sp.

XX Location/qualifiers

XX 24..35

XX /label= CDR1L

XX /note= "all CDR regions are claimed"

XX 51..57

XX /label= CDR2L

XX /note= "all CDR regions are claimed"

XX 90..98

XX /label= CDR3L

XX /note= "all CDR regions are claimed"

XX JP07165799-A.

XX 27-JUN-1995.

XX 22-OCT-1993; 93JP-00264792.

XX 22-OCT-1993; 93JP-00264792.

XX (TSUR/) TSURA T.

XX (ASAK) ASAH BREMERIES LTD.

XX (TORI) TORII YAKUJIN KK.

XX (NIKK-) NIKKA WHISKY KK.

XX WPI; 1995-261292/34.

XX N-PSDB; AAO96289.

XX Novel monoclonal antibody against human high-affinity Igr receptor - and  
XX DNA fragment encoding the MAb, for the specific identification of human  
XX Fe-epitope R1.

XX Claim 9; Page 16-17; 20pp; Japanese.

Polypeptides which specifically recognise human IgE receptor (Fc-epsilon-R1) have been isolated and sequenced. The new peptides are related to a monoclonal antibody against Fc-epsilon-R1 and are either heavy or light chain molecules. The heavy chain molecules have the general formula FR1-CDRH1-FR2-CDRH1-FR3-CDRH1-FR4 (corrected to AAR79153, AAR79155, AAR79157, AAR79159 and AAR79161) and are encoded by AA096280, AA096282, AA096284, AA096286 and AA096288. FR1 is a polypeptide having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide, FR3 is a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide. Similarly the light chains have the general formula FR5-CDRL1-FR6-CDRL1-FR7-CDRL1-FR8 (corrected to AAR79154, AAR79156, AAR79158, AAR79160 and AAR79162) and are encoded by AA096281, AA096283, AA096285, AA096287 and AA096289. FR5 is a 23-28 aa polypeptide, FR6 is a 14-16 aa polypeptide, FR7 is a 30-34 aa polypeptide and FR8 is a 9-11 aa polypeptide. All the peptides are derived from mouse hybridoma cells and are useful in the detection of the human Fc-epsilon-R1 or for the elucidation of an antigen recognising region of a monoclonal antibody against human Fc-epsilon-R1. (Updated on 25-MAR-2003 to correct PA field.)

Sequence 109 AA;

Query Match 93.8%; Score 528; DB 2; Length 109;  
Best Local Similarity 92.7%; Pred. No. 5.7e-34;  
Matches 101; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTQSPTTMAASPGKITTTCSSASSISSNVLMHYOORPGFSPKLIYRTSNLASGV 60  
DB 1 DQMTQSPPTTMAASPGKITTTCSSASSISSNVLMHYOORPGFSPKLIYRTSNLASGV 60

QY 61 AAFSGSGSTSYSLTIGTMEADVATYYCOQGSIPRTFGGKLEIKR 109  
DB 61 AAFSGSGSTSYSLTIGTMEADVATYYCOQGSIPRTFGGKLEIKR 109

RESULT 11

AAU72866 standard; protein; 256 AA.

AAU72866;

26-FEB-2002 (first entry)

P5-3 single chain Fv.

Human; NKGD2; NKGD2 receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytotoxic; antimicrobial; immunomodulatory; 1182D10; 6H787; 8G7C10; 6E5A7; 1182D10x4-7; 8G7C10x4-7; P4-2; P4-3; P4-14; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14; P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.

Homo sapiens.

WO200171005-A2.

27-SEP-2001.

26-MAR-2001; 2001WO-BP003414.

24-MAR-2000; 2000EP-00106467.

(KUFE/) KUFER P.

Kuifer P, Riettmueller G, Lutterbuese R, Borschert K, Kischel R;

Mayer M, Hofmeister R;

WPI: 2002-055119/07.

N-PSDB; AAS37140.

Multi-functional polypeptides comprising binding sites that specifically

recognize extracellular groups of the NKGD2 receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases.

Example 7; Fig 16; 114pp; English.

The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKGD2 receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated polynucleotide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protozoa or helminths. The autoimmune diseases include multiple sclerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKGD2 receptor and the polypeptides of the invention

Sequence 256 AA;

Query Match 93.4%; Score 526; DB 5; Length 256;  
Best Local Similarity 96.2%; Pred. No. 1.9e-33;  
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPPTTMAASPGKITTTCSSASSISSNVLMHYOORPGFSPKLIYRTSNLASGV 63  
DB 140 LTQSPPTTMAASPGKITTTCSSASSISSNVLMHYOORPGFSPKLIYRTSNLASGV 199

QY 64 SSGSGSTSYSLTIGTMEADVATYYCOQGSIPRTFGGKLEIKR 109  
DB 200 SSGSGSTSYSLTIGTMEADVATYYCOQGSIPRTFGGKLEIKR 245

RESULT 12

AAU72874 standard; protein; 503 AA.

AAU72874;

26-FEB-2002 (first entry)

3B10xP5-23 bispecific single chain Fv.

Human; NKGD2; NKGD2 receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytotoxic; antimicrobial; immunomodulatory; 1182D10; 6H787; 8G7C10; 6E5A7; 1182D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14; P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.

Homo sapiens.

WO200171005-A2.

27-SEP-2001.

26-MAR-2001; 2001WO-BP003414.

24-MAR-2000; 2000EP-00106467.

(KUFE/) KUFER P.

Kuifer P, Riettmueller G, Lutterbuese R, Borschert K, Kischel R;

Mayer M, Hofmeister R;

XX MPI; 2002-055119/07.  
 DR N-PSDB; AAS97148.  
 XX Multifunctional polypeptides comprising binding sites that specifically  
 PT recognize extracellular groups of the NKG2D receptor complex and domains  
 PT which function as receptors or ligands, useful for treating cancers and  
 PT infectious diseases.  
 XX  
 PS Example 5; Fig 16; 114pp; English.  
 XX The invention relates to a multifunctional polypeptide comprising a  
 CC domain with a binding site that specifically recognizes an extracellular  
 CC group of the NKG2D receptor complex and a second domain which functions  
 CC as a receptor or ligand. The polypeptide and its associated  
 CC polynucleotide are used for the preparation of a pharmaceutical  
 CC composition for the treatment of cancer, infections and/or autoimmune  
 CC conditions. The cancer may be a tumour of the head and neck, stomach,  
 CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,  
 CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,  
 CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.  
 CC The infectious diseases can be caused by viruses, bacteria, fungi,  
 CC protozoa or helminths. The autoimmune diseases include multiple  
 CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior  
 CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent  
 CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and  
 CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D  
 CC receptor and the polypeptides of the invention  
 XX  
 SQ Sequence 503 AA;  
 Query Match 93.4%; Score 526; DB 5; Length 503;  
 Best Local Similarity 96.2%; Pred. No. 3.7e-33;  
 Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 LTGSPPTMAASPGKITTTCASASSISSNVLMYQQRGFSFKLLIYRTSNLAGVGP 63  
 DB 387 LTGSPPTMAASPGKITTTCASASSISSNVLMYQQRGFSFKLLIYRTSNLAGVGP 446  
 QY 64 SGSSGSGTSTLTGTMEAEADVATYYCOGSSISPTFGGTLEIKR 109  
 DB 447 SGSSGSGTSTLTGTMEAEADVATYYCOGSSISPTFGGTLEIKR 492

RESULT 13  
 ADR38693  
 ID ADR38693 standard; peptide; 109 AA.  
 XX ADR38693;  
 AC  
 XX 02-DEC-2004 (first entry)  
 DT  
 XX Mouse light chain variable region scfv seqid 95.  
 DE  
 XX Antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 KW light chain variable region; single chain antibody; scfv.  
 XX  
 OS Mus sp.  
 XX  
 PN US2004175385-A1.  
 PD  
 XX 09-SEP-2004.  
 PF  
 XX 01-AUG-2003; 2003US-00632706.  
 PR 31-AUG-1998; 98US-00144886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Marks JD, Ameredorfer P;  
 PI

XX MPI; 2004-652009/63.  
 DR  
 XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 XX  
 PS Example 1; SEQ ID NO 95; 110pp; English.  
 XX The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of a mouse light chain variable fragment anti-botulinum toxin  
 CC scfv.  
 XX  
 SQ Sequence 109 AA;  
 Query Match 93.3%; Score 525; DB 8; Length 109;  
 Best Local Similarity 92.7%; Pred. No. 9.8e-34;  
 Matches 101; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DSELTOSPTMAASPGKITTTCASASSISSNVLMYQQRGFSFKLLIYRTSNLAGV 60  
 DB 1 DIELTOSPTMAASPGKITTTCASASSISSNVLMYQQRGFSFKLLIYRTSNLAGV 60  
 QY 61 ARFSGSGSGTSTLTGTMEAEADVATYYCOGSSISPTFGGTLEIKR 109  
 DB 61 ARFSGSGSGTSTLTGTMEAEADVATYYCOGSSISPTFGGTLEIKR 109

RESULT 14  
 AAR21300  
 ID AAR21300 standard; protein; 110 AA.  
 XX AAR21300;  
 AC  
 XX 21-MAY-1992 (first entry)  
 DT  
 XX Murine VL kappa group V chain o specific for phox.  
 DE  
 XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;  
 KW g3p; binding; adsorption; gene VIII; diverse repertoire;  
 KW specific binding pairs; replicable genetic display package.  
 XX  
 OS Synthetic.  
 XX  
 PN Key  
 XX Binding-site 24..35 Location/Qualifiers  
 FT Binding-site /label= CDR1  
 FT Binding-site 51..57  
 FT Binding-site /label= CDR2  
 FT Binding-site 90..98



```

FT      /label= CDR3
PT      /note= "D-X-G-X-X motif "
XX
XX      MO9201047-A.
XX
XX      23-JAN-1992.
XX
XX      10-JUL-1990; 90GB-00015198.
XX
XX      10-JUL-1990; 90GB-00015198.
XX
XX      10-JUL-1990; 90GB-00015198.
XX
XX      19-OCT-1990; 90GB-00022845.
XX
XX      12-NOV-1990; 90GB-00024503.
XX
XX      06-MAR-1991; 91GB-00004744.
XX
XX      15-MAY-1991; 91GB-00010549.
XX
XX      (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX      (MEDI-) MED RES COUNCIL.
XX
XX      McCaferly J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
XX
XX      Jackson RH, Holliger KP, Marks JD;
XX
XX      WPI, 1992-056862/07.
XX
XX      Producing members of specific binding pairs - by expression in
XX
XX      recombinant host cells with a secreting replicable genetic display
XX
XX      package.
XX
XX      Example 22; Fig 24; 209pp; English.
XX
XX      The VK sequence is one of 23 (AAR21286-308) expressed from a single chain
XX
XX      Fv library. The library produces a diverse repertoire of antibody
XX
XX      fragments specific for 2-phenyl-5-oxazolone (phox). It was prep'd. using
XX
XX      cDNA generated from mRNA from mice immunised with phox coupled to chicken
XX
XX      serum albumin. The VH and VL kappa sequences were separately amplified by
XX
XX      PCR (AAG2374-84) and ligated into fdCAT2 (AAG22463) for expression on
XX
XX      the phage surface as fusions with gene III. The resulting library of
XX
XX      clones was diverse; 23 hapten binding clones were sequenced revealing 8
XX
XX      VH genes (A-H; AAR21264-71) in a variety of pairings with 7 VK genes (a-g
XX
XX      / AAR21286-92). Most clones were VH-B combinations so a further
XX
XX      hierarchical library was prep'd. by "crossing" VH-B with the VK
XX
XX      repertoire. The resulting library was screened for hapten binding and 24
XX
XX      clones sequenced. 14 new partners (AAR21293-308) for VH-B were
XX
XX      identified. Nearly all the VK genes were "ox-like"; only f, (from the
XX
XX      original library) and h, p, q, and r (from the hierarchical library) were
XX
XX      Vkoxi type genes. Of the 24 hierarchical clones, two were of type "o".
XX
XX      The kd of VH-B/VK-d for phox-GABA was 10 nM, one of the highest values
XX
XX      found. This suggests that phage bearing scFv fragments having weak
XX
XX      affinity-ies can be selected with antigen, probably due to the avidity of
XX
XX      the multiple antibody heads on the phage. The different combinations
XX
XX      could also be isolated on a basis of antigen affinity. See also AAR21260-
XX
XX      307, 309-311; AAR22450, 565-581
XX
XX      Sequence 110 AA;
SQ
Query Match      92.5%; Score 521; DB 2; Length 110;
Best Local Similarity 93.6%; Pred. No. 2e-33;
Matches 102; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
OY      1 DSELTOSPTTMAASPEKITTTCASASSISSNYLHWYQORPGRSPKLLIYRTSNLASGVP 60
DB      1 DIELTQSPAIMAASPEKITTTCASASSISSNYLHWYQOKPGSPKLLIYRTSNLASGVP 60
OY      61 AAFSGSGSTSYSLTIGTMEADVATYYCOGSSSIPRTFGGSKLEIKR 109
DB      61 AAFSGSGSTSYSLTIGTMEADVATYYCOGSSSIPRTFGGSKLEIKR 109
RESULT 15
AA17963
ID      AA17963 standard; protein; 239 AA.
AC      AA17963;
XX

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```

DT      04-AUG-1999 (first entry)
XX
XX      Mouse scFv fragment 5-3.
XX
XX      Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
XX
XX      autoimmune disease; scFv-antibody; single-chain Fv; mouse.
XX
XX      Mus sp.
XX
XX      WO9925818-A1.
XX
XX      27-MAY-1999.
XX
XX      16-NOV-1998; 98WO-EP007313.
XX
XX      17-NOV-1997; 97EP-00120096.
XX
XX      (KUPE/) KUPER P.
XX
XX      Kufer P, Raum T, Borchert K, Zetl F, Lutterbuese R;
XX
XX      WPI, 1999-338004/28.
XX
XX      N-Psdb; AAX77246.
XX
XX      Phage display system for identification of binding site domains retaining
XX
XX      capacity to bind an epitope.
XX
XX      Claim 27; Fig 6.9; 152pp; English.
XX
XX      The invention relates to a method of identifying binding site domains
XX
XX      (BSD) that retain the capacity of binding to a predetermined epitope when
XX
XX      positioned C-terminal of at least one further domain in a recombinant bi-
XX
XX      or multivalent polypeptide. The method comprises (a) testing a panel of
XX
XX      BSD displayed on the surface of a biological display system as part of a
XX
XX      fusion protein for binding to a predetermined epitope, where the fusion
XX
XX      protein comprises an additional domain positioned N-terminal of the BSD
XX
XX      and an amino acid sequence that mediates anchoring of the fusion protein
XX
XX      to the surface of the display system; and (b) identifying a BSD that
XX
XX      binds to the predetermined epitope. The method is useful to identify bi-
XX
XX      or multivalent polypeptides that comprise antibody binding sites capable
XX
XX      of efficiently binding to the corresponding antigen. The polypeptides or
XX
XX      antibodies identified by the method are useful therapeutically and
XX
XX      diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
XX
XX      fragments that bind independently of their position within bifunctional
XX
XX      single-chain fusion proteins can be isolated from combinatorial antibody
XX
XX      libraries using the new in vitro method. Sequences AA17957-965 represent
XX
XX      mouse scFv fragments
XX
XX      Sequence 239 AA;
SQ
Query Match      92.5%; Score 521; DB 2; Length 239;
Best Local Similarity 96.2%; Pred. No. 4.4e-33;
Matches 101; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY      4 LTQSPPTMAASPEKITTTCASASSISSNYLHWYQORPGRSPKLLIYRTSNLASGVPAR 63
DB      135 LTQSPPTMAASPEKITTTCASASSISSNYLHWYQOKPGSPKLLIYRTSNLASGVPAR 194
OY      64 SSGSGSTSYSLTIGTMEADVATYYCOGSSSIPRTFGGSKLEIKR 108
DB      195 SSGSGSTSYSLTIGTMEADVATYYCOGSSSIPRTFGGSKLEIKR 239
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 / Search time 26.5513 seconds  
(without alignments)  
394.995 Million cell updates/sec

Title: US-10-632-706-89

Perfect score: 563

Sequence: 1 DSELTQSPTTMAASPEKITT.....QQGSSIPRTGGGTLEIKR 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	533	94.7	123 2 S05269	Ig kappa chain pre
2	522	92.7	109 2 S13699	Ig kappa chain V r
3	522	92.7	124 2 S05267	Ig kappa chain pre
4	520	92.4	108 2 PS0069	Ig kappa chain V r
5	516	91.7	106 2 S29583	Ig kappa chain V r
6	515	91.5	120 2 S66536	Ig light chain V r
7	504	89.5	103 2 S13695	Ig kappa chain - m
8	497	88.3	102 2 S29588	Ig kappa chain V r
9	493	87.6	102 2 S29582	Ig kappa chain V r
10	478	84.9	101 2 S13696	Ig heavy chain V r
11	478	84.9	102 2 S13697	Ig heavy chain V r
12	473.5	84.1	103 2 S13698	Ig heavy chain V r
13	468	83.1	93 2 S17633	Ig kappa chain V r
14	467	82.9	93 2 S17635	Ig kappa chain V r
15	464	82.4	93 2 S17631	Ig kappa chain V r
16	462	82.1	93 2 S17624	Ig kappa chain V r
17	459	81.5	93 2 S17634	Ig kappa chain V r
18	458	81.3	93 2 S17636	Ig kappa chain V r
19	445	79.0	93 2 S17625	Ig kappa chain V r
20	440	78.2	93 2 S17632	Ig kappa chain V r
21	436	77.4	130 2 A32513	Ig kappa chain pre
22	433	76.9	108 2 P10278	Ig kappa chain V r
23	431	76.6	108 2 P10276	Ig kappa chain V r
24	427	75.8	107 2 PC4405	Ig kappa chain V r
25	426	75.7	140 2 P10013	Ig kappa chain pre
26	425	75.5	130 2 S04573	Ig kappa chain pre
27	424	75.3	130 2 B32456	Ig kappa chain pre
28	424	75.3	130 2 B32456	Ig kappa chain pre
29	423	75.1	107 2 A30562	Ig kappa chain V r

30	419	74.4	105 2 S26338	Ig kappa chain V r
31	418	74.2	107 2 B30562	Ig kappa chain V r
32	418	74.2	132 2 S05268	Ig kappa chain pre
33	417	74.1	113 2 S03410	Ig kappa chain pre
34	416	73.9	129 1 KVM578	Ig kappa chain pre
35	414	73.5	106 2 B54378	Ig light chain V r
36	414	73.5	108 2 S29581	Ig kappa chain V r
37	412	73.2	106 2 PS0070	Ig kappa chain V r
38	410	72.8	109 2 P10405	Ig light chain V r
39	407	72.3	130 1 J10079	Ig kappa chain pre
40	404	71.8	107 2 PD0011	Ig kappa chain V r
41	404	71.8	109 2 PT0404	Ig light chain V r
42	403	71.6	103 2 S29591	Ig kappa chain V r
43	403	71.6	120 2 A34871	Ig kappa chain V r
44	402	71.4	104 2 UC6076	anti-D-dimer monoc
45	401	71.2	106 2 PS0071	Ig kappa chain V r

#### ALIGNMENTS

RESULT 1  
S05269  
Ig kappa chain precursor V-J region (38C13-V4) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Jan-2000  
C/Accession: S05269; J10064; S03847  
R/Levy, S.  
submitted to the EMBL Data Library, February 1989  
A/Accession: S05267  
A/Accession: S05269  
A/Molecule type: mRNA  
A/Residues: 1-123 <LBV>  
A/Cross-references: UNIPARC:UPI0000115DED; EMBL:X14099; NID:952568; PIDN:CAA32261.1; PID  
R/Carroll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.  
J. Exp. Med. 168, 1607-1620, 1988  
A/Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An explanation  
A/Reference number: J10061; MUID:89035985; PMID:3141553  
A/Accession: J10064  
A/Molecule type: mRNA  
A/Residues: 1-121 <CAR>  
A/Cross-references: UNIPARC:UPI0000176799; EMBL:X14099  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/1-13/Domain: signal sequence (fragment) #status predicted <Sig>  
F/14-123/Product: Ig kappa chain (fragment) #status predicted <Mat>  
F/14-107/Domain: V region (V-kappa-4) <VRB>  
F/28-104/Domain: immunoglobulin homology <IMH>  
F/108-123/Domain: J region (J-kappa-4) (fragment) <JRB>

Query Match 94.7%; Score 533; DB 2; Length 123;  
Best Local Similarity 97.2%; Pred. No. 4.2e-38;  
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LTGSPPTMAASPEKITTGSSASSSTSSNYLHWYQQPGSPKLLIRTSNLSGVPAF 63  
DB 17 LTGSPPTMAASPEKITTGSSASSSTSSNYLHWYQQPGSPKLLIRTSNLSGVPAF 76

QY 64 SGSGSGTYSILTIGTMEAEADVATYYCQGGSSIPRTFGGTYLBIKR 109  
DB 77 SGSGSGTYSILTIGTMEAEADVATYYCQGGSSIPRTFGGTYLBIKR 122

RESULT 2  
S13699  
Ig kappa chain V region (hybridoma NCI9-B8G2) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S13699  
R/Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.  
Eur. J. Immunol. 19, 1289-1295, 1989  
A/Title: B1ased immunoglobulin variable region gene expression by Ly-1 B cells due to clc  
A/Reference number: S13685; MUID:89338557; PMID:2503389

A:Accession: S13699  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-109 <PEN>  
 A:Cross-references: UNIPARC:UPI000011377B; EMBL:X53352; NID:G55303; PIDN:CAA37438.1; PID  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 522; DB 2; Length 109;  
 Best Local Similarity 95.3%; Pred. No. 1.6e-37;  
 Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOQRPFSPKLIYRTSNLASGVPAKF 63  
 DB 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOQRPFSPKLIYRTSNLASGVPAKF 63  
 QY 64 SSGSGGTSTLTGTMEADVAATYCCQGSIPRTFGGTLEIKR 109  
 DB 64 SSGSGGTSTLTGTMEADVAATYCCQGSIPRTFGGTLEIKR 109

## RESULT 3

S05267  
 Ig kappa chain precursor V-J region (38C13-V3) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Jan-2000  
 C:Accession: S05267; J10063; S03845  
 R:Levy, S.  
 submitted to the EMBL Data Library, February 1989

A:Reference number: S05267  
 A:Accession: S05267  
 A:Molecule type: mRNA  
 A:Residues: 1-124 <LEV>  
 A:Cross-references: UNIPARC:UPI0000115DB; EMBL:X14097; NID:G52565; PIDN:CAA32259.1; PID  
 R:Carroll, W.L.; Stearns, C.O.; Levy, R.; Levy, S.  
 J. Exp. Med. 168, 1607-1620, 1988  
 A:Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An explant  
 A:Reference number: J10063; MUID:89035985; PMID:3141553  
 A:Accession: J10063  
 A:Molecule type: mRNA  
 A:Residues: 1-123 <CAR>  
 A:Cross-references: UNIPARC:UPI0000176798; EMBL:X14097  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:1-11/Domain: signal sequence (fragment) #status predicted <SIG>  
 F:14-124/Product: Ig kappa chain (fragment) #status predicted <Mat>  
 F:14-111/Domain: V region (V-kappa-3) <VRB>  
 F:29-104/Domain: immunoglobulin homology <IMM>  
 F:112-124/Domain: J region (J-kappa-4) (fragment) <JRB>

Query Match 92.7%; Score 522; DB 2; Length 124;  
 Best Local Similarity 95.4%; Pred. No. 1.9e-37;  
 Matches 103; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOQRPFSPKLIYRTSNLASGVPAKF 63  
 DB 17 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOQRPFSPKLIYRTSNLASGVPAKF 76  
 QY 64 SSGSGGTSTLTGTMEADVAATYCCQGSIPRTFGGTLEIKR 109  
 DB 77 SSGSGGTSTLTGTMEADVAATYCCQGSIPRTFGGTLEIKR 124

## RESULT 4

PS0069  
 Ig kappa chain V region (38C13.V6) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
 C:Accession: PS0069  
 R:Levy, S.; Campbell, M.J.; Levy, R.  
 J. Exp. Med. 170, 1-13, 1989  
 A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement

A:Reference number: A92781; MUID:89310348; PMID:2501443  
 A:Accession: PS0069  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-108 <LEV>  
 A:Cross-references: UNIPROT:Q9JL78; UNIPARC:UPI00001767C7  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 520; DB 2; Length 108;  
 Best Local Similarity 96.2%; Pred. No. 2.4e-37;  
 Matches 101; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOQRPFSPKLIYRTSNLASGVPAKF 63  
 DB 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOQRPFSPKLIYRTSNLASGVPAKF 63  
 QY 64 SSGSGGTSTLTGTMEADVAATYCCQGSIPRTFGGTLEIKR 108  
 DB 64 SSGSGGTSTLTGTMEADVAATYCCQGSIPRTFGGTLEIKR 108

## RESULT 5

S29583  
 Ig kappa chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C:Accession: S29583  
 R:Kavaler, J.  
 submitted to the EMBL Data Library, April 1991

A:Reference number: S29583  
 A:Accession: S29583  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-106 <KAV>  
 A:Cross-references: UNIPARC:UPI0000113791; EMBL:X59098; NID:G52203; PIDN:CAA41824.1; PID  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 91.7%; Score 516; DB 2; Length 106;  
 Best Local Similarity 97.1%; Pred. No. 5.1e-37;  
 Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOQRPFSPKLIYRTSNLASGVPAKF 63  
 DB 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOQRPFSPKLIYRTSNLASGVPAKF 63  
 QY 64 SSGSGGTSTLTGTMEADVAATYCCQGSIPRTFGGTLEIKR 106  
 DB 64 SSGSGGTSTLTGTMEADVAATYCCQGSIPRTFGGTLEIKR 106

## RESULT 6

S66536  
 Ig light chain V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
 C:Accession: S66536  
 R:Tsotolis, G.; Haase, W.; Engel, A.; Michel, H.  
 Eur. J. Biochem. 231, 823-830, 1995  
 A:Title: Isolation and structural characterization of trimetric cyanobacterial photosystem  
 A:Reference number: S66536; MUID:95377318; PMID:7649183  
 A:Accession: S66536  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-120 <TSI>  
 A:Cross-references: UNIPARC:UPI00001137B0; EMBL:X88903; NID:G895870; PIDN:CAA61365.1; PID  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 91.5%; Score 515; DB 2; Length 120;

Best Local Similarity 91.7%; Pred. No. 7, 1e-37;  
Matches 100; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DSEIOTPTMAASPGKITTTCGASSSISNNYLMHWQORPGFSPKLLIYRTSNLASGVP 60  
Db 1 DSEIOTPTMAASPGKITTTCGASSSISNNYLMHWQORPGFSPKLLIYRTSNLASGVP 60

Qy 61 ARSGSGGTYSLLTGTMEADVATYYCOQGSIPRTFGGTLBIKR 109  
Db 61 ARSGSGGTYSLLTGTMEADVATYYCOQGSIPRTFGGTLBIKR 109

## RESULT 7

S13695  
Ig kappa chain - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000

C/Accession: S13695

R/Pennell, C.A.; Mercollino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

Eur. J. Immunol. 19, 1289-1295, 1989

A/Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl

A/Reference number: S13685; MUID:89338557; PMID:2503389

A/Accession: S13695

A/Molecule type: mRNA

A/Residues: 1-103 <PEN>

A/Cross-references: UNIPARC:UPI0000113777; EMBL:X53348; NID:955296; PIDN:CAA37434.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 89.5%; Score 504; DB 2; Length 103;  
Best Local Similarity 97.0%; Pred. No. 5, 2e-36;  
Matches 97; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LTOSPTTMAASPGKITTTCGASSSISNNYLMHWQORPGFSPKLLIYRTSNLASGVPARF 63  
Db 4 LTOSPTTMAASPGKITTTCGASSSISNNYLMHWQORPGFSPKLLIYRTSNLASGVPARF 63

Qy 64 SGSGSGTYSLLTGTMEADVATYYCOQGSIPRTFGGCT 103  
Db 64 SGSGSGTYSLLTGTMEADVATYYCOQGSIPRTFGGCT 103

RESULT 8  
S29588  
Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C/Accession: S29588

R/Kavaler, J.

submitted to the EMBL Data Library, April 1991

A/Reference number: S26459

A/Accession: S29588

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-102 <KAV>

A/Cross-references: UNIPARC:UPI0000115F54; EMBL:X59091; NID:952221; PIDN:CAA41817.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 497; DB 2; Length 102;  
Best Local Similarity 97.0%; Pred. No. 2e-35;  
Matches 96; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LTOSPTTMAASPGKITTTCGASSSISNNYLMHWQORPGFSPKLLIYRTSNLASGVPARF 63  
Db 4 LTOSPTTMAASPGKITTTCGASSSISNNYLMHWQORPGFSPKLLIYRTSNLASGVPARF 63

RESULT 9  
S29582  
Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000

C/Accession: S29582

R/Kavaler, J.

submitted to the EMBL Data Library, April 1991

A/Reference number: S26459

A/Accession: S29582

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-102 <KAV>

A/Cross-references: UNIPARC:UPI0000115F59; EMBL:X59091; NID:952201; PIDN:CAA41823.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 87.6%; Score 493; DB 2; Length 102;  
Best Local Similarity 96.0%; Pred. No. 4, 4e-35;  
Matches 95; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LTOSPTTMAASPGKITTTCGASSSISNNYLMHWQORPGFSPKLLIYRTSNLASGVPARF 63  
Db 4 LTOSPTTMAASPGKITTTCGASSSISNNYLMHWQORPGFSPKLLIYRTSNLASGVPARF 63

Qy 64 SGSGSGTYSLLTGTMEADVATYYCOQGSIPRTFGG 102  
Db 64 SGSGSGTYSLLTGTMEADVATYYCOQGSIPRTFGG 102

RESULT 10  
S13696  
Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000

C/Accession: S13696

R/Pennell, C.A.; Mercollino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

Eur. J. Immunol. 19, 1289-1295, 1989

A/Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl

A/Reference number: S13685; MUID:89338557; PMID:2503389

A/Accession: S13696

A/Molecule type: mRNA

A/Residues: 1-101 <PEN>

A/Cross-references: UNIPARC:UPI0000113778; EMBL:X53349; NID:955297; PIDN:CAA37435.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 84.9%; Score 478; DB 2; Length 101;  
Best Local Similarity 95.9%; Pred. No. 8e-34;  
Matches 93; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LTOSPTTMAASPGKITTTCGASSSISNNYLMHWQORPGFSPKLLIYRTSNLASGVPARF 63  
Db 4 LTOSPTTMAASPGKITTTCGASSSISNNYLMHWQORPGFSPKLLIYRTSNLASGVPARF 63

Qy 64 SGSGSGTYSLLTGTMEADVATYYCOQGSIPRTFG 100  
Db 64 SGSGSGTYSLLTGTMEADVATYYCOQGSIPRTFG 100

RESULT 11  
S13697  
Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C/Accession: S13697

R/Pennell, C.A.; Mercollino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

Eur. J. Immunol. 19, 1289-1295, 1989

A/Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl

A/Reference number: S13685; MUID:89338557; PMID:2503389

A/Accession: S13697  
A/Molecule type: mRNA  
A/Residues: 1-102 <PEN>  
A/Cross-references: UNIPROT:Q9JL78; UNIPARC:UPI00001767B5; EMBL:X53350  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin

Query Match 84.9%; Score 478; DB 2; Length 102;  
Best Local Similarity 93.9%; Pred. No. 8.1e-34;  
Matches 93; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 ITQSPPTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARF 63  
DB 4 LTQSPPTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARF 63  
QY 64 GSGSGSTSLITGTMEADVAITYCCQGSIPRTFGG 102  
DB 64 GSGSGSTSLITGTMEADVAITYCCQGSIPRTFGG 102

## RESULT 12

S13698  
Ig heavy chain V region - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C/Accession: S13698  
R/Clauckson, T.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.  
Bur. J. Immunol. 19, 1289-1295, 1989  
A/Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl  
A/Reference number: S13685; MUID:89338557; PMID:2503389  
A/Accession: S13698  
A/Molecule type: mRNA  
A/Residues: 1-103 <PEN>  
A/Cross-references: UNIPROT:Q9JL78; UNIPARC:UPI00001767B6; EMBL:X53351  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/16-91/Domain: immunoglobulin homology <IMV>

Query Match 84.1%; Score 473.5; DB 2; Length 103;  
Best Local Similarity 94.0%; Pred. No. 2e-33;  
Matches 94; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 4 ITQSPPTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARF 63  
DB 4 LTQSPPTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARF 63  
QY 64 GSGSGSTSLITGTMEADVAITYCCQGSIPRTFGG 102  
DB 64 GSGSGSTSLITGTMEADVAITYCCQGSIPRTFGG 102

## RESULT 13

S17633  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S17633  
R/Clauckson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352, 624-628, 1991  
A/Title: Making antibody fragments using phage display libraries.  
A/Reference number: S17230; MUID:91326098; PMID:1907718  
A/Accession: S17633  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-93 <CLA>  
A/Cross-references: UNIPARC:UPI00001767FA  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/18-83/Domain: immunoglobulin homology <IMV>

Query Match 83.1%; Score 468; DB 2; Length 93;  
Best Local Similarity 96.8%; Pred. No. 5.2e-33;  
Matches 90; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 TTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARFSGSGS 68  
DB 1 TTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARFSGSGS 60  
QY 69 GTSYSLITGTMEADVAITYCCQGSIPRTFGG 101  
DB 61 GTSYSLITGTMEADVAITYCCQGSIPRTFGG 93

## RESULT 14

S17635  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
C/Accession: S17635  
R/Clauckson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352, 624-628, 1991  
A/Title: Making antibody fragments using phage display libraries.  
A/Reference number: S17230; MUID:91326098; PMID:1907718  
A/Accession: S17635  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-93 <CLA>  
A/Cross-references: UNIPARC:UPI00001767FC  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/18-83/Domain: immunoglobulin homology <IMV>

Query Match 82.9%; Score 467; DB 2; Length 93;  
Best Local Similarity 96.8%; Pred. No. 6.3e-33;  
Matches 90; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 TTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARFSGSGS 68  
DB 1 TTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARFSGSGS 60  
QY 69 GTSYSLITGTMEADVAITYCCQGSIPRTFGG 101  
DB 61 GTSYSLITGTMEADVAITYCCQGSIPRTFGG 93

## RESULT 15

S17631  
Ig kappa chain V region - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C/Accession: S17631  
R/Clauckson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.  
Nature 352, 624-628, 1991  
A/Title: Making antibody fragments using phage display libraries.  
A/Reference number: S17230; MUID:91326098; PMID:1907718  
A/Accession: S17631  
A/Status: preliminary  
A/Molecule type: nucleic acid  
A/Residues: 1-93 <CLA>  
A/Cross-references: UNIPROT:Q9JL78; UNIPARC:UPI00001767F8  
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotrimer; immunoglobulin  
F/18-83/Domain: immunoglobulin homology <IMV>

Query Match 82.4%; Score 464; DB 2; Length 93;  
Best Local Similarity 95.7%; Pred. No. 1.1e-32;  
Matches 89; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 TTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARFSGSGS 68  
DB 1 TTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARFSGSGS 60  
QY 69 GTSYSLITGTMEADVAITYCCQGSIPRTFGG 101  
DB 61 GTSYSLITGTMEADVAITYCCQGSIPRTFGG 93

Search completed: November 21, 2005, 12:22:13  
Job time : 26.5513 secs

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OW protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55 ; Search time 161.304 Seconds  
(without alignments)  
476.756 Million cell updates/sec

Title: US-10-632-706-89  
Perfect score: 563  
Sequence: 1 DSELTQSPPTMAASPGEKIT.....QQGSSIPRTGGGTGLKIR 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	ID	Description
1	494.5	87.8	Q9JL78_MOUSE	Q9JL78 mus musculu
2	454	80.6	Q8K1P1_MOUSE	Q8K1P1 mus musculu
3	431	76.6	Q8K1P2_MOUSE	Q8K1P2 mus musculu
4	431	76.6	Q8K1P3_MOUSE	Q8K1P3 mus musculu
5	428	76.0	Q8VD00_MOUSE	Q8VD00 mus musculu
6	417.5	74.2	Q811C3_MOUSE	Q811C3 mus musculu
7	417	74.1	Q569Y8_MOUSE	Q569Y8 mus musculu
8	416	73.9	Q569Y8_MOUSE	Q569Y8 mus musculu
9	411	73.0	Q9U4I0_MOUSE	Q9U4I0 mus musculu
10	409	72.6	Q8K1P0_MOUSE	Q8K1P0 mus musculu
11	405	71.9	Q58EV6_MOUSE	Q58EV6 mus musculu
12	401	71.2	Q8K1P1_MOUSE	Q8K1P1 mus musculu
13	398	70.3	Q8K1P2_MOUSE	Q8K1P2 mus musculu
14	396	70.3	Q8K1P3_MOUSE	Q8K1P3 mus musculu
15	395	70.2	Q8K1P0_MOUSE	Q8K1P0 mus musculu
16	395	70.2	Q8K1P1_MOUSE	Q8K1P1 mus musculu
17	394	70.0	Q8K1P2_MOUSE	Q8K1P2 mus musculu
18	394	70.0	Q8K1P3_MOUSE	Q8K1P3 mus musculu
19	379.5	67.4	Q8K1P0_MOUSE	Q8K1P0 mus musculu
20	376.5	66.9	Q8K1P1_MOUSE	Q8K1P1 mus musculu
21	376	66.8	Q8K1P2_MOUSE	Q8K1P2 mus musculu
22	376	66.8	Q8K1P3_MOUSE	Q8K1P3 mus musculu
23	374.5	66.5	Q8K1P0_MOUSE	Q8K1P0 mus musculu
24	374.5	66.5	Q8K1P1_MOUSE	Q8K1P1 mus musculu
25	374.5	66.5	Q8K1P2_MOUSE	Q8K1P2 mus musculu
26	373.5	66.3	Q8K1P3_MOUSE	Q8K1P3 mus musculu
27	372.5	66.2	Q8K1P0_MOUSE	Q8K1P0 mus musculu
28	371	65.9	Q8K1P1_MOUSE	Q8K1P1 mus musculu
29	370	65.7	Q8K1P2_MOUSE	Q8K1P2 mus musculu
30	368.5	65.5	Q8K1P3_MOUSE	Q8K1P3 mus musculu
31	368.5	65.5	Q8K1P0_MOUSE	Q8K1P0 mus musculu

32	368	65.4	107	1	KV6C_MOUSE	P01677 mus musculu
33	367.5	65.3	111	1	KV3R_MOUSE	P01670 mus musculu
34	366	65.0	109	2	Q9JL78_HUMAN	Q9JL78 homo sapien
35	364.5	64.7	236	2	Q6P1H7_HUMAN	Q6P1H7 homo sapien
36	363	64.5	107	2	Q96SA9_HUMAN	Q96SA9 homo sapien
37	362.5	64.4	244	2	Q65ZC8_HUMAN	Q65ZC8 homo sapien
38	362	64.3	129	1	KV1L_HUMAN	P18135 homo sapien
39	361.5	64.2	108	1	KV5P_MOUSE	P01649 mus musculu
40	360.5	64.0	111	2	Q920E9_MOUSE	Q920E9 mus musculu
41	360.5	64.0	236	1	Q7TS98_MOUSE	Q7TS98 mus musculu
42	359.5	63.9	108	1	KV1O_HUMAN	P01607 homo sapien
43	359	63.8	109	1	KV3E_HUMAN	P01623 homo sapien
44	358.5	63.7	108	2	Q9JL77_HUMAN	Q9JL77 homo sapien
45	357.5	63.5	236	2	Q6CKX8_HUMAN	Q6CKX8 homo sapien

ALIGNMENTS

RESULT 1  
Q9JL78\_MOUSE  
ID Q9JL78\_MOUSE PRELIMINARY; PRT; 101 AA.  
AC Q9JL78;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Anti-myosin immunoglobulin light chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Oryzomyiidae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC SPRAIN-A, CA.  
RX MEDLINE=20448942; PubMed=10992488;  
RX DOI=10.1128/IAI.68.10.5803-5808.2000;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin";  
RT Infect. Immun. 68:5803-5808 (2000).  
RL J. Exp. Med. 170:1-13 (1989).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1907718;  
RA Claesson T., Hoogenboom R.R., Griffiths A.D., Winter G.;  
RT "Making antibody fragments using phage display libraries";  
RL Nature 352:624-628 (1991).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=89338557; PubMed=2503389;  
RA Pennell C.A., Mercollino T.J., Grdina T.A., Arnold L.W., Houghton G., Clarke S.H.;  
RT "Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection";  
RL Eur. J. Immunol. 19:1289-1295 (1989).  
DR EMBL, AF206028; AF69326.1; -, mRNA.  
DR PIR, PS0069; PS0069.  
DR PIR, S13697; S13697.  
DR PIR, S13698; S13698.  
DR PIR, S17631; S17631.  
DR HSSP, P01679; 2PBJ.  
DR SMR, Q9JL78; 3-101.  
DR Ensemble; ENSMUSG00000056850; Mus musculus.

DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 101  
 SQ SEQUENCE 101 AA; 10778 MW; 0A7F6586A7E6F14D CRC64;

Query Match 87.8%; Score 494.5; DB 2; Length 101;  
 Best Local Similarity 96.0%; Pred. No. 1.3e-41;  
 Matches 97; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 9 TMAASPGKITTTSASSSISNLYLHWYQGRPGFSPKLIYRTSNLASGVPARFSGSS 68  
 DB 1 TMAASPGKITTTSASSSISNLYLHWYQGRPGFSPKLIYRTSNLASGVPARFSGSS 60  
 QY 69 GTSYSLTIGTMEADVATYTCQGSISPR-TFGGQTKLEIK 108  
 DB 61 GTSYSLTIGTMEADVATYTCQGSISPR-TFGGQTKLEIK 101

## RESULT 2

Q8K1F1\_MOUSE  
 ID Q8K1F1\_MOUSE PRELIMINARY; PRT; 114 AA.  
 AC Q8K1F1;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Anti-VIPase light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;  
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC PubMed:2499887;  
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;  
 RT "Two murine natural polyreactive autoantibodies are encoded by  
 RT nonmutated germ-line genes."; Genomic\_DNA.  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;  
 RA Tildman D.M., Jou N.T., Hill R.J., Marion T.N.;  
 RT "Both IGM and IGG anti-DNA antibodies are the products of clonally  
 RT selective B cell stimulation in (NZB x NZM) F1 mice.";  
 RL J. Exp. Med. 176:761-779 (1992).  
 DR EMBL; AF516284; AAM64202.1; -; Genomic\_DNA.  
 DR PIR; A33933; A33933.  
 DR PIR; PH1058; PH1058.  
 DR HSSP; P01837; 25C8.  
 DR SMR; Q8K1F1; 2-114.  
 DR Ensembl; ENSMUSG0000059896; Mus musculus.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 114  
 SQ SEQUENCE 114 AA; 12163 MW; 8BD9833DBF3BEFD1 CRC64;

Query Match 80.6%; Score 454; DB 2; Length 114;  
 Best Local Similarity 80.7%; Pred. No. 1.7e-37;  
 Matches 88; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 DSELQSPPTMAASPGKITTTSASSSISNLYLHWYQGRPGFSPKLIYRTSNLASGVP 60  
 DB 1 DSELQSPPTMAASPGKITTTSASSSISNLYLHWYQGRPGFSPKLIYRTSNLASGVP 60

DB 1 DIVLTQSPAIMSAPGKIVTTCRASSVSSYLHWYQKSGASPKLIYRTSNLASGVP 60  
 QY 61 ARFSGSGGTSTSLTIGTMEADVATYTCQGSISPR-TFGGQTKLEIK 109  
 DB 61 ARFSGSGGTSTSLTIGTMEADVATYTCQGSISPR-TFGGQTKLEIK 109

## RESULT 3

Q8K1F2\_MOUSE  
 ID Q8K1F2\_MOUSE PRELIMINARY; PRT; 112 AA.  
 AC Q8K1F2;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Anti-VIPase light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;  
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC PubMed:2499887;  
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;  
 RT "Two murine natural polyreactive autoantibodies are encoded by  
 RT nonmutated germ-line genes."; Genomic\_DNA.  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).  
 DR EMBL; AF516283; AAM64201.1; -; Genomic\_DNA.  
 DR PIR; H33932; H33932.  
 DR HSSP; P01837; 25C8.  
 DR SMR; Q8K1F2; 2-112.  
 DR Ensembl; ENSMUSG0000064150; Mus musculus.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 112  
 SQ SEQUENCE 112 AA; 11953 MW; 4716887FADB543BD CRC64;

Query Match 76.6%; Score 431; DB 2; Length 112;  
 Best Local Similarity 77.1%; Pred. No. 3.3e-35;  
 Matches 84; Conservative 8; Mismatches 15; Indels 2; Gaps 1;

QY 1 DSELQSPPTMAASPGKITTTSASSSISNLYLHWYQGRPGFSPKLIYRTSNLASGVP 60  
 DB 1 DIVLTQSPAIMSAPGKIVTTCRASSVSSYLHWYQKSGASPKLIYRTSNLASGVP 58  
 QY 61 ARFSGSGGTSTSLTIGTMEADVATYTCQGSISPR-TFGGQTKLEIK 109  
 DB 59 ARFSGSGGTSTSLTIGTMEADVATYTCQGSISPR-TFGGQTKLEIK 107

## RESULT 4

Q8K1F3\_MOUSE  
 ID Q8K1F3\_MOUSE PRELIMINARY; PRT; 112 AA.  
 AC Q8K1F3;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Anti-VIPase light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.  
 RN [1]



RC STRAIN=BALE/c; TISSUE=Hyperimmunized spleen;  
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed:2499887.  
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;  
 RT "Two murine natural polyreactive autoantibodies are encoded by  
 RT nonmutated germ-line genes."  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE:92381444; PubMed:1512540; DOI=10.1084/jem.176.3.761;  
 RA Tilieman D.M., Jou N.T., Hill R.J., Marion T.N.;  
 RT "Both IgM and IgG anti-DNA antibodies are the products of clonally  
 RT selective B cell stimulation in (NZB x NZW)F1 mice."  
 RL J. Exp. Med. 176:761-779(1992).  
 DR EMBL; AF516282; AA64200.1; -; Genomic\_DNA.  
 DR PIR; A33933; A33933.  
 DR HSSP; P01837; 25C8.  
 DR SMR; Q8KLF3; 2-112.  
 DR Ensembl; ENSMUSG0000063156; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;  
 SQ  
 Query Match 76.6%; Score 431; DB 2; Length 112;  
 Best Local Similarity 78.0%; Pred. No. 3.3e-35;  
 Matches 85; Conservative 8; Mismatches 14; Indels 2; Gaps 1;  
 QY 1 DSELTQPTMAASPGKKTITTCASASSISNTLHWYQQRPGSPKLLYRTSNTLASGV 60  
 DB 1 DIVLTQSPAIMSASPGKKTITTCASASSIS--YMYWYQQRPGSPKMWIRTSNLASGV 58  
 QY 61 ARPSGSGTSYSLTGTMEADVATYTCQGSISIPRTFGGTFKLEIKR 109  
 DB 59 ARPSGSGTSYSLTISMEADATYTCQGHSHYPTFGGTFKLEIKR 107  
 DB  
 RESULT 5  
 Q8VDD0 MOUSE PRELIMINARY; PRT; 134 AA.  
 ID Q8VDD0  
 AC Q8VDD0  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Anti-MOG Z12 variable light chain (fragment).  
 GN Name=gmi502; Synonym=anti-MOG kappa;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BALE/c;  
 RA Sembli P.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BALE/c;  
 RA Chernajovsky Y.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed:2427335;  
 RA Cation A.J., Brownlee G.G., Staedt L.M., Gerhard W.;  
 RT "Structural and functional implications of a restricted antibody

RT response to a defined antigenic region on the influenza virus  
 RT hemagglutinin.";  
 RL EMBL; AJ41577-1587(1986).  
 DR EMBL; AJ415331; CAC94866.1; -; mRNA.  
 DR PIR; G27887; G27887.  
 DR HSSP; P01834; 1M1M.  
 DR SMR; Q8VDD0; 23-134.  
 DR Ensembl; ENSMUSG0000062047; Mus musculus.  
 DR MGI; MGI:2686348; Gm1502.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 134  
 FT SEQUENCE 134 AA; 14525 MW; CFPD8E2236E2DC6 CRC64;  
 SQ  
 Query Match 76.0%; Score 428; DB 2; Length 134;  
 Best Local Similarity 80.2%; Pred. No. 8.1e-35;  
 Matches 85; Conservative 5; Mismatches 14; Indels 2; Gaps 1;  
 QY 4 LTQSPPTMAASPGKKTITTCASASSISNTLHWYQQRPGSPKLLYRTSNTLASGV 63  
 DB 26 LTQSPAIMSASPGKKTITTCASASSIS--YMYWYQQRPGSPKMWIRTSNLASGV 63  
 QY 64 SSGSGSGTSYSLTGTMEADVATYTCQGSISIPRTFGGTFKLEIKR 109  
 DB 84 SSGSGSGTSYSLTISMEADATYTCQGHSHYPTFGGTFKLEIKR 129  
 DB  
 RESULT 6  
 Q81IC3 MOUSE PRELIMINARY; PRT; 131 AA.  
 ID Q81IC3  
 AC Q81IC3  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Immunoglobulin gamma-3 kappa chain precursor (fragment).  
 OS Mus musculus (mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=MRL/MPJ-1pr/1pr; TISSUE=spleen;  
 RX MEDLINE=93156722; PubMed=8429833; DOI=10.1016/0161-5890(93)90089-T;  
 RA Takahashi S., Itoh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;  
 RT "Cloning and cDNA sequence analysis of dephlogenic monoclonal  
 RT antibodies derived from an MRL/lpr lupus mouse."  
 RL Mol. Immunol. 30:177-182(1993).  
 DR EMBL; D14629; BAA03482.1; -; mRNA.  
 DR HSSP; P01679; 2FBJ.  
 DR SMR; Q81IC3; 23-131.  
 DR Ensembl; ENSMUSG0000058987; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 KW Signal.  
 FT SIGNAL 1 22 Potential.  
 FT CHAIN 23 >131 immunoglobulin gamma-3 kappa chain.  
 FT NON\_TER 131  
 FT SEQUENCE 131 AA; 14083 MW; SE83656946689E CRC64;  
 SQ  
 Query Match 74.2%; Score 417.5; DB 2; Length 131;  
 Best Local Similarity 76.4%; Pred. No. 8.8e-34;  
 Matches 81; Conservative 8; Mismatches 16; Indels 1; Gaps 1;  
 QY 4 LTQSPPTMAASPGKKTITTCASASSISNTLHWYQQRPGSPKLLYRTSNTLASGV 63  
 DB 26 LTQSPAIMSASPGKKTITTCASASSISNTLHWYQQRPGSPKMWIRTSNLASGV 63  
 QY 64 SSGSGSGTSYSLTGTMEADVATYTCQGSISIPRTFGGTFKLEIKR 108

Db 86 SGGSGTSTLTSSVEAEDATYCCQYDSSPSITFGAGTLELK 131

	RESULT	7		
ID	Q569Y8_MOUSE	PRELMINARY;	PRT;	237 AA.
AC	Q569Y8_			
DT	10-MAY-2005 (TrEMBLrel. 30,			Created)
DT	10-MAY-2005 (TrEMBLrel. 30,			last sequence update)
DT	10-MAY-2005 (TrEMBLrel. 30,			last annotation update)
DE	Igk-C protein.			
GN	Name=Igk-C;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteleia; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Myrodidae; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NCITROTIDE SEQUENCE.			
RC	STRAIN=FVB/N; TISSUE=Kidney;			
RX	MEDLINE=223825; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Braunberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D.,			
RA	Altshul S.F., Zeeberg B., Buco K.H., Scheffer C.J., Bhut N.K.,			
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heish F.,			
RA	Diatchenko L., Marninska K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udell T.B., Tohyuki S., Carruth P., Prange C.,			
RA	Raita S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren R.J., Lu X., Gibbs R.A.,			
RA	Fahy U., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmuetz J., Myers R.M.,			
RA	Buchanan A., Schein J.E., Jones S.J.M., Skatela U., Smallos D.E.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	NCITROTIDE SEQUENCE.			
RC	STRAIN=FVB/N; TISSUE=Kidney;			
RG	NIH MGC project:			
RL	Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; BC092251; AAH92251.1; -, mRNA.			
DR	BNR; Q569Y8; 23-237.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig cl.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF07654; Cl-sect; 1.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 1.			
DR	PROSITE; PSS0835; IG_LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN; 1.			
DR	SEQUENCE 237 AA; 25978 MW; A88596AA47F7B932 CRC64;			

ID	NAME	STANDARD	PROT	AA
KV4A_MOUSE				
AC	P01680			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	IG kappa chain V-IV region S107B precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muroidea; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NCBIROTOR SEQUENCE.			
RX	MEDLINE=82115300; PubMed=6799208; DOI=10.1016/0092-8674(81)90033-7;			
RA	Kwan S.-P., Max E.E., Seidman J.G., Leder P., Schaff E.M.D.;			
RT	"Two kappa immunoglobulin genes are expressed in the myeloma S107.";			
RL	Cell 26:57-66 (1981).			
CC	-1- MISCELLANEOUS: This protein, in which there is a deletion of two			
CC	amino acids at the V-J recombination site (after position 118), is			
CC	synthesized but not secreted in cells that express and secrete the			
CC	normal kappa chain S107.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			

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          RESULT 9
          Q9U410 MOUSE
          ID  Q9U410_ MOUSE PRELIMINARY;      PRT;      106 AA
          AC  Q9U410;

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DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DB Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30  
 DB Immunoglobulin light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX PubMed=12567627;  
 RP NUCLEOTIDE SEQUENCE.  
 RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Yu X.C., Xiong Y., Yin C.C.,  
 RA Huang H.L., Guan X.H.;  
 RT "Cloning and sequence analysis of the light chain variable region  
 RT gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma  
 RT japonicum".  
 RL Zhongguo Ji Sheng Chong Xue Yu Ji Sheng Chong Bing Za Zhi  
 RL 18:257-259(2000).  
 DR EMBL; AF207620; AAF19434.1; -; Genomic\_DNA.  
 DR HSSP; P01679; 2PBJ.  
 DR SMR; Q9U410; 4-106.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 106  
 SQ SEQUENCE 106 AA; 11478 MW; P20F544426BAE63B CRC64;  
  
 Query Match 72.6%; Score 411; DB 2; Length 106;  
 Best Local Similarity 76.2%; Pred. No. 3.1e-33;  
 Matches 80; Conservative 9; Mismatches 14; Indels 2; Gaps 1;  
  
 QY 4 LTGSPPTMAASPEKIKTTTCSASSISNTLHWYQQRPGSPKLLIRTSNLASGV 63  
 DB 4 LTGSPAIMASPEKIKTTTCSASSISNTLHWYQQRPGSPKLLIRTSNLASGV 61  
 64 SGSSGSGSYSLTIGTMEADVATYCCQGSISIPRTFGGTLKLR 108  
 DB 62 SGSSGSGSYSLTISRMEADVATYCCQGSISIPRTFGGTLKLR 106  
  
 RESULT 10  
 OSKIF0 MOUSE PRELIMINARY; PRT; 112 AA.  
 AC OSKIF0;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Anti-viral light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX PubMed=249887;  
 RP NUCLEOTIDE SEQUENCE.  
 RA STRAIN=BAJB/c; TISSUE=Hyperimmunized spleen;  
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Baccala R., Quang T.V., Gilbert M., Terynck T., Avrameas S.;  
 RT "Two murine natural polyclonal autoantibodies are encoded by  
 RT Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).  
 DR EMBL; AF516285; AAM64203.1; -; Genomic\_DNA.  
 DR PIR; A33933; A33933.  
 DR PIR; PC4405; PC4405.  
 DR HSSP; P01837; 10KQ.

DR SMR; OSKIF0; 3-112.  
 DR Ensemble; ENSMUSG00000062047; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
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 DR PROSITE; PSS0835; IG\_LIKE; 1.  
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 FT NON\_TER 112  
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 Query Match 72.6%; Score 409; DB 2; Length 112;  
 Best Local Similarity 74.3%; Pred. No. 5.2e-33;  
 Matches 81; Conservative 8; Mismatches 18; Indels 2; Gaps 1;  
  
 QY 1 DSELTGSPPTMAASPEKIKTTTCSASSISNTLHWYQQRPGSPKLLIRTSNLASGV 60  
 DB 1 DSELTGSPAIMASPEKIKTTTCSASSISNTLHWYQQRPGSPKLLIRTSNLASGV 58  
 61 ARPSGSGSYSLTIGTMEADVATYCCQGSISIPRTFGGTLKLR 109  
 DB 59 ARPSGSGSYSLTISRMEADVATYCCQGSISIPRTFGGTLKLR 107  
  
 RESULT 11  
 OS8EV6 MOUSE PRELIMINARY; PRT; 235 AA.  
 AC OS8EV6;  
 DT 10-MAY-2005 (TREMBlrel. 30, Created)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
 DE Igk-C protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX PubMed=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ugin T.B., Toibolyuk J., Abramson R.D., Mullaby S.J.,  
 RA Rana S.S., Loughran N.A., Peters G.J., Malek J.A., Gunaratne P.H.,  
 RA Bosak S.A., McEwan P.O., McKernan K.J., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,  
 RA Krotzfeldt Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA STRAIN=FVB/N; TISSUE=Colon;  
 RG NIH MGC Project;  
 DR EMBL; BC091738; AA91738.1; -; mRNA.  
 DR SMR; OS8EV6; 23-235.  
 DR GO; GO:0003823; P:antigen binding; IEA.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF07654; Cl-secl.1.  
 DR SMART; SM00409; Igc1.2.  
 DR SMART; SM00407; Igc1.1.  
 DR SMART; SM00406; Igc1.1.  
 DR PROSITE; PS00835; IG\_LIKE.2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN.1.  
 DR SEQUENCE 235 AA; 25719 MW; BE454ABDD2578252 CRC64;

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QY 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOORPFGSPKLIYRTSNLASGVPAF 63  
 AC P04945; 1-107.  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE IG kappa chain V-VI region NQ2-17.4.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=83271467; PubMed=6877353;  
 RA Kaattinen M., Griffiths G.M., Markham A.F., Milestein C.;  
 RT "mRNA sequences define an unusually restricted Igg response to 2-phenylloxazolone and its early diversification.";  
 RL Nature 304:320-324(1983).  
 CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.  
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 CC EMBL; K00735; AAA38680.1; -; mRNA.  
 DR HSSP; P01679; 2FB7.  
 DR SMR; P04940; 1-107.  
 DR Ensembl; ENSMUSG0000062047; Mus musculus.  
 DR InterPro; IPR007110; IG\_LIKE.  
 DR InterPro; IPR003596; IG\_V.  
 DR SMART; SM00406; Igc1.1.  
 DR PROSITE; PS00835; IG\_LIKE.1.  
 DR Hybridoma; Immunoglobulin domain; Immunoglobulin V region.  
 FT REGION 1 23 Framework-1.  
 FT REGION 24 33 Complementarity-determining-1.  
 FT REGION 34 48 Framework-2.  
 FT REGION 49 55 Complementarity-determining-2.  
 FT REGION 56 87 Framework-3.  
 FT REGION 88 96 Complementarity-determining-3.  
 FT REGION 97 106 Framework-4.  
 FT DISULFID 23 87 By similarity.  
 FT NON TER 107 107  
 SQ SEQUENCE 107 AA; 11561 MW; 6F694284E6A686 CRC64;

Query Match 71.2%; Score 401; DB 1; Length 107;  
 Best Local Similarity 74.5%; Pred. No. 3.1e-32;  
 Matches 79; Conservative 9; Mismatches 16; Indels 2; Gaps 1;

QY 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOORPFGSPKLIYRTSNLASGVPAF 63  
 AC P04945; 1-107.  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE IG kappa chain V-VI region NQ2-17.4.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=83271467; PubMed=6877353;  
 RA Kaattinen M., Griffiths G.M., Markham A.F., Milestein C.;  
 RT "mRNA sequences define an unusually restricted Igg response to 2-phenylloxazolone and its early diversification.";  
 RL Nature 304:320-324(1983).  
 CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.  
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 CC EMBL; K00735; AAA38680.1; -; mRNA.  
 DR HSSP; P01679; 2FB7.  
 DR SMR; P04940; 1-107.  
 DR Ensembl; ENSMUSG0000062047; Mus musculus.  
 DR InterPro; IPR007110; IG\_LIKE.  
 DR InterPro; IPR003596; IG\_V.  
 DR SMART; SM00406; Igc1.1.  
 DR PROSITE; PS00835; IG\_LIKE.1.  
 DR Hybridoma; Immunoglobulin domain; Immunoglobulin V region.  
 FT REGION 1 23 Framework-1.  
 FT REGION 24 33 Complementarity-determining-1.  
 FT REGION 34 48 Framework-2.  
 FT REGION 49 55 Complementarity-determining-2.  
 FT REGION 56 87 Framework-3.  
 FT REGION 88 96 Complementarity-determining-3.  
 FT REGION 97 106 Framework-4.  
 FT DISULFID 23 87 By similarity.  
 FT NON TER 107 107  
 SQ SEQUENCE 108 AA; 11713 MW; DABF235CDB680AC6 CRC64;

Query Match 70.7%; Score 398; DB 1; Length 108;  
 Best Local Similarity 73.8%; Pred. No. 6.3e-32;  
 Matches 79; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

QY 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOORPFGSPKLIYRTSNLASGVPAF 63  
 AC P04945; 1-107.  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE IG kappa chain V-VI region NQ2-17.4.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=83271467; PubMed=6877353;  
 RA Kaattinen M., Griffiths G.M., Markham A.F., Milestein C.;  
 RT "mRNA sequences define an unusually restricted Igg response to 2-phenylloxazolone and its early diversification.";  
 RL Nature 304:320-324(1983).  
 CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.  
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 CC EMBL; K00735; AAA38680.1; -; mRNA.  
 DR HSSP; P01679; 2FB7.  
 DR SMR; P04940; 1-107.  
 DR Ensembl; ENSMUSG0000062047; Mus musculus.  
 DR InterPro; IPR007110; IG\_LIKE.  
 DR InterPro; IPR003596; IG\_V.  
 DR SMART; SM00406; Igc1.1.  
 DR PROSITE; PS00835; IG\_LIKE.1.  
 DR Hybridoma; Immunoglobulin domain; Immunoglobulin V region.  
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 FT REGION 24 33 Complementarity-determining-1.  
 FT REGION 34 48 Framework-2.  
 FT REGION 49 55 Complementarity-determining-2.  
 FT REGION 56 87 Framework-3.  
 FT REGION 88 96 Complementarity-determining-3.  
 FT REGION 97 106 Framework-4.  
 FT DISULFID 23 87 By similarity.  
 FT NON TER 108 108  
 SQ SEQUENCE 108 AA; 11713 MW; DABF235CDB680AC6 CRC64;

Query Match 70.7%; Score 398; DB 1; Length 108;  
 Best Local Similarity 73.8%; Pred. No. 6.3e-32;  
 Matches 79; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

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AC P04943;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NO6-8.3.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MBDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
phenyloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; K00740; AAA38685.1; -; mRNA.
DR HSSP; P01679; 2PBJ.
DR SMR; P04943; 1-107.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR POSITE; PSS0835; Ig_LIKE; 1.
KM Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 106 Framework-4.
FT REGION 107 107 By similarity.
FT DISULFID 23 87
FT NON TER 107
SQ SEQUENCE 107 AA; 11573 MW; 6F694824ECF0C8E6 CRC64;

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Best Local Similarity 73.6%; Pred. No. 9.8e-32;
Matches 78; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 4 LTOSPTMAASPGKITTTCGASSSSISNTLHWYQORPGFSPKLLIYRTSLNLAGVPAF 63
DB 4 LTOSPAIMASPGQKVTMTCSASSVS--YHWYQORSGTSPKWIYDTSKLASGPAF 61

QY 64 SSGSGSGSYSLTIGTMEADVATYYCOQGSIPRTFGGTGLIKR 109
DB 62 SSGSGSATSYSLTITSMQADATYYCQOWSNPLTFAGTGLIKR 107

RESULT 15
KV6G MOUSE STANDARD; PRT; 107 AA.
ID KV6G MOUSE
AC P04941;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NO2-48.2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
phenyloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
CC -----
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CC removed.
CC -----
DR EMBL; K00737; AAA38682.1; -; mRNA.
DR HSSP; Q91W12; IAY1.
DR SMR; P04941; 1-103.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR POSITE; PSS0835; Ig_LIKE; 1.
KM Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 106 Framework-4.
FT DISULFID 23 87
FT NON TER 107
SQ SEQUENCE 107 AA; 11557 MW; 7248DA9BF354934 CRC64;

Query Match 70.2%; Score 395; DB 1; Length 107;
Best Local Similarity 73.6%; Pred. No. 1.2e-31;
Matches 78; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 4 LTOSPTMAASPGKITTTCGASSSSISNTLHWYQORPGFSPKLLIYRTSLNLAGVPAF 63
DB 4 LTOSPAIMASPGQKVTMTCSASSVS--YHWYQORSGTSPKWIYDTSKLASGPAF 61

QY 64 SSGSGSGSYSLTIGTMEADVATYYCOQGSIPRTFGGTGLIKR 109
DB 62 SSGSGSATSYSLTITSMQADATYYCQOWSNPLTFAGTGLIKR 107

Search completed: November 21, 2005, 12:04:06
Job time : 161.304 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:31 ; Search time 41.1245 Seconds  
(without alignments)  
219.131 Million cell updates/sec

Title: US-10-632-706-89

Perfect score: 563  
Sequence: 1 DSELTQSPPTMAASPERKIT.....QQGSSIPRTFGGTLLEIKR 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/1aa/5 COMB.pep:\*
  - 2: /cgn2\_6/ptodata/1/1aa/6 COMB.pep:\*
  - 3: /cgn2\_6/ptodata/1/1aa/H COMB.pep:\*
  - 4: /cgn2\_6/ptodata/1/1aa/PCTUS COMB.pep:\*
  - 5: /cgn2\_6/ptodata/1/1aa/RE COMB.pep:\*
  - 6: /cgn2\_6/ptodata/1/1aa/backfilestl.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	97.3	109	1	US-08-553-497A-14 Sequence 14, Appl
2	541	96.1	110	2	US-09-726-219A-247 Sequence 247, App
3	541	96.1	110	2	US-09-196-522-247 Sequence 247, App
4	540	95.9	110	2	US-09-726-219A-249 Sequence 249, App
5	540	95.9	110	2	US-09-196-522-249 Sequence 249, App
6	537	95.4	110	2	US-09-726-219A-245 Sequence 245, App
7	537	95.4	110	2	US-09-196-522-245 Sequence 245, App
8	535	95.0	110	2	US-09-726-219A-258 Sequence 258, App
9	535	95.0	110	2	US-09-196-522-258 Sequence 258, App
10	532	94.5	110	2	US-09-726-219A-238 Sequence 238, App
11	532	94.5	110	2	US-09-726-219A-248 Sequence 248, App
12	532	94.5	110	2	US-09-196-522-238 Sequence 238, App
13	532	94.5	110	2	US-09-196-522-248 Sequence 248, App
14	530	94.1	297	2	US-09-486-814A-2 Sequence 2, Appl1
15	527	93.6	110	2	US-09-726-219A-250 Sequence 250, App
16	527	93.6	110	2	US-09-196-522-250 Sequence 250, App
17	524	93.1	110	2	US-09-726-219A-246 Sequence 246, App
18	524	93.1	110	2	US-09-196-522-246 Sequence 246, App
19	518	92.0	110	2	US-09-726-219A-239 Sequence 239, App
20	518	92.0	110	2	US-09-196-522-239 Sequence 239, App
21	496	88.1	103	2	US-09-486-814A-6 Sequence 6, Appl1
22	455	80.8	108	2	US-08-881-037-74 Sequence 74, Appl
23	455	80.8	110	2	US-09-726-219A-255 Sequence 255, App
24	455	80.8	110	2	US-09-726-219A-256 Sequence 256, App
25	455	80.8	110	2	US-09-196-522-255 Sequence 255, App
26	455	80.8	110	2	US-09-196-522-256 Sequence 256, App
27	452	80.3	110	2	US-09-726-219A-257 Sequence 257, App

28	452	80.3	110	2	US-09-196-542-257 Sequence 257, App
29	450	79.9	110	2	US-09-726-219A-237 Sequence 237, App
30	450	79.9	110	2	US-09-196-542-237 Sequence 237, App
31	447	79.4	108	2	US-09-726-219A-240 Sequence 240, App
32	447	79.4	108	2	US-09-196-542-240 Sequence 240, App
33	444	78.9	110	2	US-09-726-219A-254 Sequence 254, App
34	444	78.9	110	2	US-09-196-542-254 Sequence 254, App
35	440	78.2	129	1	US-08-116-776B-2 Sequence 2, Appl1
36	440	78.2	129	1	US-08-438-542-2 Sequence 2, Appl1
37	440	78.2	129	1	US-08-483-528B-92 Sequence 92, Appl
38	439	78.0	108	2	US-09-726-219A-242 Sequence 242, App
39	439	78.0	108	2	US-09-196-522-242 Sequence 242, App
40	439	78.0	256	2	US-09-526-738A-2 Sequence 2, Appl1
41	439	78.0	258	2	US-09-526-738A-4 Sequence 4, Appl1
42	437	77.6	106	2	US-09-798-688-8 Sequence 8, Appl1
43	437	77.6	235	2	US-09-171-945-17 Sequence 17, Appl
44	437	77.6	235	2	US-09-910-059-17 Sequence 17, Appl
45	437	77.6	238	2	US-09-798-689-21 Sequence 21, Appl

#### ALIGNMENTS

RESULT 1  
US-08-553-497A-14  
Sequence 14, Application US/08553497A  
Patent No. 5844093  
GENERAL INFORMATION:  
APPLICANT: KETTERBOROUGH, C. A.  
APPLICANT: BENDIG, MARY M.  
APPLICANT: ANSELL, KEITH H.  
APPLICANT: GUSSON, DETLEF  
APPLICANT: ADAM, JAUME  
APPLICANT: MITJANS, FRANCESC  
APPLICANT: ROSEIL, ELISABET  
APPLICANT: BLASCO, FRANCESC  
APPLICANT: PILATS, JAUME  
TITLE OF INVENTION: ANTI-BGFR SINGLE-CHAIN FVS AND ANTI-BGFR  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MILLEN WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD. SUITE 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,497A  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP95/00978  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94104160.0  
FILING DATE: 17-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94118970.6  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1726  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-553-497A-14

Query Match 97.3%; Score 548; DB 1; Length 109;  
Best Local Similarity 97.2%; Pred. No. 4,9e-46;  
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DSELTOSPTTMAASPGKITTTCASASSISNNYLMWYQRRGFPKLLIYRTSNLAGVP 60  
DB 1 DIELTOSPTTMAASPGKITTTCASASSISNNYLMWYQRRGFPKLLIYRTSNLAGVP 60  
QY 61 ARFGSGSGTSTSLTIGTMEADVATYYCOOGSSIPRTFGGTLEIKR 109  
DB 61 ARFGSGSGTSTSLTIGTMEADVATYYCOOGSSIPRTFGGTLEIKR 109

## RESULT 2

US-09-726-219A-247  
Sequence 247, Application US/09726219A  
Patent No. 6806079

GENERAL INFORMATION:  
APPLICANT: Cambridge Antibody Technology  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Johnson, Kevin  
APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew  
APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kaeper  
APPLICANT: Marks, James  
APPLICANT: Clackson, Timothy  
APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory  
APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
FILE REFERENCE: 213839-00013  
CURRENT APPLICATION NUMBER: US/09/726,219A  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1990-11-12  
PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-06  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 247  
LENGTH: 110  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VL of scfv from mouse immunized with 2-phenyl-5-oxazolone  
US-09-726-219A-247

Query Match 96.1%; Score 541; DB 2; Length 110;

Best Local Similarity 96.3%; Pred. No. 2.3e-45;  
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DSELTOSPTTMAASPGKITTTCASASSISNNYLMWYQRRGFPKLLIYRTSNLAGVP 60  
DB 1 DIELTOSPTTMAASPGKITTTCASASSISNNYLMWYQRRGFPKLLIYRTSNLAGVP 60  
QY 61 ARFGSGSGTSTSLTIGTMEADVATYYCOOGSSIPRTFGGTLEIKR 109  
DB 61 ARFGSGSGTSTSLTIGTMEADVATYYCOOGSSIPRTFGGTLEIKR 109

## RESULT 3

US-09-196-522-247  
Sequence 247, Application US/09196522  
Patent No. 6916605

GENERAL INFORMATION:  
APPLICANT: Cambridge Antibody Technology  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Johnson, Kevin  
APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew  
APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kaeper  
APPLICANT: Marks, James  
APPLICANT: Clackson, Timothy  
APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory  
APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
FILE REFERENCE: 213839-00004  
CURRENT APPLICATION NUMBER: US/09/196,522  
PRIOR FILING DATE: 1998-11-28  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1990-11-12  
PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-06  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 247  
LENGTH: 110  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VL of scfv from mouse immunized with 2-phenyl-5-oxazolone  
US-09-196-522-247

Query Match 96.1%; Score 541; DB 2; Length 110;  
Best Local Similarity 96.3%; Pred. No. 2.3e-45;  
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DSELTOSPTTMAASPGKITTTCASASSISNNYLMWYQRRGFPKLLIYRTSNLAGVP 60  
DB 1 DIELTOSPTTMAASPGKITTTCASASSISNNYLMWYQRRGFPKLLIYRTSNLAGVP 60  
QY 61 ARFGSGSGTSTSLTIGTMEADVATYYCOOGSSIPRTFGGTLEIKR 109



Db 61 ARFSGSGSTSYSLTIGTMEADVATYYCOQSSIPYFGGTYKLEIKR 109

RESULT 4  
US-09-726-219A-249  
Sequence 249, Application US/09726219A  
Patent No. 6806079

## GENERAL INFORMATION:

APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Johnson, Kevin  
APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew  
APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kasper  
APPLICANT: Marks, James  
APPLICANT: Clackson, Timothy  
APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory  
APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
FILE REFERENCE: 213839-00013  
CURRENT APPLICATION NUMBER: US/09/726,219A  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1990-11-12  
PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 249  
LENGTH: 110  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone  
US-09-726-219A-249

Query Match 95.9%; Score 540; DB 2; Length 110;  
Best Local Similarity 96.3%; Pred. No. 2.9e-45;  
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DSELTOSPTTMAASPGKITTTCASSSISSNVLAHWYQORPGFSPKLLIYRTSNLASGVP 60  
Db 1 DIELTOSPTTMAASPGKITTTCASSSISSNVLAHWYQORPGFSPKLLIYRTSNLASGVP 60

Qy 61 ARFSGSGSTSYSLTIGTMEADVATYYCOQSSIPRTFGGTYKLEIKR 109  
Db 61 ARFSGSGSTSYSLTIGTMEADVATYYCOQSSIPRTFGGTYKLEIKR 109

RESULT 5  
US-09-196-522-249  
Sequence 249, Application US/09196522  
Patent No. 691605

## GENERAL INFORMATION:

APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Johnson, Kevin  
APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew  
APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kasper  
APPLICANT: Marks, James  
APPLICANT: Clackson, Timothy  
APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory  
APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
FILE REFERENCE: 213839-00004  
CURRENT APPLICATION NUMBER: US/09/196,522  
CURRENT FILING DATE: 1998-11-28  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1990-11-12  
PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 249  
LENGTH: 110  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone  
US-09-196-522-249

Query Match 95.9%; Score 540; DB 2; Length 110;  
Best Local Similarity 96.3%; Pred. No. 2.9e-45;  
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DSELTOSPTTMAASPGKITTTCASSSISSNVLAHWYQORPGFSPKLLIYRTSNLASGVP 60  
Db 1 DIELTOSPTTMAASPGKITTTCASSSISSNVLAHWYQORPGFSPKLLIYRTSNLASGVP 60

Qy 61 ARFSGSGSTSYSLTIGTMEADVATYYCOQSSIPRTFGGTYKLEIKR 109  
Db 61 ARFSGSGSTSYSLTIGTMEADVATYYCOQSSIPRTFGGTYKLEIKR 109

RESULT 6  
US-09-726-219A-245  
Sequence 245, Application US/09726219A  
Patent No. 6806079

GENERAL INFORMATION:  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Johnson, Kevin  
APPLICANT: Hoogenboom, Hendricus

```
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 245
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-245
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```
Query Match 95.4% Score 537, DB 2, Length 110;
Best Local Similarity 95.4%; Pred. No. 5,7e-45;
Matches 104; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DSELTQSPTTMAASRGKITTTCSSASSISSNYLHWYQORGFSPKLIYRTSNLAGVP 60
Db 1 DIELQSPPTMAASRGKITTTCSSASSISSNYLHWYQORGFSPKLIYRTSNLAGVP 60

Qy 61 ARFSGSGSGTSYSLITGTMEADVATYYCCQSSSIPTFGGKTLKIR 109
Db 61 ARFSGSGSGTSYSLITGTMEADVATYYCCQSSSIPTFGGKTLKIR 109

RESULT 7
US-09-196-522-245
Sequence 245, Application US/09196522
Patent No. 6916605
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
```

```
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00004
CURRENT APPLICATION NUMBER: US/09/196,522
CURRENT FILING DATE: 1998-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 245
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-196-522-245
```

```
Query Match 95.4% Score 537, DB 2, Length 110;
Best Local Similarity 95.4%; Pred. No. 5,7e-45;
Matches 104; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DSELTQSPTTMAASRGKITTTCSSASSISSNYLHWYQORGFSPKLIYRTSNLAGVP 60
Db 1 DIELQSPPTMAASRGKITTTCSSASSISSNYLHWYQORGFSPKLIYRTSNLAGVP 60

Qy 61 ARFSGSGSGTSYSLITGTMEADVATYYCCQSSSIPTFGGKTLKIR 109
Db 61 ARFSGSGSGTSYSLITGTMEADVATYYCCQSSSIPTFGGKTLKIR 109

RESULT 8
US-09-726-219A-258
Sequence 258, Application US/09726219A
Patent No. 6806079
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
```

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/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 258
/ LENGTH: 110
/ TYPE: PR1
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-258

Query Match          95.0%; Score 535; DB 2; Length 110;
Best Local Similarity 95.4%; Pred. No. 9e-45;
Matches 104; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTQSPTTMAASPGKITTTCSSASSISSNTLHWYQQRPGFSPKLLIYRTSNLASGVP 60
DB 1 DIELTQSPTTMAASPGKITTTCSSASSISSNTLHWYQQRPGFSPKLLIYRTSNLASGVP 60
QY 61 ARPSGSGSTYSLTITGTMEADVAITYCOQSSSIPTFGGKLEIKR 109
DB 61 ARPSGSGSTYSLTITGTMEADVAITYCOQSSSIPTFGGKLEIKR 109

RESULT 9
US-09-196-522-258
/ Sequence 238, Application US/09196522
/ Patent No. 6916605
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Jackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 213839-00004
/ CURRENT APPLICATION NUMBER: US/09/196,522
/ PRIOR FILING DATE: 1998-11-28
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patent version 3.1
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/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 258
/ LENGTH: 110
/ TYPE: PR1
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-196-522-258

Query Match          95.0%; Score 535; DB 2; Length 110;
Best Local Similarity 95.4%; Pred. No. 9e-45;
Matches 104; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTQSPTTMAASPGKITTTCSSASSISSNTLHWYQQRPGFSPKLLIYRTSNLASGVP 60
DB 1 DIELTQSPTTMAASPGKITTTCSSASSISSNTLHWYQQRPGFSPKLLIYRTSNLASGVP 60
QY 61 ARPSGSGSTYSLTITGTMEADVAITYCOQSSSIPTFGGKLEIKR 109
DB 61 ARPSGSGSTYSLTITGTMEADVAITYCOQSSSIPTFGGKLEIKR 109

RESULT 10
US-09-726-219A-238
/ Sequence 238, Application US/09726219A
/ Patent No. 6806079
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Jackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 213839-00003
/ CURRENT APPLICATION NUMBER: US/09/726,219A
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patent version 3.1
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; SEQ ID NO 238
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
; OS-09-726-219A-238

```

Query Match 94.5%; Score 532; DB 2; Length 110;  
Best Local Similarity 94.5%; Pred. No. 1.8e-4;  
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

[illegible]

RESULT 11  
US-09-726-219A-248

GENERAL INFORMATION:  
 APPLICANT: Cambridge Antibody Technology  
 APPLICANT: Cambridge Antibody Technology Limited  
 APPLICANT: Medical Research Council  
 APPLICANT: McCafferty, John  
 APPLICANT: Pope, Anthony  
 APPLICANT: Johnson, Kevin  
 APPLICANT: Hoogenboom, Hendricus  
 APPLICANT: Grifflths, Andrew  
 APPLICANT: Jackson, Ronald  
 APPLICANT: Holliger, Kaspar  
 APPLICANT: Marks, James  
 APPLICANT: Claesoon, Timothy  
 APPLICANT: Chiswell, David  
 APPLICANT: Winter, Gregory  
 APPLICANT: Bonert, Timothy  
 TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs

Query Match	94.5%	Score 532;	DB 2;	Length 110;
Best Local Similarity	94.5%	Pred. No. 1,8e-44;		
Matches 103; Conservative	2;	Mismatches	4;	Indels 0;
				Gaps 0;

Oy DSELTGSPPTMAASPGSEKITTTCASASS1:SSNVTLHYHOORPGSPPLLIRYTSNLSAGVP 60  
 Db 1 DILHTGSPPTMAASPGSEKITTTCASASS1:SSNHTLHYHOORPGSPPLLIRYTSNLSAGVP 60  
 Oy 61 ARFPGSGSGTSYSLTIGTMEAEADVATYYCOQSS1PRTTGGGKTLEIKR 109  
 Db 61 ARFPGSGSGTSYSLTIGTMEAEADVATYYCOQSG1PYRTGGGKTLEIKR 109

RESULT 12  
US-09-196-522-238  
; Sequence 238, Application US/09196522

```

1  GENERAL INFORMATION:
2  APPLICANT: Cambridge Antibody Technology
3  APPLICANT: Cambridge Antibody Technology Limited
4  APPLICANT: Medical Research Council
5  APPLICANT: McCafferty, John
6  APPLICANT: Pope, Anthony
7  APPLICANT: Johnson, Kevin
8  APPLICANT: Hoogenboom, Hendricus
9  APPLICANT: Griffiths, Andrew
10 APPLICANT: Jackson, Ronald
11 APPLICANT: Holliger, Kasper
12 APPLICANT: Marks, James
13 APPLICANT: Claesdon, Timothy
14 APPLICANT: Chiswell, David
15 APPLICANT: Winter, Gregory
16 APPLICANT: Bonert, Timothy
17 TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs

```

Query Match	94.5%	Score 532,	DB 2,	Length 110,
Best Local Similarity	94.5%	Pred. No. 1.8e+4,		
Matches 103; Conservative	2;	Mismatches 4;	Indels 0;	Gaps 0;

```
Oy      I DSELTQSPPTMAASPGKEITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVP    600
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 DIELTQSPTTMAASPGKEITTTCSASSISSNYLHWYQOKPGEFPKLLIYRTSNLASGVP    600
```

QY 61 ARFGSGSGTSLTGTGMEADVATYYCCQSSIPRTFGGTRKLEIKR 109  
DB 61 ARFGSGSGTSLTGTGMEADVATYYCCQSSIPRTFGGTRKLEIKR 109

RESULT 13  
US-09-196-522-248

Sequence 248, Application US/09196522  
Patent No. 6916605

## GENERAL INFORMATION:

APPLICANT: Cambridge Antibody Technology  
APPLICANT: Cambridge Antibody Technology Limited

APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John

APPLICANT: Pope, Anthony  
APPLICANT: Johnson, Kevin

APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew

APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kasper

APPLICANT: Marks, James  
APPLICANT: Clackson, Timothy

APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory

APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs

FILE REFERENCE: 213839-00004  
CURRENT FILING DATE: 1998-11-28

CURRENT FILING DATE: 1998-11-28  
PRIOR FILING DATE: 1990-07-10

PRIOR FILING DATE: 1990-07-10  
PRIOR FILING DATE: 1990-11-12

PRIOR FILING DATE: 1990-11-12  
PRIOR FILING DATE: 1990-03-06

PRIOR FILING DATE: 1990-03-06  
PRIOR FILING DATE: 1991-05-15

PRIOR FILING DATE: 1991-05-15  
PRIOR FILING DATE: 1991-07-10

PRIOR FILING DATE: 1991-07-10  
PRIOR FILING DATE: 1993-01-08

PRIOR FILING DATE: 1993-01-08  
PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272

NUMBER OF SEQ ID NOS: 272  
SOFTWARE: Patentin version 3.1

SEQ ID NO 248  
LENGTH: 110

TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone

US-09-196-522-248

Query Match 94.5%; Score 532; DB 2; Length 110;  
Best Local Similarity 94.5%; Pred. No. 1.8e-44;

Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTOSTTMAASPEKITTTCASSSSISNLYHWYQORPFGSPKLLIYRTSNLASGVP 60  
DB 1 DIELTOSTTMAASPEKITTTCASSSSISNLYHWYQORPFGSPKLLIYRTSNLASGVP 60  
QY 61 ARFGSGSGTSLTGTGMEADVATYYCCQSSIPRTFGGTRKLEIKR 109  
DB 61 ARFGSGSGTSLTGTGMEADVATYYCCQSSIPRTFGGTRKLEIKR 109

RESULT 14  
US-09-486-814A-2  
Sequence 2, Application US/09486814A

Patent No. 6562599  
GENERAL INFORMATION:  
APPLICANT: YAMAMOTO, Masato  
APPLICANT: YAMAMOTO, Masato

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APPLICANT: YAMAMOTO, Masato

Query Match 94.1%; Score 530; DB 2; Length 297;  
Best Local Similarity 93.7%; Pred. No. 8.7e-44;  
Matches 104; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 DSELTOSTTMAASPEKITTTCASSSSISNLYHWYQORPFGSPKLLIYRTSNLASGVP 60  
DB 169 DIELTOSTTMAASPEKITTTCASSSSISNLYHWYQORPFGSPKLLIYRTSNLASGVP 228  
QY 61 ARFGSGSGTSLTGTGMEADVATYYCCQSSIPRTFGGTRKLEIKR 109  
DB 229 ARFGSGSGTSLTGTGMEADVATYYCCQSSIPRTFGGTRKLEIKR 279

RESULT 15  
US-09-726-219A-250  
Sequence 250, Application US/09726219A

Patent No. 6806079  
GENERAL INFORMATION:

APPLICANT: Cambridge Antibody Technology  
APPLICANT: Cambridge Antibody Technology Limited

APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John

APPLICANT: Pope, Anthony  
APPLICANT: Johnson, Kevin

APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew

APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kasper

APPLICANT: Marks, James  
APPLICANT: Clackson, Timothy

APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory

APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs

FILE REFERENCE: 213839-00013  
CURRENT FILING DATE: 2000-11-28

CURRENT FILING DATE: 2000-11-28  
PRIOR FILING DATE: 1990-07-10

PRIOR FILING DATE: 1990-07-10  
PRIOR FILING DATE: 1990-10-19

PRIOR FILING DATE: 1990-10-19  
PRIOR FILING DATE: 1990-11-12

PRIOR FILING DATE: 1990-11-12  
PRIOR FILING DATE: 1990-11-12

PRIOR FILING DATE: 1990-11-12  
PRIOR FILING DATE: 1990-11-12

PRIOR FILING DATE: 1990-11-12  
PRIOR FILING DATE: 1990-11-12

PRIOR FILING DATE: 1990-11-12  
PRIOR FILING DATE: 1990-11-12

PRIOR FILING DATE: 1990-11-12  
PRIOR FILING DATE: 1990-11-12

PRIOR FILING DATE: 1990-11-12  
PRIOR FILING DATE: 1990-11-12



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:50:51 / Search time 134.952 Seconds  
(without alignments)  
337.478 Million cell updates/sec

Title: US-10-632-706-89

Perfect score: 1 DSELTQSPTTMAASPGKKT.....QQSSIPRTGGGTLEIKR 109

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	563	100.0	109	3	US-09-144-886-92
2	563	100.0	109	4	US-10-632-706-89
3	541	96.1	110	4	US-10-803-622-247
4	541	96.1	110	4	US-10-803-653-247
5	540	95.9	110	4	US-10-803-622-249
6	540	95.9	110	4	US-10-803-653-245
7	537	95.4	110	4	US-10-803-622-245
8	537	95.4	110	4	US-10-803-653-245
9	535	95.0	110	4	US-10-803-622-258
10	535	95.0	110	4	US-10-803-653-258
11	532	94.5	109	3	US-09-144-886-88
12	532	94.5	110	4	US-10-803-622-238
13	532	94.5	110	4	US-10-803-622-248
14	532	94.5	110	4	US-10-803-653-238
15	532	94.5	110	4	US-10-803-653-248
16	527	93.6	110	4	US-10-803-622-250
17	527	93.6	110	4	US-10-803-653-250
18	526	93.4	256	4	US-10-233-656-61
19	526	93.4	503	4	US-10-233-656-77
20	525	93.3	109	4	US-10-632-706-95
21	524	93.1	110	4	US-10-803-622-246
22	524	93.1	110	4	US-10-803-653-246
23	518	92.0	110	4	US-10-803-622-239
24	518	92.0	110	4	US-10-803-653-239
25	494	87.7	109	5	US-10-831-459-19
26	455	80.8	110	4	US-10-803-622-255
27	455	80.8	110	4	US-10-803-622-256

28	455	80.8	110	4	US-10-803-643-255	Sequence 255, App
29	455	80.8	110	4	US-10-803-622-256	Sequence 256, App
30	452	80.3	110	4	US-10-803-622-257	Sequence 257, App
31	452	80.3	110	4	US-10-803-653-257	Sequence 257, App
32	450	79.9	109	3	US-09-144-886-91	Sequence 91, App1
33	450	79.9	109	4	US-10-632-706-88	Sequence 88, App1
34	450	79.9	110	4	US-10-803-622-237	Sequence 237, App
35	450	79.9	110	4	US-10-803-653-237	Sequence 237, App
36	447	79.4	108	4	US-10-803-622-240	Sequence 240, App
37	447	79.4	108	4	US-10-803-653-240	Sequence 240, App
38	444	78.9	107	4	US-10-632-706-87	Sequence 87, App1
39	444	78.9	110	4	US-10-803-622-254	Sequence 254, App
40	444	78.9	110	4	US-10-803-653-254	Sequence 254, App
41	444	78.9	242	4	US-10-259-087A-20	Sequence 20, App1
42	444	78.9	242	4	US-10-689-006-20	Sequence 20, App1
43	443	78.7	109	4	US-10-461-878-12	Sequence 12, App1
44	443	78.7	109	5	US-10-461-885-12	Sequence 12, App1
45	442	78.5	107	3	US-09-144-886-90	Sequence 90, App1

## ALIGNMENTS

RESULT 1  
US-09-144-886-92  
Sequence 92, Application US/09144886  
Patent No. US20020155114A1  
GENERAL INFORMATION:  
APPLICANT: Marks, James D  
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize Botulinum Neurotoxin  
FILE REFERENCE: 2500.117USO  
CURRENT APPLICATION NUMBER: US/09/144, 886  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 92  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-92

Query Match 100.0%; Score 563; DB 3; Length 109;  
Best Local Similarity 100.0%; Pred. No. 5.7e-42;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSELTQSPTTMAASPGKKTITTCSSASSIS\$NYLHWYQORPSPKLLITRTSLAGVP 60  
DB 1 DSELTQSPTTMAASPGKKTITTCSSASSIS\$NYLHWYQORPSPKLLITRTSLAGVP 60  
QY 61 ARFGSGSGTSTLTITGMAEDVATYCCOQSSIPRTGGGTLEIKR 109  
DB 61 ARFGSGSGTSTLTITGMAEDVATYCCOQSSIPRTGGGTLEIKR 109

RESULT 2  
US-10-632-706-89  
Sequence 89, Application US/10632706  
Publication No. US20040175385A1  
GENERAL INFORMATION:  
APPLICANT: MARKS, JAMES D.  
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM

FILE REFERENCE: 407T-895120US  
CURRENT APPLICATION NUMBER: US/10/632, 706  
CURRENT FILING DATE: 2003-08-01  
PRIOR APPLICATION NUMBER: US 60/400, 721  
PRIOR FILING DATE: 2002-08-01

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/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 89
/ LENGTH: 109
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody
US-10-632-706-89

Query Match          100.0%; Score 563; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5-42;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DSELTOSPTTMAASPEKITTTCSSASSISSNVLMHYOORPFPSPKLLYRTSNLASGVP 60
Db      1 DSELTOSPTTMAASPEKITTTCSSASSISSNVLMHYOORPFPSPKLLYRTSNLASGVP 60

Qy      61 ARFSGSGGTSTSLTGTMEADVATYYCCQSSSIPTFTGGGKLEIKR 109
Db      61 ARFSGSGGTSTSLTGTMEADVATYYCCQSSSIPTFTGGGKLEIKR 109

RESULT 3
US-10-803-622-247
/ Sequence 247, Application US/10803622
/ Publication No. US2004015721A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT FILING DATE: US/10/803,622
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 247
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
```

```

/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-247

Query Match          96.1%; Score 541; DB 4; Length 110;
Best Local Similarity 96.3%; Pred. No. 5e-40;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 DSELTOSPTTMAASPEKITTTCSSASSISSNVLMHYOORPFPSPKLLYRTSNLASGVP 60
Db      1 DSELTOSPTTMAASPEKITTTCSSASSISSNVLMHYOORPFPSPKLLYRTSNLASGVP 60

Qy      61 ARFSGSGGTSTSLTGTMEADVATYYCCQSSSIPTFTGGGKLEIKR 109
Db      61 ARFSGSGGTSTSLTGTMEADVATYYCCQSSSIPTFTGGGKLEIKR 109

RESULT 4
US-10-803-653-247
/ Sequence 247, Application US/10803653
/ Publication No. US20040157215A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT FILING DATE: US/10/803,653
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 247
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-247

Query Match          96.1%; Score 541; DB 4; Length 110;
Best Local Similarity 96.3%; Pred. No. 5e-40;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Qy	1	USELTOGPTTMAASGEKITTTCASASSISSNYLHWYQORPSPKLLYRTSNLASGVP	60
Db	1	DIELTOSPTTMAASGEKITTTCASASSISSNYLHWYQORPSPKLLYRTSNLASGVP	60
Qy	61	ARFGSGSGTSTLTIGTMEADVATYYTTCQSSSIPTFGGKTLEIKR	109
Db	61	ARFGSGSGTSTLTIGTMEADVATYYTTCQSSSIPTFGGKTLEIKR	109
RESULT 5			
US-10-803-622-249			
Sequence 249, Application US/10803622			
Publication No. US2004015721A1			
GENERAL INFORMATION:			
APPLICANT: Cambridge Antibody Technology Limited			
APPLICANT: Cambridge Antibody Technology Limited			
APPLICANT: Medical Research Council			
APPLICANT: McCafferty, John			
APPLICANT: Pope, Anthony			
APPLICANT: Johnson, Kevin			
APPLICANT: Hoogendoorn, Hendricus			
APPLICANT: Griffiths, Andrew			
APPLICANT: Jackson, Ronald			
APPLICANT: Holliger, Kasper			
APPLICANT: Marks, James			
APPLICANT: Clarkson, Timothy			
APPLICANT: Chiswell, David			
APPLICANT: Winter, Gregory			
APPLICANT: Bonert, Timothy			
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs			
FILE REFERENCE: 13839-00013			
CURRENT APPLICATION NUMBER: US/10/803,622			
CURRENT FILING DATE: 2004-03-18			
PRIOR APPLICATION NUMBER: GB 9015198.6			
PRIOR FILING DATE: 1990-07-10			
PRIOR APPLICATION NUMBER: GB 9022845.3			
PRIOR FILING DATE: 1990-10-19			
PRIOR APPLICATION NUMBER: GB 9022845.3			
PRIOR FILING DATE: 1990-10-19			
PRIOR APPLICATION NUMBER: GB 9024503.6			
PRIOR FILING DATE: 1990-11-12			
PRIOR APPLICATION NUMBER: GB 9104744.9			
PRIOR FILING DATE: 1991-03-06			
PRIOR APPLICATION NUMBER: GB 9110549.4			
PRIOR FILING DATE: 1991-05-15			
PRIOR APPLICATION NUMBER: PCT/GB91/01134			
PRIOR FILING DATE: 1991-07-10			
PRIOR APPLICATION NUMBER: US 07/971,857			
PRIOR FILING DATE: 1993-01-08			
PRIOR APPLICATION NUMBER: US 08/464,893			
PRIOR FILING DATE: 1995-06-07			
NUMBER OF SEQ ID NOS: 272			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 249			
LENGTH: 110			
TYPE: PRT			
ORGANISM: Artificial Sequence			
FEATURES:			
OTHER INFORMATION: VL of bcfv from mouse immunized with 2-phenyl-5-oxazolone			
US-10-803-622-249			
Query Match 95.9%; Score 540; DB 4; Length 110;			
Best Local Similarity 96.3%; Pred. No. 6,1e-40;			
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;			
Qy	1	DSELTGSPPTMAASGEKITTTCASASSISSNYLHWYQORPSPKLLYRTSNLASGVP	60
Db	1	DIELTOSPTTMAASGEKITTTCASASSISSNYLHWYQORPSPKLLYRTSNLASGVP	60
Qy	61	ARFGSGSGTSTLTIGTMEADVATYYTTCQSSSIPTFGGKTLEIKR	109
Db	61	ARFGSGSGTSTLTIGTMEADVATYYTTCQSSSIPTFGGKTLEIKR	109

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RESULT 6
US-10-803-653-249
/ Sequence 249, Application US/10803653
/ Publication No. US20040157215A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonnett, Timothy
/ TITLE OR INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,653
/ CURRENT FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 249
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-249

Query Match          95.9%; Score 540; DB 4; Length 110;
Best Local Similarity 96.3%; Pred. No. 6,1e-40;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 DSELTQSTTMAASPGKRIITTSASSSISSNYLHWYQORPGSPDLLIRTSNLAAGVP 60
DB      1 DIETQSTTMAASPGKRIITTSASSSISSNYLHWYQORPGSPDLLIRTSNLAAGVP 60
QY      61 ARFGSGSGTYSYLTIGTMEADVATYYCCQSSIPRTFGGTKLEIKR 109
DB      61 ARFGSGSGTYSYLTIGTMEADVATYYCCQSSIPRTFGGTKLEIKR 109

RESULT 7
US-10-803-622-245
/ Sequence 245, Application US/10803622
/ Publication No. US20040157214A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited

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/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clarkson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,622
/ PRIOR FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 245
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-245

Query Match          95.4%; Score 537; DB 4; Length 110;
Best Local Similarity 95.4%; Pred. No. 1.1e-39;
Matches 104; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 DSELTGSPPTMAAPGKRIITTCASSSISSNYLHWYQKRGFSPKLIYTSNLASGVP 60
Db 1 DIELTQSPPTMAAPGKRIITTCASSSISSNYLHWYQKRGFSPKLIYTSNLASGVP 60

Cy 61 ARFGSSGSGTSYSLITGTMEADVAITYCCQSSSIPTFGGDTLEIKR 109
Db 61 ARFGSSGSGTSYSLITGTMEADVAITYCCQSSSIPTFGGDTLEIKR 109

RESULT 8
US-10-803-653-245
/ Sequence 245, Application US/10803653
/ Publication No. US20040157215A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clarkson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,622
```

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/ APPLICANT: Marks, James
/ APPLICANT: Clarkson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,653
/ PRIOR FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 245
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-245

Query Match          95.4%; Score 537; DB 4; Length 110;
Best Local Similarity 95.4%; Pred. No. 1.1e-39;
Matches 104; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 DSELTGSPPTMAAPGKRIITTCASSSISSNYLHWYQKRGFSPKLIYTSNLASGVP 60
Db 1 DIELTQSPPTMAAPGKRIITTCASSSISSNYLHWYQKRGFSPKLIYTSNLASGVP 60

Cy 61 ARFGSSGSGTSYSLITGTMEADVAITYCCQSSSIPTFGGDTLEIKR 109
Db 61 ARFGSSGSGTSYSLITGTMEADVAITYCCQSSSIPTFGGDTLEIKR 109

RESULT 9
US-10-803-622-258
/ Sequence 258, Application US/10803622
/ Publication No. US20040157214A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clarkson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,622
```

CURRENT FILING DATE: 2004-03-18  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6  
PRIOR FILING DATE: 1990-11-12  
PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 258  
LENGTH: 110  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazalone  
US-10-803-622-258

Query Match 95.0%; Score 535; DB 4; Length 110;  
Best Local Similarity 95.4%; Pred. No. 1.7e-39;  
Matches 104; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTGSPPTMAASPGKITTTCSSASSISNYLHWYQORPGSPKLLIYRTSNLASGVP 60  
DB 1 DIELTOSPTTMAASPGKITTTCSSASSISNYLHWYQORPGSPKLLIYRTSNLASGVP 60  
QY 61 ARPSGSGSGTSYSLTGTGMEADVATYYCOQSSISPTFGGKTKLEIKR 109  
DB 61 ARPSGSGSGTSYSLTGTGMEADVATYYCOQSSISPTFGGKTKLEIKR 109

RESULT 10  
US-10-803-653-258  
Sequence 258, Application US/10803653  
Publication No. US20040157215A1  
GENERAL INFORMATION:  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Cambridge Antibody Technology Limited  
APPLICANT: Medical Research Council  
APPLICANT: McCafferty, John  
APPLICANT: Pope, Anthony  
APPLICANT: Uomson, Kevin  
APPLICANT: Hoogenboom, Hendricus  
APPLICANT: Griffiths, Andrew  
APPLICANT: Jackson, Ronald  
APPLICANT: Holliger, Kasper  
APPLICANT: Marks, James  
APPLICANT: Clackson, Timothy  
APPLICANT: Chiswell, David  
APPLICANT: Winter, Gregory  
APPLICANT: Bonert, Timothy  
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
FILE REFERENCE: 1839-00013  
CURRENT APPLICATION NUMBER: US/10/803,653  
CURRENT FILING DATE: 2004-03-18  
PRIOR APPLICATION NUMBER: GB 9015198.6  
PRIOR FILING DATE: 1990-07-10  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9022845.3  
PRIOR FILING DATE: 1990-10-19  
PRIOR APPLICATION NUMBER: GB 9024503.6

PRIOR FILING DATE: 1990-11-12  
PRIOR APPLICATION NUMBER: GB 9104744.9  
PRIOR FILING DATE: 1991-03-06  
PRIOR APPLICATION NUMBER: GB 9110549.4  
PRIOR FILING DATE: 1991-05-15  
PRIOR APPLICATION NUMBER: PCT/GB91/01134  
PRIOR FILING DATE: 1991-07-10  
PRIOR APPLICATION NUMBER: US 07/971,857  
PRIOR FILING DATE: 1993-01-08  
PRIOR APPLICATION NUMBER: US 08/484,893  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 272  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 258  
LENGTH: 110  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazalone  
US-10-803-653-258

Query Match 95.0%; Score 535; DB 4; Length 110;  
Best Local Similarity 95.4%; Pred. No. 1.7e-39;  
Matches 104; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTGSPPTMAASPGKITTTCSSASSISNYLHWYQORPGSPKLLIYRTSNLASGVP 60  
DB 1 DIELTOSPTTMAASPGKITTTCSSASSISNYLHWYQORPGSPKLLIYRTSNLASGVP 60  
QY 61 ARPSGSGSGTSYSLTGTGMEADVATYYCOQSSISPTFGGKTKLEIKR 109  
DB 61 ARPSGSGSGTSYSLTGTGMEADVATYYCOQSSISPTFGGKTKLEIKR 109

RESULT 11  
US-09-144-886-98  
Sequence 98, Application US/09144886  
Patent No. US20020155114A1  
GENERAL INFORMATION:  
APPLICANT: Marks, James D  
APPLICANT: Amersdorfer, Peter  
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
TITLE OF INVENTION: Botulinum Neurotoxins  
FILE REFERENCE: 2500.117050  
CURRENT APPLICATION NUMBER: US/09/144,886  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 98  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
OTHER INFORMATION: 2B8 region VL epitope 4  
US-09-144-886-98

Query Match 94.5%; Score 532; DB 3; Length 109;  
Best Local Similarity 94.5%; Pred. No. 3.1e-39;  
Matches 103; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DSELTGSPPTMAASPGKITTTCSSASSISNYLHWYQORPGSPKLLIYRTSNLASGVP 60  
DB 1 DIELTOSPTTMAASPGKITTTCSSASSISNYLHWYQORPGSPKLLIYRTSNLASGVP 60  
QY 61 ARPSGSGSGTSYSLTGTGMEADVATYYCOQSSISPTFGGKTKLEIKR 109  
DB 61 ARPSGSGSGTSYSLTGTGMEADVATYYCOQSSISPTFGGKTKLEIKR 109

RESULT 12  
US-10-803-622-238  
Sequence 238, Application US/10803622

```
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Jackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1991-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-238
Query Match          94.5%; Score 532; DB 4; Length 110;
Best Local Similarity 94.5%; Pred. No. 3,1e-39;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DSELTQSPTTMAASPGKITTTCSSASSISSNVLMHYOQRPFSFKLITRTSNLASGP 60
Db 1 DIELTQSPTTMAASPGKITTTCSSASSISSNVLMHYOQKPFSPKLIYRTSNLASGP 60

Qy 61 ARFSGSGSGTYSYSLTIGTMEADVAITYYCOQSSSIPRTFGGDTKLEIKR 109
Db 61 ARFSGSGSGTYSYSLTIGTMEADVAITYYCOQSGSTIPRTFGAGTKLEIKR 109

RESULT 13
US-10-803-622-248
; Sequence 248, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
```

```
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Jackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-248
Query Match          94.5%; Score 532; DB 4; Length 110;
Best Local Similarity 94.5%; Pred. No. 3,1e-39;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DSELTQSPTTMAASPGKITTTCSSASSISSNVLMHYOQRPFSFKLITRTSNLASGP 60
Db 1 DIELTQSPTTMAASPGKITTTCSSASSISSNVLMHYOQKPFSPKLIYRTSNLASGP 60

Qy 61 ARFSGSGSGTYSYSLTIGTMEADVAITYYCOQSSSIPRTFGGDTKLEIKR 109
Db 61 ARFSGSGSGTYSYSLTIGTMEADVAITYYCOQSGSTIPRTFGAGTKLEIKR 109

RESULT 14
US-10-803-653-238
; Sequence 238, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Jackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
```

```
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,653
/ CURRENT FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 238
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-238

Query Match          94.5%; Score 532; DB 4; Length 110;
Best Local Similarity 94.5%; Pred. No. 3.1e-39; Indels 0; Gaps 0;
Matches 103; Conservative 2; Mismatches 4;

QY 1 DSELTGSPPTMAASPEKITTTCASASSISNHYLHWYQORPGFSPKLLIYRTSNLASGVP 60
DB 1 DIELTSPPTMAASPEKITTTCASASSISNHYLHWYQORPGFSPKLLIYRTSNLASGVP 60

QY 61 ARPSGSGSTSYSLTIGTMEADVATYYCOQSSSIPTFGGTKLEIKR 109
DB 61 ARPSGSGSTSYSLTIGTMEADVATYYCOQSGSTIPLTFAGTKLEIKR 109

RESULT 15
US-10-803-653-248
/ Sequence 248, Application US/10803653
/ Publication No. US20040157215A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Grifflths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kaeper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,653
/ CURRENT FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
```

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/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 248
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-248

Query Match          94.5%; Score 532; DB 4; Length 110;
Best Local Similarity 94.5%; Pred. No. 3.1e-39; Indels 0; Gaps 0;
Matches 103; Conservative 2; Mismatches 4;

QY 1 DSELTGSPPTMAASPEKITTTCASASSISNHYLHWYQORPGFSPKLLIYRTSNLASGVP 60
DB 1 DIELTSPPTMAASPEKITTTCASASSISNHYLHWYQORPGFSPKLLIYRTSNLASGVP 60

QY 61 ARPSGSGSTSYSLTIGTMEADVATYYCOQSSSIPTFGGTKLEIKR 109
DB 61 ARPSGSGSTSYSLTIGTMEADVATYYCOQSGSTIPLTFAGTKLEIKR 109

Search completed: November 21, 2005, 12:33:35
Job time : 135.952 secs
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; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: light chain
US-11-174-186-42
```

```

Query Match      70.7%; Score 398; DB 7; Length 213;
Best Local Similarity 73.6%; Pred. No. 4, 1e-19;
Matches 78; Conservative 9; Mismatches 17; Indels 2; Gaps 1;
```

```

Qy 4 LTGSPPTMAASPGKRTTTCASASSISSNYLHMVQORPGFSPKLLIYRTSNLAGVPAF 63
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 4 LTGSPATLSLSPGRVTLTCSASSSV--YMLWYQKQKQSSPKWIPDTSNLASGFPARF 61
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 64 SSGSGTSTSLTGTMEADVAITYCCQSSIPRTFGGTYLEIK 109
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 62 SSGSGTSTSLTISMEADATYVCHQSGVPYTFGGTYLEIKR 107
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

## RESULT 3

```

US-11-174-186-9
; Sequence 9, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VK8 light chain
US-11-174-186-9
```

```

Query Match      69.8%; Score 393; DB 7; Length 106;
Best Local Similarity 73.3%; Pred. No. 4, 9e-19;
Matches 77; Conservative 9; Mismatches 17; Indels 2; Gaps 1;
```

```

Qy 4 LTGSPPTMAASPGKRTTTCASASSISSNYLHMVQORPGFSPKLLIYRTSNLAGVPAF 63
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 4 LTGSPATLSLSPGRVTLTCSASSSV--YMLWYQKQKQSSPKWIPDTSNLASGFPARF 61
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 64 SSGSGTSTSLTGTMEADVAITYCCQSSIPRTFGGTYLEIK 108
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 62 SSGSGTSTSLTISMEADATYVCHQSGVPYTFGGTYLEIKR 106
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

## RESULT 4

```

US-11-174-186-7
; Sequence 7, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
```

```

; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VK6 light chain
US-11-174-186-7
```

```

Query Match      69.4%; Score 391; DB 7; Length 106;
Best Local Similarity 70.5%; Pred. No. 6, 4e-19;
Matches 74; Conservative 13; Mismatches 16; Indels 2; Gaps 1;
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```

Qy 4 LTGSPPTMAASPGKRTTTCASASSISSNYLHMVQORPGFSPKLLIYRTSNLAGVPAF 63
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 4 LTGSPATLSLSPGRVTLTCSASSSV--YMLWYQKQKQAPKLLIPDTSNLASGFPARF 61
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 64 SSGSGTSTSLTGTMEADVAITYCCQSSIPRTFGGTYLEIK 108
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 62 SSGSGTSTSLTISLEPDEFAVYVCHQSGVPYTFGGTYLEIKR 106
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

## RESULT 5

```

US-11-172-320-4
; Sequence 4, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates and
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BiMA 4 Light Chain
US-11-172-320-4
```

```

Query Match      69.4%; Score 391; DB 7; Length 213;
Best Local Similarity 70.8%; Pred. No. 1, 1e-16;
Matches 75; Conservative 14; Mismatches 15; Indels 2; Gaps 1;
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```

Qy 4 LTGSPPTMAASPGKRTTTCASASSISSNYLHMVQORPGFSPKLLIYRTSNLAGVPAF 63
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 4 LTGSPATLSLSPGRVTLTCSASSSV--NYTWYQKQKQAPKLLIPDTSNLASGFPARF 61
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 64 SSGSGTSTSLTGTMEADVAITYCCQSSIPRTFGGTYLEIKR 109
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 62 SSGSGTSTSLTISLEPDEFAVYVCHQSSNPYTFGGTYLEIKR 107
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

## RESULT 6

```

US-11-174-186-8
; Sequence 8, Application US/11174186
```



Publication No. US20050244418A1  
GENERAL INFORMATION:  
APPLICANT: Gullies, Stephen  
APPLICANT: Lo, Kin-Ming  
APPLICANT: Qian, Xiang  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/11/174,186  
CURRENT FILING DATE: 2005-07-01  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 8  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: VK7 light chain  
US-11-174-186-8

Query Match 69.3%; Score 390; DB 1; Length 106;  
Best Local Similarity 73.3%; Pred. No. 7, 4e-19;  
Matches 77; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

QY 4 LTQSPPTMAASPGKITTTCASASSISNYLHWYQORPGFSPKLLIYRTSNLASGVPARF 63  
DB 4 LTQSPMAASPGKITTTCASASSIS--YMLWYQKPGSSPKWIFDTSNLASGVPARF 61  
QY 64 SSGSGSGTSLTIGTMEADVATYYCOGSSIPRTGGGKLEIK 108  
DB 62 SSGSGSGTSLTISMEADVATYYCHORSGYPTGGGKLEIK 106

## RESULT 7

US-10-512-184-36  
Sequence 36, Application US/10512184  
Publication No. US20050244901A1  
GENERAL INFORMATION:  
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.  
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant  
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease  
FILE REFERENCE: 3581.01US01  
CURRENT APPLICATION NUMBER: US/10/512,184  
CURRENT FILING DATE: 2004-10-22  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1.  
SEQ ID NO 36  
LENGTH: 248  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: scFv SS2 with  
OTHER INFORMATION: specificity against Sclerotinia sclerotiorum,  
OTHER INFORMATION: originates from Mus musculus.  
US-10-512-184-36

Query Match 69.3%; Score 390; DB 1; Length 248;  
Best Local Similarity 70.6%; Pred. No. 1, 4e-18;  
Matches 77; Conservative 11; Mismatches 19; Indels 2; Gaps 1;

QY 1 DSELTQSPPTMAASPGKITTTCASASSISNYLHWYQORPGFSPKLLIYRTSNLASGVP 60  
DB 141 DIVLQSPPTMAASPGKITTTCASASSIS--NYLWYQKPGSSPKWIFDTSNLASGVP 198  
QY 61 ARPSGSGTSLTIGTMEADVATYYCOGSSIPRTGGGKLEIK 109  
DB 199 VRPSGSGTSLTISMEADVATYYCOGSSPPLTGGGKLEIK 247

RESULT 8  
US-10-512-184-50

Sequence 50, Application US/10512184  
Publication No. US20050244901A1  
GENERAL INFORMATION:  
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.  
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant  
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease  
FILE REFERENCE: 3581.01US01  
CURRENT APPLICATION NUMBER: US/10/512,184  
CURRENT FILING DATE: 2004-10-22  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 50  
LENGTH: 615  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: fusion protein  
OTHER INFORMATION: comprising the leader peptide - chitinase - linker  
OTHER INFORMATION: - scFv SS2 - cmc/his6.  
US-10-512-184-50

Query Match 69.3%; Score 390; DB 1; Length 615;  
Best Local Similarity 70.6%; Pred. No. 2, 6e-18;  
Matches 77; Conservative 11; Mismatches 19; Indels 2; Gaps 1;

QY 1 DSELTQSPPTMAASPGKITTTCASASSISNYLHWYQORPGFSPKLLIYRTSNLASGVP 60  
DB 482 DIVLQSPPTMAASPGKITTTCASASSIS--YMLWYQKPGSSPKWIFDTSNLASGVP 539  
QY 61 ARPSGSGTSLTIGTMEADVATYYCOGSSIPRTGGGKLEIK 109  
DB 540 VRPSGSGTSLTISMEADVATYYCHORSGYPTGGGKLEIK 588

## RESULT 9

US-11-174-186-15  
Sequence 15, Application US/11174186  
Publication No. US20050244418A1  
GENERAL INFORMATION:  
APPLICANT: Gullies, Stephen  
APPLICANT: Lo, Kin-Ming  
APPLICANT: Qian, Xiang  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/11/174,186  
CURRENT FILING DATE: 2005-07-01  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 15  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: KS de-immunized VK5  
US-11-174-186-15

Query Match 68.7%; Score 387; DB 7; Length 106;  
Best Local Similarity 71.4%; Pred. No. 1, 1e-18;  
Matches 75; Conservative 11; Mismatches 17; Indels 2; Gaps 1;

QY 4 LTQSPPTMAASPGKITTTCASASSISNYLHWYQORPGFSPKLLIYRTSNLASGVPARF 63  
DB 4 LTQSPMAASPGKITTTCASASSIS--YMLWYQKPGSSPKWIFDTSNLASGVPARF 61  
QY 64 SSGSGSGTSLTIGTMEADVATYYCOGSSIPRTGGGKLEIK 108  
DB 62 SSGSGSGTSLTISMEADVATYYCHORSGYPTGGGKLEIK 106

RESULT 10

US-11-174-186-16  
; Sequence 16, Application US/11174186  
; Publication No. US20050244418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilless, Stephen  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Qian, Xiang  
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
; FILE REFERENCE: LEX-019  
; CURRENT APPLICATION NUMBER: US/11/174,186  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: US 60/288,564  
; PRIOR FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURES:  
; OTHER INFORMATION: KS VK mouse  
US-11-174-186-16  
  
Query Match 67.9%; Score 382; DB 7; Length 106;  
Best Local Similarity 70.5%; Pred. No. 2,2e-18;  
Matches 74; Conservative 12; Mismatches 17; Indels 2; Gaps 1;  
  
QY 4 LTQSPFTMAAPGEEKITTCASASSISNLYLHWYQRRGFSPKLIYRTSNLASGVPAF 63  
DB 4 LTQSPATISASPGERVTTCASASSVS--YMLMWYQKQSSPKPIPTSNLASGVPAF 61  
QY 64 SSGSGGTSTSLTIGMEADVATYCCQGSSTPRTFGGTKEIK 108  
DB 62 SSGSGGTSTSLTISLEADATYCHQRRGVPYTFGGTKEIK 106  
  
RESULT 11  
US-11-172-320-8  
; Sequence 8, Application US/11172320  
; Publication No. US20050244413A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, Guenther  
; APPLICANT: Baum, Anke  
; APPLICANT: Heider, Karl-Heinz  
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using  
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates and  
; FILE REFERENCE: 1/1383  
; CURRENT APPLICATION NUMBER: US/11/172,320  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: US/10/645,215  
; PRIOR FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: EP 02 018 686.2  
; PRIOR FILING DATE: August 21, 2002  
; PRIOR APPLICATION NUMBER: US 60/405,956  
; PRIOR FILING DATE: August 26, 2002  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1.  
; SEQ ID NO 8  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Humanised Antibody BIWA 8 Light Chain  
US-11-172-320-8  
  
Query Match 67.7%; Score 381; DB 7; Length 213;  
Best Local Similarity 68.9%; Pred. No. 4,2e-18;  
Matches 73; Conservative 15; Mismatches 16; Indels 2; Gaps 1;  
  
QY 4 LTQSPFTMAAPGEEKITTCASASSISNLYLHWYQRRGFSPKLIYRTSNLASGVPAF 63  
DB 4 LTQSPATISASPGERVTTCASASSIS--NYIWMYQKQKQAPRIIYITSNLASGVPAF 61

QY 64 SSGSGGTSTSLTIGMEADVATYCCQGSSTPRTFGGTKEIKR 109  
DB 62 SSGSGGTSTSLTISLEADATYCHQRRGVPYTFGGTKEIKR 107  
  
RESULT 12  
US-10-648-816-5  
; Sequence 5, Application US/10648816  
; Publication No. US20050244405A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Bruggen, Nicholas  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists  
; FILE REFERENCE: P1717D1  
; CURRENT APPLICATION NUMBER: US/10/648,816  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: US/09/718,694  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: US 09/218,481  
; PRIOR FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SEQ ID NO 5  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-648-816-5  
  
Query Match 67.4%; Score 379.5; DB 1; Length 110;  
Best Local Similarity 65.1%; Pred. No. 3,2e-18;  
Matches 71; Conservative 22; Mismatches 15; Indels 1; Gaps 1;  
  
QY 1 DSELTQSPFTMAAPGEEKITTCASASSISNLYLHWYQRRGFSPKLIYRTSNLASGV 60  
DB 1 DIQLTQSPSSISASVGVGRVTTCASADPI-SKYNLWYQKQKQKAPKVIYFTSSLSHSGVP 59  
QY 61 ARFGSGSGTSTSLTIGMEADVATYCCQGSSTPRTFGGTKEIKR 109  
DB 60 SRFGSGSGTSTFTLITSSLOPEDATYCCQYSTVPWTFGGTKEIKR 108  
  
RESULT 13  
US-10-648-816-1  
; Sequence 1, Application US/10648816  
; Publication No. US20050244405A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Bruggen, Nicholas  
; APPLICANT: Ferrara, Napoleone  
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists  
; FILE REFERENCE: P1717D1  
; CURRENT APPLICATION NUMBER: US/10/648,816  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: US/09/718,694  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: US 09/218,481  
; PRIOR FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SEQ ID NO 1  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-648-816-1  
  
Query Match 67.1%; Score 377.5; DB 1; Length 110;  
Best Local Similarity 64.2%; Pred. No. 4,2e-18;  
Matches 70; Conservative 23; Mismatches 15; Indels 1; Gaps 1;  
  
QY 1 DSELTQSPFTMAAPGEEKITTCASASSISNLYLHWYQRRGFSPKLIYRTSNLASGV 60  
DB 1 DIQMTQSPSSISASVGVGRVTTCASADPI-SNLYLWYQKQKQKAPKVIYFTSSLSHSGVP 59

QY 61 ARFSGSGSTSYLTIGTMEADVATYYCQGSIPRTFGGTKLEIK 109  
DB 60 SRFSGSGSTYLTITLISLQPEDFATYYCQGVSTVPTFGGTKVEIKR 108

RESULT 14  
US-11-174-186-10  
Sequence 10, Application US/11174186  
Publication No. US2005024418A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
APPLICANT: Lo, Kin-Ming  
APPLICANT: Qian, Xiang  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/11/174,186  
CURRENT FILING DATE: 2005-07-01  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 10  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: KS VK veneered  
US-11-174-186-10

Query Match 67.0%; Score 377; DB 7; Length 106;  
Best Local Similarity 69.5%; Pred. No. 4.4e-18;  
Matches 73; Conservative 12; Mismatches 18; Indels 2; Gaps 1;

QY 4 LTOSPPTMAASPGKITTTCSSASSISNTLHWYQGRPGSPKLIYRTSNLASGVPARF 63  
DB 4 LTOSPASLAVSPGPRATITCSASSVS--YMLMTQQRKPGPPKPIPTDTSNLSGFPARF 61  
QY 64 SGSGSGSTSYLTIGTMEADVATYYCQGSIPRTFGGTKLEIK 108  
DB 62 SGSGSGSTSYLTITLISLQPEDFATYYCQGVSTVPTFGGTKVEIKR 106

RESULT 15  
US-11-174-186-14  
Sequence 14, Application US/11174186  
Publication No. US2005024418A1  
GENERAL INFORMATION:  
APPLICANT: Gillies, Stephen  
APPLICANT: Lo, Kin-Ming  
APPLICANT: Qian, Xiang  
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof  
FILE REFERENCE: LEX-019  
CURRENT APPLICATION NUMBER: US/11/174,186  
CURRENT FILING DATE: 2005-07-01  
PRIOR APPLICATION NUMBER: US 60/288,564  
PRIOR FILING DATE: 2001-05-03  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 14  
LENGTH: 106  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: KS de-immunized VK4  
US-11-174-186-14

Query Match 67.0%; Score 377; DB 7; Length 106;  
Best Local Similarity 69.5%; Pred. No. 4.4e-18;  
Matches 73; Conservative 12; Mismatches 18; Indels 2; Gaps 1;

QY 4 LTOSPPTMAASPGKITTTCSSASSISNTLHWYQGRPGSPKLIYRTSNLASGVPARF 63  
DB 4 LTOSPASLAVSPGPRATITCSASSVS--YMLMTQQRKPGPPKPIPTDTSNLSGFPARF 61

QY 64 SGSGSGSTSYLTIGTMEADVATYYCQGSIPRTFGGTKLEIK 108  
DB 62 SGSGSGSTSYLTITLISLQPEDFATYYCQGVSTVPTFGGTKVEIKR 106

Search completed: November 21, 2005, 12:33:51  
Job time: 3.09634 sec

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CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I) and a composition (II) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain variable region complementarily determining  
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX Sequence 11 AA;  
 SQ

Query Match 100.0%; Score 60; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0017;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATYYFGGLDV 11  
 DB 1 LATYYFGGLDV 11

RESULT 2  
 ID ADR38725 standard; peptide; 11 AA.  
 XX ADR38725;  
 AC  
 XX 02-DEC-2004 (first entry)  
 DT  
 XX Mouse heavy chain variable region CDR3 seqid 127.  
 DE  
 XX antibody; botulinum neurotoxin type A; BONT/A;  
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 KW heavy chain variable region; complementarily determining region; CDR3.  
 KM  
 XX Mus sp.  
 OS  
 XX US2004175385-A1.  
 PN  
 XX 09-SEP-2004.  
 PD  
 XX 01-AUG-2003; 2003US-00632706.  
 PF  
 XX 31-AUG-1998; 98US-00144886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Marks JD, Amerdorfer P;  
 PI  
 XX WPI, 2004-652009/63.  
 DR  
 XX New isolated antibody that neutralises botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 PT  
 XX Example 3; SEQ ID NO 127; 110P; English.

CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WRI(V), WRI(T), 3-1,  
 CC

CC 3-8, 3-10 and INGI, where (I) binds to and neutralises botulinum  
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
 CC comprising BONT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I) and a composition (II) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain variable region complementarily determining  
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX Sequence 11 AA;  
 SQ

Query Match 100.0%; Score 60; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0017;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATYYFGGLDV 11  
 DB 1 LATYYFGGLDV 11

RESULT 3  
 ID AEB45960 standard; protein; 122 AA.  
 XX AEB45960;  
 AC  
 XX 06-OCT-2005 (first entry)  
 DT  
 XX Human monoclonal anti-MadCAM antibody related protein #4.  
 DE  
 XX Monoclonal antibody; mucosal addressin cell adhesion molecule; MadCAM;  
 KW inflammation; inflammatory bowel disease; Crohn's disease;  
 KW ulcerative colitis; diverticular disease; gastritis; liver disease;  
 KW primary biliary cirrhosis; primary sclerosing cholangitis;  
 KW insulin dependent diabetes; graft versus host disease; anti-inflammatory;  
 KW gastrointestinal-gen.; antitumor; hepatotropic; antidiabetic;  
 KW immunosuppressive; antibody.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO2005067620-A2.  
 PN  
 XX 28-JUL-2005.  
 PD  
 XX 07-JAN-2005; 2005MO-US000370.  
 PF  
 XX 09-JAN-2004; 2004US-0535490P.  
 PR  
 XX (PFIZ ) PFIZER INC.  
 PA (ABGR-) ABGENIX INC.  
 XX (PFIZ ) PFIZER LTD.  
 PA  
 XX Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendelcho M;  
 PI  
 XX WPI; 2005-554958/56.  
 DR  
 XX New antibody to Mucosal Addressin Cell Adhesion Molecule, useful for  
 PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel  
 PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or  
 PT graft versus host disease.  
 PT

PS Example 5, Fig 1, 167pp; English.

XX The invention relates to a human monoclonal antibody or its antigen-  
 CC binding portion that specifically binds to mucosal addressin cell  
 CC adhesion molecule (MAdCAM). The invention also relates to a hybridoma  
 CC cell line that produces the human monoclonal antibody, a pharmaceutical  
 CC composition comprising an amount of the monoclonal antibody or its  
 CC antigen-binding portion and a pharmaceutical carrier, a method of  
 CC treating inflammatory disease in a subject, an isolated cell line that  
 CC produces the monoclonal antibody or its antigen-binding portion or the  
 CC heavy chain or light chain of the antibody or of its portion, an isolated  
 CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy  
 CC chain or its antigen-binding portion or the light chain or its antigen-  
 CC binding portion of an antibody described above, a vector comprising the  
 CC nucleic acid molecule, where the vector optionally comprises an  
 CC expression control sequence operably linked to the nucleic acid molecule,  
 CC a host cell comprising the vector or the nucleic acid molecule above, a  
 CC method of producing a human monoclonal antibody or its antigen-binding  
 CC portion that specifically binds MAdCAM, a method of isolating an antibody  
 CC or its antigen-binding portion that specifically binds to MAdCAM, a  
 CC method of treating a subject in need of a human antibody or its antigen-  
 CC binding portion that specifically binds to MAdCAM and inhibits binding to  
 CC alpha<sub>5</sub>beta<sub>1</sub>, a method of inhibiting alpha<sub>5</sub>beta<sub>1</sub> binding to cells  
 CC expressing human MAdCAM, a method of inhibiting MAdCAM-mediated leukocyte  
 CC -endothelial cell adhesion, migration and infiltration into tissues, a  
 CC method of inhibiting alpha<sub>5</sub>beta<sub>1</sub>/MAdCAM-dependent cellular adhesion,  
 CC inhibiting the MAdCAM-mediated recruitment of lymphocytes to  
 CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder  
 CC characterized by circulating soluble human MAdCAM and detecting  
 CC inflammation in a subject. The antibody, composition and methods are  
 CC useful for diagnosing and treating inflammatory disease, e.g.,  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC diverticular disease, gastritis, liver disease, primary biliary  
 CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and  
 CC graft versus host disease. This sequence represents a human monoclonal  
 CC anti-MAdCAM antibody related protein of the invention.  
 CC XX

SO Sequence 122 AA;

Query Match 80.0%; Score 48; DB 9; Length 122;  
 Best Local Similarity 63.6%; Pred. No. 2.5;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LATYYFGLDV 11  
 :|||:|:|:  
 DB 100 VTTYTYGMDV 110

RESULT 4

ADD28082  
 ID ADD28082 standard; protein; 114 AA.

AC ADD28082;

DT 15-JAN-2004 (first entry)

DE Lymphoma related immunoglobulin variable region.

XX B-cell; malignant; immunoglobulin; immunoglobulin variable region;  
 KW Ig variable region; glycosylation site; lymphoma; B cell receptor;  
 KW cytostatic; gene therapy; glycosylation inhibitor;  
 KW non-Hodgkin's lymphoma.  
 XX

OS Synthetic.  
 OS Homo sapiens.

XX WO2003074059-A2.

XX 12-SBP-2003.

XX 24-FEB-2003; 2003WO-GB000783.

XX 07-MAR-2002; 2002GB-0005395.

XX (CANC-) CANCER RES TECHNOLOGY LTD.

PA Zhu D, Stevenson F,

PI WPI, 2003-902720/82.

PT Classifying a B-cell as malignant or normal by isolating a sequence  
 PT representing an Ig variable region from the B cell, detecting the  
 PT presence of a glycosylation site and classifying the cell as malignant or  
 PT normal.

PS Disclosure, Fig 3; 61pp; English.

XX The present invention describes a method for classifying a B-cell as  
 CC malignant or normal comprising: (a) isolating a sequence representing an  
 CC immunoglobulin (Ig) variable region from the B cell; (b) detecting the  
 CC presence of a glycosylation site; and (c) classifying the cell as  
 CC malignant or normal on the basis of the presence or absence of a  
 CC glycosylation site. Also described: (1) treating a patient suffering from  
 CC or at risk of having lymphoma; (2) screening for substances capable of  
 CC inhibiting glycosylation of the Ig variable region of the B cell receptor  
 CC ; and (3) screening for substances (S) capable of inhibiting the  
 CC interaction between lectins of the type found in the germinal centre and  
 CC N-glycans found on the surface of Ig of lymphoma cells. (S) has  
 CC cyostatic activity, and can be used in gene therapy, and as a  
 CC glycosylation inhibitor. The method is useful in classifying a B-cell as  
 CC malignant or normal. The glycosylation inhibitor is useful in preparing a  
 CC medicament for treating non-Hodgkin's lymphoma. The present sequence  
 CC represents an Ig variable region sequence which is used in the  
 CC exemplification of the present invention.  
 CC XX

SO Sequence 114 AA;

Query Match 78.3%; Score 47; DB 7; Length 114;  
 Best Local Similarity 77.8%; Pred. No. 3.4;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTYTFFGLDV 11  
 |||:|:|:  
 DB 106 TTYTYGMDV 114

RESULT 5

ADD28323  
 ID ADD28323 standard; protein; 129 AA.

AC ADD28323;

DT 15-JAN-2004 (first entry)

DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:101.

XX human heterodimeric antibody; human; antibody; binding affinity;  
 KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;  
 KW edema factor; lethal factor; anthracis; anthracis; immunotherapy;  
 KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;  
 KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.  
 XX

OS Synthetic.  
 OS Homo sapiens.

XX WO2003076568-A2.

XX 18-SBP-2003.

XX 11-FEB-2003; 2003WO-US004206.

XX 11-FEB-2002; 2002US-0356086P.

XX 29-APR-2002; 2002US-0376408P.

XX 27-SBP-2002; 2002US-0414053P.

XX 25-NOV-2002; 2002US-0428807P.

PA (ALEX-) ALEXION PHARM INC.  
XX  
XX Bowdish KS, Wild MA;  
XX  
XX WPI, 2003-722327/68.  
XX  
XX New human heterodimeric antibodies or their antibody fragments, useful as  
PT anti-toxins or anti-infectives with respect to infective agents, e.g.  
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West  
PT Nile virus.  
XX  
XX  
XX Claim 11; SEQ ID NO 101; 67pp; English.  
XX  
XX The present invention describes a human heterodimeric antibody (I)  
CC (fragment) having a binding affinity of at least 1x10<sup>-8</sup> M to the  
CC protective antigen of Bacillus anthracis or a molecule involved in  
CC anthrax infection that blocks binding of the antigen or molecule to cell  
CC receptors, edema factor and lethal factor. (I) has virulence and  
CC antibacterial activities, and can be used in immunotherapy. The  
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect  
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan  
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The  
CC present sequence represents a human heterodimeric antibody heavy chain  
CC variable region amino acid sequence, which is used in the exemplification  
CC of the present invention.  
XX  
XX Sequence 129 AA;

Query Match 78.3%; Score 47; DB 7; Length 129;  
Best Local Similarity 77.8%; Pred. No. 3.9;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
||||:|  
Db 105 TTYTGMVDV 113

RESULT 6  
ADD28237  
ID ADD28237 standard; protein; 134 AA.

AC ADD28237;  
XX  
DT 15-JAN-2004 (first entry)

DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:15.

XX human heterodimeric antibody; human; antibody; binding affinity;  
KM protective antigen; Bacillus anthracis; anthrax infection; cell receptor;  
KM edema factor; lethal factor; virulence; antibacterial; immunotherapy;  
KM anti-toxin; anti-infective; anthrax; botulinum; smallpox;  
KM Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.

XX Synthetic.  
OS Homo sapiens.

XX MO2003076568-A2.

XX 18-SEP-2003.

XX 11-FEB-2003; 2003WO-US004206.

XX 11-FEB-2002; 2002US-0356086P.

XX 29-APR-2002; 2002US-0376408P.

XX 27-SEP-2002; 2002US-0414053P.

XX 25-NOV-2002; 2002US-042807P.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Wild MA;  
XX WPI, 2003-722327/68.  
XX

PT New human heterodimeric antibodies or their antibody fragments, useful as  
PT anti-toxins or anti-infectives with respect to infective agents, e.g.  
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West  
PT Nile virus.  
XX  
XX  
XX Claim 6; SEQ ID NO 15; 67pp; English.

XX The present invention describes a human heterodimeric antibody (I)  
CC (fragment) having a binding affinity of at least 1x10<sup>-8</sup> M to the  
CC protective antigen of Bacillus anthracis or a molecule involved in  
CC anthrax infection that blocks binding of the antigen or molecule to cell  
CC receptors, edema factor and lethal factor. (I) has virulence and  
CC antibacterial activities, and can be used in immunotherapy. The  
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect  
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan  
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The  
CC present sequence represents a human heterodimeric antibody heavy chain  
CC variable region amino acid sequence, which is used in the exemplification  
CC of the present invention.  
XX  
XX Sequence 134 AA;

Query Match 78.3%; Score 47; DB 7; Length 134;  
Best Local Similarity 77.8%; Pred. No. 4;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
||||:|  
Db 110 TTYTGMVDV 118

RESULT 7  
ADV86824  
ID ADV86824 standard; protein; 134 AA.

AC ADV86824;

XX 10-MAR-2005 (first entry)

DE Bacillus anthracis toxin Fab 9 K 2e G pro heavy chain variable region.

XX Bioreactor; Bacillus anthracis infection; vaccine; diagnosis;

KM antibacterial; antibody; heavy chain variable region.

XX Homo sapiens.

XX NO2004110362-A2.

XX 23-DEC-2004.

XX 26-MAY-2004; 2004MO-US016557.

XX 02-JUN-2003; 2003US-00452593.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Frederickson S, Wild MA, Maruyama T, Nolan MJ;

XX WPI, 2005-057715/06.

XX Treating an animal with anthrax infection by administering an antibody to  
PT the protective antigen of Bacillus anthracis, and blocking binding to  
PT cell receptors, edema factor or lethal factor.

XX Claim 7; SEQ ID NO 15; 87pp; English.

XX A claimed method for treating an animal infected with Bacillus anthracis  
CC comprises administering an antibody or antibody fragment that binds to a  
CC molecule involved in anthrax infection and which has the ability to block  
CC the binding of the molecule to at least one of a cell receptor, PA63,  
CC PA63 heptamer, PA83, edema factor and lethal factor. A claimed method for  
CC determining exposure to B. anthracis comprises assaying a sample for the  
CC presence of a molecule selected from cell receptors, PA63, PA63 heptamer,



CC PA83, edema factor or lethal factor with an antibody that has binding  
 CC affinity for the molecule, where the presence of elevated levels of the  
 CC antibody correlates with the presence of a disease associated with B.  
 CC anthrax. Alternatively, the method involves assaying for the presence  
 CC of an antibody to a cell receptor, PA63, PA63 heptamer, PA83, edema  
 CC factor or lethal factor with a secondary antibody having binding affinity  
 CC for the antibody, where the presence of elevated levels of the secondary  
 CC antibody correlates with the presence of B. anthracis in a subject. In  
 CC all cases, the antibody (full-length or functional fragment) may comprise  
 CC a heavy chain variable region selected from a group of sequences ADV86810  
 CC -ADV86827, a light chain kappa region selected from a group of sequences  
 CC ADV86828-ADV86835 and a light chain lambda region selected from a group  
 CC of sequences ADV86836-ADV86847. Diagnostic kits are provided. A claimed  
 CC vaccine comprises a multimer of anthrax toxin PA63. The methods and  
 CC compositions of the present invention are also useful for producing anti-  
 CC toxins or anti-infectives to infective agents such as anthrax, botulinum,  
 CC smallpox, Venezuelan equine encephalomyelitis and West Nile virus. The  
 CC present sequence is that of the heavy chain variable region of a human  
 CC Fab (designated 9 K 2e G pro) with positive reactivity to anthrax  
 CC proteins PA63 and PA83. Phage libraries were developed from mRNA isolated  
 CC from blood and bone marrow samples of donors who had been vaccinated  
 CC against anthrax. The libraries were panned against PA83 and PA63, and  
 CC sequence analysis was performed on positive responders. Neutralization of  
 CC anthrax toxin activity by purified Fabs was demonstrated.

SO Sequence 134 AA;

Query Match 78.3%; Score 47; DB 9; Length 134;  
 Best Local Similarity 77.8%; Pred. No. 4;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTYTGGLDV 11  
 ||||:|:|  
 Db 110 TTYTGGMDV 118

RESULT 8

ID ADR28082 standard; protein; 244 AA.

AC ADR28082;

DT 07-OCT-2004 (first entry)

DE NPB polypeptide scFv27, seq id 29.

KW Cytostatic; metastasis inhibitor; neuropilin binder; NPB; scFv;  
 single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.

OS Mus sp.

OS Synthetic.

Key Location/Qualifiers

Region 87..103  
 /note="complementary determining region claimed under  
 claim 5"

PN WO2004056874-A2.

PD 08-JUL-2004.

PF 22-DEC-2003; 2003WO-EP014756.

PR 20-DEC-2003; 2002US-0435893P.

PR 15-JAN-2003; 2003EP-0000615.

PA (XERI-) XERION PHARM AG.

PA (TUFT) UNIV TUFTS.

PI Unger CM, Beete G, Zehetmeier C, Iain B, Torella C, Niewoehner J;  
 Jay DG, Bustace BK, Krauer R, Jensen KH;

XX WPI; 2004-507700/48.

DR N-PSDB; ADR28116.

XX Novel neuropilin binder which is scFv, antibody fragment or bioconjugate,  
 PT that modulates neuropilin-1 function or inhibits NP-1 dependent  
 PT angiogenesis of endothelial cells and/or invasion of tumor cells useful  
 PT for treating cancer.

PS Claim 3, SEQ ID NO 29, 120pp, English.

CC The invention relates to a neuropilin binder (NPB) (1) which is a  
 CC polypeptide, antibody, scFv, antibody fragment or bioconjugate, that  
 CC modulates neuropilin-1 (NP-1) function or inhibits NP-1 dependent  
 CC angiogenesis of endothelial cells and/or invasion of tumour cells,  
 CC whereby the NPB binds to NP-1 and modulates NP-1 function. Further  
 CC disclosed is an ex vivo method of determining the dependency of the  
 CC invasiveness of a naturally occurring invasive cancer cell on the  
 CC functionality of NP-1. The NPB of the invention is an inhibitor of  
 CC metastasis of NP-1 mediated invasion and/or adhesion and an inhibitor of  
 CC tumour-associated NP-1 dependent angiogenesis. The NPB of the invention  
 CC is useful for detecting NP-1 expression, modulation of NP-1 function,  
 CC particularly modulation or inhibition of NP-dependent invasion or  
 CC adhesion of cells, preferably tumour cells. It is useful in the  
 CC manufacture of medicament for the treatment or prevention of NP-dependent  
 CC angiogenesis and non-physiological blood vessel growth, particularly  
 CC correlated with a tumour. It is also useful for treatment or prevention  
 CC of cancer and/or metastasis of tumour cells. The current sequence  
 CC represents a single chain antibody neuropilin binder (NPB) polypeptide.

SO Sequence 244 AA;

Query Match 78.3%; Score 47; DB 8; Length 244;  
 Best Local Similarity 77.8%; Pred. No. 4.7;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTYTGGLDV 11  
 ||||:|:|  
 Db 95 TTYTGGMDV 103

RESULT 9

ID AEB45891 standard; protein; 468 AA.

AC AEB45891;

DT 06-OCT-2005 (first entry)

DE Human monoclonal anti-MAdCAM antibody #37.

KW Monoclonal antibody; mucosal addressin cell adhesion molecule; MAdCAM;  
 inflammation; inflammatory bowel disease; Crohn's disease;  
 ulcerative colitis; diverticular disease; gastritis; liver disease;  
 primary biliary cirrhosis; primary sclerosing cholangitis;  
 insulin dependent diabetes; graft versus host disease; anti-inflammatory;  
 gastrointestinal-gen.; antidiabetic; hepatotropic; antidiabetic;  
 immunosuppressive; antibody.

OS Homo sapiens.

PN WO2005067620-A2.

PD 28-JUL-2005.

PF 07-JAN-2005; 2005WO-US000370.

PR 09-JAN-2004; 2004US-0535490P.

PA (PFIZ) PFIZER INC.

PA (ABGE-) ABGENIX INC.

PA (PFIZ) PFIZER LTD.

PI Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendescho M;

DR WPI; 2005-554958/56.  
 DR N-PSDB; AEB45890.  
 XX  
 PT New antibody to Mucosal Addressin Cell Adhesion Molecule, useful for  
 PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel  
 PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or  
 PT graft versus host disease.  
 XX  
 PS Claim 8; SEQ ID NO 56; 167bp; English.  
 XX  
 CC The invention relates to a human monoclonal antibody or its antigen-  
 CC binding portion that specifically binds to mucosal addressin cell  
 CC adhesion molecule (MAdCAM). The invention also relates to a hybridoma  
 CC cell line that produces the human monoclonal antibody, a pharmaceutical  
 CC composition comprising an amount of the monoclonal antibody or its  
 CC antigen-binding portion and a pharmaceutical carrier, a method of  
 CC treating inflammatory disease in a subject, an isolated cell line that  
 CC produces the monoclonal antibody or its antigen-binding portion or the  
 CC heavy chain or light chain of the antibody or of its portion, an isolated  
 CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy  
 CC chain or its antigen-binding portion or the light chain or its antigen-  
 CC binding portion of an antibody described above, a vector comprising the  
 CC nucleic acid molecule, where the vector optionally comprises an  
 CC expression control sequence operably linked to the nucleic acid molecule,  
 CC a host cell comprising the vector or the nucleic acid molecule above,  
 CC a method of producing a human monoclonal antibody or its antigen-binding  
 CC portion that specifically binds MAdCAM, a method of isolating an antibody  
 CC or its antigen-binding portion that specifically binds to MAdCAM, a  
 CC method of treating a subject in need of a human antibody or its antigen-  
 CC binding portion that specifically binds to MAdCAM and inhibits binding to  
 CC alpha/beta7, a method of inhibiting alpha/beta7 binding to cells  
 CC expressing human MAdCAM, a method of inhibiting MAdCAM-mediated leukocyte  
 CC endothelial cell adhesion, migration and infiltration into tissues, a  
 CC method of inhibiting alpha/beta7/MAdCAM-dependent cellular adhesion,  
 CC inhibiting the MAdCAM-mediated recruitment of lymphocytes to  
 CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder  
 CC characterized by circulating soluble human MAdCAM and detecting  
 CC inflammation in a subject. The antibody, composition and methods are  
 CC useful for diagnosing and treating inflammatory disease, e.g.  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC diverticular disease, gastritis, liver disease, primary biliary  
 CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and  
 CC graft versus host disease. This sequence represents a human monoclonal  
 CC anti-MAdCAM antibody of the invention.  
 XX  
 SQ Sequence 468 AA;  
 Query Match 78.3%; Score 47; DB 9; Length 468;  
 Best Local Similarity 77.8%; Pred. No. 15;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 TTYTFFGADV 11  
 DB 123 TTYTFFGADV 131  
 RESULT 10  
 ID AEB45853 standard; protein; 469 AA.  
 XX  
 AC AEB45853;  
 XX  
 DT 06-OCT-2005 (first entry)  
 XX  
 XX Human monoclonal anti-MAdCAM antibody #9.  
 XX  
 KM Monoclonal antibody; mucosal addressin cell adhesion molecule; MAdCAM;  
 KM inflammation; inflammatory bowel disease; Crohn's disease;  
 KM ulcerative colitis; diverticular disease; gastritis; liver disease;  
 KM primary biliary cirrhosis; primary sclerosing cholangitis;  
 KM insulin dependent diabetes; graft versus host disease; antiinflammatory;  
 KM gastrointestinal-gen.; antineur; hepatotropic; antidiabetic;  
 KM immunosuppressive; antibody.

XX  
 OS Homo sapiens.  
 XX  
 PN WO2005067620-A2.  
 XX  
 PD 28-JUL-2005.  
 XX  
 PF 07-JAN-2005; 2005WO-US000370.  
 XX  
 PR 09-JAN-2004; 2004US-0535490P.  
 XX  
 PA (PFIZ ) PFIZER INC.  
 PA (ABGE-) ABGENIX INC.  
 PA (PFIZ ) PFIZER LTD.  
 PI Pollen N, Molloy E, Kellermann S, Green LL, Haak-Frendelcho M;  
 DR WPI; 2005-554958/56.  
 DR N-PSDB; AEB45852.  
 XX  
 PT New antibody to Mucosal Addressin Cell Adhesion Molecule, useful for  
 PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel  
 PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or  
 PT graft versus host disease.  
 XX  
 PS Claim 8; SEQ ID NO 18; 167bp; English.  
 XX  
 CC The invention relates to a human monoclonal antibody or its antigen-  
 CC binding portion that specifically binds to mucosal addressin cell  
 CC adhesion molecule (MAdCAM). The invention also relates to a hybridoma  
 CC cell line that produces the human monoclonal antibody, a pharmaceutical  
 CC composition comprising an amount of the monoclonal antibody or its  
 CC antigen-binding portion and a pharmaceutical carrier, a method of  
 CC treating inflammatory disease in a subject, an isolated cell line that  
 CC produces the monoclonal antibody or its antigen-binding portion or the  
 CC heavy chain or light chain of the antibody or of its portion, an isolated  
 CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy  
 CC chain or its antigen-binding portion or the light chain or its antigen-  
 CC binding portion of an antibody described above, a vector comprising the  
 CC nucleic acid molecule, where the vector optionally comprises an  
 CC expression control sequence operably linked to the nucleic acid molecule,  
 CC a host cell comprising the vector or the nucleic acid molecule above,  
 CC a method of producing a human monoclonal antibody or its antigen-binding  
 CC portion that specifically binds MAdCAM, a method of isolating an antibody  
 CC or its antigen-binding portion that specifically binds to MAdCAM, a  
 CC method of treating a subject in need of a human antibody or its antigen-  
 CC binding portion that specifically binds to MAdCAM and inhibits binding to  
 CC alpha/beta7, a method of inhibiting alpha/beta7 binding to cells  
 CC expressing human MAdCAM, a method of inhibiting MAdCAM-mediated leukocyte  
 CC endothelial cell adhesion, migration and infiltration into tissues, a  
 CC method of inhibiting alpha/beta7/MAdCAM-dependent cellular adhesion,  
 CC inhibiting the MAdCAM-mediated recruitment of lymphocytes to  
 CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder  
 CC characterized by circulating soluble human MAdCAM and detecting  
 CC inflammation in a subject. The antibody, composition and methods are  
 CC useful for diagnosing and treating inflammatory disease, e.g.  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC diverticular disease, gastritis, liver disease, primary biliary  
 CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and  
 CC graft versus host disease. This sequence represents a human monoclonal  
 CC anti-MAdCAM antibody of the invention.  
 XX  
 SQ Sequence 469 AA;  
 Query Match 78.3%; Score 47; DB 9; Length 469;  
 Best Local Similarity 77.8%; Pred. No. 15;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 TTYTFFGADV 11  
 DB 123 TTYTFFGADV 131

RESULT 11  
 ADR38712 standard; peptide; 13 AA.  
 XX ADR38712;  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Mouse heavy chain variable region CDR3 seqid 114.  
 XX  
 KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 KW heavy chain variable region; complementarity determining region; CDR3.  
 OS Mus sp.  
 XX  
 PN US2004175385-A1.  
 XX  
 PD 09-SEP-2004.  
 XX  
 PF 01-AUG-2003; 2003US-00632706.  
 XX  
 PR 31-AUG-1998; 98US-00144886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Marks JD, Amerdorter P;  
 DR WPI; 2004-652009/63.  
 XX  
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 XX  
 PS Example 3; SEQ ID NO 114; 110pp; English.  
 XX  
 CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C39, I66, 3D12, B4, 1P3, huc25, Ar1, Ar2, WRI(V), WRI(T), 3-1,  
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinum  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain variable region complementarity determining  
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.  
 XX  
 SQ Sequence 13 AA;

Query Match 76.7%; Score 46; DB 8; Length 13;  
 Best Local Similarity 70.0%; Pred. No. 0.5;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 ATYYTGGLDV 11  
 | | | | | | | | | | | | |

Db 4 ANYYTGGMDV 13  
 RESULT 12  
 ADM04816 standard; peptide; 21 AA.  
 XX ADM04816;  
 AC  
 XX  
 DT 07-APR-2005 (first entry)  
 XX  
 DE PAPP-A immunoglobulin variable domain AB b03 heavy chain CDR3 SEQ ID 141.  
 XX  
 KW Cytostatic; Vasostrictic; heavy chain variable domain;  
 KW proliferative disorder; restenosis; glioblastoma; osteosarcoma.  
 XX  
 OS Unidentified.  
 XX  
 PN US2005009136-A1.  
 XX  
 PD 13-JAN-2005.  
 XX  
 PF 19-FEB-2004; 2004US-00783311.  
 XX  
 PR 19-FEB-2003; 2003US-0448515P.  
 XX  
 PA (DYAX-) DYAX CORP.  
 XX  
 PI Nixon A, Hogan S;  
 DR WPI; 2005-080519/09.  
 XX  
 PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins  
 PT comprising immunoglobulin variable domain sequences, useful for  
 PT diagnosing, preventing or treating diseases such as cancer.  
 XX  
 PS Example; SEQ ID NO 141; 168pp; English.  
 XX  
 CC The present invention relates to novel proteins (I) that bind to  
 CC pregnancy-associated plasma protein A (PAPP-A ADM04676). (I) comprises a  
 CC first and second immunoglobulin variable domain sequence which binds to  
 CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)  
 CC and heavy chain immunoglobulin variable domain sequences which binds to  
 CC PAPP-A. The proteins are useful for diagnosing, preventing or treating  
 CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth  
 CC of vascular smooth muscle cells following e.g., balloon angioplasty  
 CC (which may cause restenosis). The proteins are especially useful for  
 CC useful for treating diseases involving IGF regulated growth. The present  
 CC sequence is one such immunoglobulin variable domain sequence.  
 XX  
 SQ Sequence 21 AA;

Query Match 76.7%; Score 46; DB 9; Length 21;  
 Best Local Similarity 63.6%; Pred. No. 0.83;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LATYYTGGLDV 11  
 | | | | | | | | | | | | |  
 Db 11 LGNTYYGMDV 21  
 | | | | | | | | | | | | |  
 RESULT 13  
 ADM241994 standard; peptide; 126 AA.  
 XX ADM241994;  
 AC  
 XX  
 DT 30-JUN-2005 (first entry)  
 XX  
 DE Ig H chain variable region, B-CLL set II peptide #4.  
 XX  
 KW Antibody; antibody engineering; antibody therapy;  
 KW light chain variable region; heavy chain variable region;

KM chronic lymphocytic leukemia; cytostatic; Hodgkins disease; lymphoma;  
 KM Burkitts lymphoma; multiple myeloma; systemic lupus erythematosus;  
 KM antiinflammatory; dermatological; immunosuppressive; myasthenia gravis;  
 KM muscular-gen.; neuroprotective; Graves disease; antithyroid;  
 KM insulin dependent diabetes; diabetes mellitus; antidiabetic;  
 KM autoimmune hemolytic anemia; antianemic.  
 OS Homo sapiens.  
 XX  
 XX MO2005034733-A2.  
 PN  
 XX  
 PD 21-APR-2005.  
 XX  
 XX 08-OCT-2004; 2004MO-US033176.  
 PF  
 XX 08-OCT-2003; 2003US-0509473P.  
 PR  
 XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.  
 PA  
 XX Messmer BT, Chiorazzi N, Albesiano E;  
 PI  
 XX WPI; 2005-306220/31.  
 DR  
 XX  
 PT New isolated and purified preparation of light chain and heavy chain  
 PT antibody genes, useful for diagnosing, preventing or treating B cell  
 PT chronic lymphocytic leukemia, or in screening for agents that may treat  
 PT such disease.  
 PS  
 XX Disclosure; Fig 2, 58pp; English.  
 CC The new invention relates to combinations of light chain antibody genes  
 CC and heavy chain antibody genes, useful for treating B cell chronic  
 CC lymphocytic leukemia (B-CLL). B-CLL is a disease of slowly proliferating  
 CC CD5+ B lymphocytes. These cells express low levels of surface membrane Ig  
 CC that serves as the receptor for antigen (BCR). Analysis of V region gene  
 CC cassette usage has shown that distribution of variable region gene  
 CC increased frequency of VH3-07, VH4-34, and VH1-69 genes. This implies  
 CC that the structure of the antibody molecule, and antigen specificity, the  
 CC play a role in the leukemic transformation of particular B cells. The  
 CC present invention discloses that a significant proportion of B-CLL  
 CC patients with aggressive disease share the same classes of VH, D, JH, VL  
 CC and JH antibody genes, forming sets of patients with highly homologous B  
 CC cell receptors. Alternatively, the patients have a disorder selected from  
 CC Hodgkins disease, non-Hodgkins lymphoma, Burkitt's lymphoma, myeloma or  
 CC systemic lupus erythematosus, myasthenia gravis, Grave's disease, type I  
 CC diabetes mellitus, autoimmune peripheral neuropathy, and autoimmune  
 CC hemolytic anemia. The new members of the antibody genes are: VH4-39/D6-  
 CC 13/JH5/VLkappa012/2/JLkappa1/kappa2 (Set II); VH4-34/D5-  
 CC 5/JH6/VLkappa017/JLkappa1/kappa2 (Set III); VH1-69/D3-  
 CC 21/JH6/VLkappa012/2/JLkappa1/kappa2 (Set IV); VH1-69/D3-  
 CC 16/JH3/VLkappa012/2/JLkappa1/kappa2 (Set V); VH1-02/D6-  
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VIa); VH1-03/D6-  
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VIb); VH1-18/D6-  
 CC 5/D6-19/JH4/VLkappa012/2/JLkappa1 (Set VIc); VH1-46/D6-19/JH4 (Set VId); VH5-  
 CC 3/JH4/VLkappa019/JLkappa4 (Set VII); and VH1-69/D2-  
 CC 2/JH6/VLkappa016/2/JLkappa3 (Set VIII). Treating a patient having B-CLL  
 CC with the above genes comprises administering an agent that binds to the  
 CC antigen-binding region of an antibody encoded by the antibody genes. The  
 CC agent is an anti-idiotypic antibody, a peptide antigen, or an aptamer. The  
 CC present sequence is an Ig H chain variable region, B-CLL set II peptide.  
 XX  
 XX Sequence 126 AA;  
 SQ

Query Match 76.7%; Score 46; DB 9; Length 126;  
 Best Local Similarity 72.7%; Pred. No. 5.6;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LATYYTGLDV 11  
 | | | | |  
 DB 105 LKRYTGLDV 115

RESULT 14  
 ADM04810  
 ID ADM04810 standard; protein; 140 AA.

AC ADM04810;  
 XX  
 XX 07-APR-2005 (first entry)  
 DT  
 XX  
 XX PAPP-A immunoglobulin variable domain AB D03 heavy chain SEQ ID 135.

XX Cytostatic; Vasotropic; heavy chain variable domain;  
 XX proliferative disorder; restenosis; glioblastoma; osteosarcoma.  
 XX  
 XX Unidentified.  
 OS

PN US2005009136-A1.  
 PD 13-JAN-2005.  
 XX

PF 19-FEB-2004; 2004US-00783311.  
 PR

PR 19-FEB-2003; 2003US-0448515P.  
 XX  
 XX (DYAX-) DYAX CORP.  
 PA  
 XX

PI Nixon A, Hogan S;  
 XX  
 XX WPI; 2005-080519/09.  
 DR

PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins  
 PT comprising immunoglobulin variable domain sequences, useful for  
 PT diagnosing, preventing or treating diseases such as cancer.  
 PS Example; SEQ ID NO 135; 168pp; English.

XX The present invention relates to novel proteins (I) that bind to  
 CC pregnancy-associated plasma protein A (PAPP-A ADM04676). (I) comprises a  
 CC first and second immunoglobulin variable domain sequence which binds to  
 CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)  
 CC and heavy chain immunoglobulin variable domain sequences which binds to  
 CC PAPP-A. The proteins are useful for diagnosing, preventing or treating  
 CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth  
 CC of vascular smooth muscle cells following e.g., balloon angioplasty  
 CC (which may cause restenosis). The proteins are especially useful for  
 CC useful for treating diseases involving IGF regulated growth. The present  
 CC sequence is one such immunoglobulin variable domain sequence.  
 XX

SQ Sequence 140 AA;

Query Match 76.7%; Score 46; DB 9; Length 140;  
 Best Local Similarity 63.6%; Pred. No. 6.3;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LATYYTGLDV 11  
 | | | | |  
 DB 109 LKNTYYTGLDV 119

RESULT 15  
 ADM04952  
 ID ADM04952 standard; peptide; 16 AA.  
 XX

AC ADM04952;  
 XX

XX 07-APR-2005 (first entry)  
 DT

XX PAPP-A immunoglobulin variable domain AB F03 heavy chain CDR3 SEQ ID 277.  
 DE

XX Cytostatic; Vasotropic; heavy chain variable domain;  
 KM proliferative disorder; restenosis; glioblastoma; osteosarcoma.  
 XX

OS Unidentified.

XX US200509136-A1.

XX 13-JAN-2005.

XX 19-FEB-2004; 2004US-00783311.

XX 19-FEB-2003; 2003US-0448515P.

XX (DYAX-) DYAX CORP.

XX Nixon A, Hogan S;

XX WPI; 2005-080519/09.

PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins  
 PT comprising immunoglobulin variable domain sequences, useful for  
 PT diagnosing, preventing or treating diseases such as cancer.

XX Example; SEQ ID NO 277; 168bp; English.

CC The present invention relates to novel proteins (I) that bind to  
 CC pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a  
 CC first and second immunoglobulin variable domain sequence which binds to  
 CC PAPP-A. Also claimed are proteins (II) which comprise light chain (Lc)  
 CC and heavy chain immunoglobulin variable domain sequences which binds to  
 CC PAPP-A. The proteins are useful for diagnosing, preventing or treating  
 CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth  
 CC of vascular smooth muscle cells following e.g., balloon angioplasty  
 CC (which may cause restenosis). The proteins are especially useful for  
 CC useful for treating diseases involving IGF regulated growth. The present  
 CC sequence is one such immunoglobulin variable domain sequence.

XX Sequence 16 AA;

Query Match 75.0%; Score 45; DB 9; Length 16;  
 Best Local Similarity 63.6%; Pred. No. 0.92;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYRGLDV 11

Db 6 VAGYYTGMVDV 16

Search completed: November 21, 2005, 12:20:00  
 Job time : 16.7271 secs

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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:36 ; Search time 2.67949 Seconds  
(without alignments)  
394.995 Million cell updates/sec

Title: US-10-632-706-126  
Perfect score: 60  
Sequence: 1 LATYYFGLDV 11

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	43	71.7	19 2 PH1307	Ig heavy chain DJ
2	43	71.7	23 2 PH1361	Ig heavy chain DJ
3	43	71.7	29 2 PH1328	Ig heavy chain DJ
4	43	71.7	160 2 D70189	conserved hypotnet
5	43	71.7	160 2 S05271	Ig heavy chain pre
6	43	71.7	408 2 E70380	Na+/H+-exchanging
7	42	70.0	19 2 PH1304	Ig heavy chain DJ
8	42	70.0	19 2 S43960	Ig mu chain V regi
9	42	70.0	23 2 PH1364	Ig heavy chain DJ
10	42	70.0	24 2 PT0258	Ig heavy chain CDR
11	42	70.0	27 2 PH1371	Ig heavy chain DJ
12	42	70.0	27 2 PH1355	Ig heavy chain V r
13	42	70.0	74 2 S26793	Ig heavy chain V r
14	42	70.0	118 2 PH1666	Ig heavy chain V r
15	42	70.0	119 2 PH0961	Ig heavy chain V r
16	42	70.0	120 2 PH1650	Ig heavy chain V r
17	42	70.0	125 2 S24686	Ig heavy chain V6
18	42	70.0	128 2 S46797	Ig heavy chain V r
19	42	70.0	132 2 PH0954	Ig heavy chain V r
20	42	70.0	133 2 C33548	Ig heavy chain V-1
21	42	70.0	136 2 A49047	Ig heavy chain V r
22	42	70.0	147 2 I37780	Ig variable region
23	42	70.0	627 2 S14683	Ig mu chain precur
24	40	66.7	22 2 PH1325	Ig heavy chain DJ
25	39.5	65.8	581 2 E83729	adenine deaminase
26	39	65.0	126 2 S44107	Ig heavy chain V-D
27	39	65.0	375 2 A83788	spore germination
28	38	63.3	22 2 PH1359	Ig heavy chain DJ
29	38	63.3	45 2 PL0094	Ig heavy chain V r

30	38	63.3	287 2 T27056	hypothetical prote
31	38	63.3	473 2 H86240	hypothetical prote
32	38	63.3	979 2 A39792	transcription acti
33	37	61.7	14 2 PH1601	Ig H chain V-D-J r
34	37	61.7	126 1 MHHUOU	Ig heavy chain V-I
35	37	61.7	276 2 S16892	probable transposa
36	37	61.7	447 2 T09809	NADH2 dehydrogenas
37	37	61.7	448 2 T12006	glycerol-3-phospha
38	37	61.7	527 2 C70130	conditioned medium
39	37	61.7	571 2 A42138	conditioned medium
40	37	61.7	571 2 S24482	bel-1 protein - Ca
41	37	61.7	685 2 T22223	Ig heavy chain V r
42	36.5	60.8	120 2 E49590	hypothetical prote
43	36.5	60.8	316 2 C75205	Ig heavy chain DJ
44	36	60.0	18 2 PH1368	30S ribosomal prot
45	36	60.0	145 2 H97707	

## ALIGNMENTS

### RESULT 1

PH1307  
Ig heavy chain DJ region (clone C96-119) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_rev1sion 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1307  
R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymphic  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1307  
A/Molecule type: DNA  
A/Residues: 1-19 <WAS>  
A/Cross-references: UNIPARC:UPI0000176935  
C/Suprafamily: immunoglobulin V region; immunoglobulin  
C/Keywords: heterotetramer; immunoglobulin

Query Match  
Best Local Similarity 71.7%; Score 43; DB 2; Length 19;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYFGLDV 11  
DB 6 SYYYGMDV 14

### RESULT 2

PH1361  
Ig heavy chain DJ region (clone C178-122B) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_rev1sion 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1361  
R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymphic  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1361  
A/Molecule type: DNA  
A/Residues: 1-23 <WAS>  
A/Cross-references: UNIPARC:UPI0000176948  
C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match  
Best Local Similarity 71.7%; Score 43; DB 2; Length 23;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11  
DB 8 LFPYYGMDV 18

```
RESULT 3
PH1328
Ig heavy chain DJ region (clone C113-148) - human (fragment)
A/Residues: 1-144 <KIS2>
A/Cross-references: UNIPARC:UPI0000176B51; EMBL:X14584
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1328
R/Maserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovere, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:11460419
A/Accession: PH1328
A/Molecule type: DNA
A/Residues: 1-29 <MAS>
A/Cross-references: UNIPARC:UPI0000176939
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

Query Match      71.7%; Score 43; DB 2; Length 29;
Best Local Similarity 66.7%; Pred. No. 0.36;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTYTFFGLDV 11
       :|:|:|:|:|
Db      16 SYTYGMDV 24

RESULT 4
D70189
Conserved hypothetical integral membrane protein B80717 - Lyme disease spirochete
C/Species: Borrelia burgdorferi (Lyme disease spirochete)
C/Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C/Accession: D70189
R/Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A/Authors: Smith, H.O.; Venter, J.C.
A/Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A/Reference number: A70100; MUID:98065943; PMID:9403685
A/Accession: D70189
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-160 <KLE>
A/Cross-references: UNIPROT:O51659; UNIPARC:UPI0000575B2; GB:AE001171; GB:AE000783; NID
A/Experimental source: strain B31

Query Match      71.7%; Score 43; DB 2; Length 160;
Best Local Similarity 60.0%; Pred. No. 2;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 ATYYTFFGLDV 11
       |||:|:|:|
Db      23 ATYYTFSIDI 32

RESULT 5
S05271
Ig heavy chain precursor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C/Accession: S05271; S04602
R/Kishimoto, T.
Submitted to the EMBL Data Library, March 1989
A/Reference number: S05270
A/Accession: S05271
A/Molecule type: mRNA
A/Residues: 1-160 <KSI>
A/Cross-references: UNIPROT:Q96BB9; UNIPARC:UPI0000176B50; EMBL:X14584
R/Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A/Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A/Reference number: S04601; MUID:89296497; PMID:2500644
A/Accession: S04602
```

```
A/Molecule type: mRNA
A/Residues: 1-144 <KIS2>
A/Cross-references: UNIPARC:UPI0000176B51; EMBL:X14584
C/Superfamily: immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/1-19/Domain: signal sequence #status predicted <Sig>
F/20-160/Product: Ig heavy chain (fragment) #status predicted <Mat>
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match      71.7%; Score 43; DB 2; Length 160;
Best Local Similarity 66.7%; Pred. No. 2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTYTFFGLDV 11
       :|:|:|:|:|
Db      125 SYTYGMDV 133

RESULT 6
E70380
Na+/H+-exchanging protein - Aquifex aeolicus
N/Alternate names: Na+/H+ antiporter
C/Species: Aquifex aeolicus
C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C/Accession: E70380
R/Decker, G.; Warren, P.V.; Gassterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.B.; Ove
r Nature 392, 353-358, 1998
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A/Reference number: A70300; MUID:98196666; PMID:9537320
A/Accession: E70380
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1408 <AGP>
A/Cross-references: UNIPROT:O67072; UNIPARC:UPI0000564AB; GB:AE000714; NID:92983446; PII
C/Genetic:
A/Experimental source: strain VFS
A/Gene: napA2
C/Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napA1

Query Match      71.7%; Score 43; DB 2; Length 408;
Best Local Similarity 54.5%; Pred. No. 5.2;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 LATYYTFFGLDV 11
       :|:|:|:|:|
Db      116 TVSYTFFGLDL 126

RESULT 7
PH1304
Ig heavy chain DJ region (clone C439-111) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1304
R/Maserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovere, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:11460419
A/Accession: PH1304
A/Molecule type: DNA
A/Residues: 1-19 <MAS>
A/Cross-references: UNIPARC:UPI0000176934
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

Query Match      70.0%; Score 42; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 YYYTFFGLDV 11
       |||:|:|:|
Db      7 YYYTGMDV 14
```



## RESULT 8

S43960  
Ig mu chain V region (clone 18) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 20-Oct-1994 #sequence\_revision 26-Jul-1996 #text\_change 17-Mar-1999  
C/Accession: S43960  
R/Magnier, S.D.; Williams, G.T.; Larson, T.; Neuburger, M.S.; Kitamura, D.; Rajewsky, K.  
Nucleic Acids Res. 22, 1389-1393, 1994  
A/Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.  
A/Reference number: S43956; MUID:94248036; PMID:8190623  
A/Accession: S43960  
A/Molecule type: DNA  
A/Residues: 1-19 <WAG>  
A/Cross-references: UNIPARC:UPI000017690D  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: immunoglobulin

Query Match  
Best Local Similarity 70.0%; Score 42; DB 2; Length 19;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGADV 11  
|||:|:|  
DB 10 YYYGMDV 17

## RESULT 9

PH1364  
Ig heavy chain DJ region (clone C178-136A) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1364  
R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1364  
A/Molecule type: DNA  
A/Residues: 1-23 <WAS>  
A/Cross-references: UNIPARC:UPI0000176949  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match  
Best Local Similarity 70.0%; Score 42; DB 2; Length 23;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGADV 11  
|||:|:|  
DB 11 YYYGMDV 18

## RESULT 10

PT0258  
Ig heavy chain CDR3 region (clone 2-118B) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 30-May-1997  
C/Accession: PT0258  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0258  
A/Molecule type: DNA  
A/Residues: 1-24 <YAM>  
A/Cross-references: UNIPARC:UPI0000176940  
A/Experimental source: B lymphocyte  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match  
70.0%; Score 42; DB 2; Length 24;

Best Local Similarity 75.0%; Pred. No. 0.44;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGADV 11  
|||:|:|  
DB 12 YYYGMDV 19

## RESULT 11

PH1371  
Ig heavy chain DJ region (clone C111-145) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1371  
R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1371  
A/Molecule type: DNA  
A/Residues: 1-27 <WAS>  
A/Cross-references: UNIPARC:UPI000017694B  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match  
Best Local Similarity 70.0%; Score 42; DB 2; Length 27;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGADV 11  
|||:|:|  
DB 15 YYYGMDV 22

## RESULT 12

PH1355  
Ig heavy chain DJ region (clone C100-136) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1355  
R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1355  
A/Molecule type: DNA  
A/Residues: 1-27 <WAS>  
A/Cross-references: UNIPARC:UPI0000176945  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match  
Best Local Similarity 70.0%; Score 42; DB 2; Length 27;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGADV 11  
|||:|:|  
DB 15 YYYGMDV 22

## RESULT 13

S26793  
Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C/Accession: S26793  
R/Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.  
Eur. J. Immunol. 22, 241-245, 1992  
A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam1  
A/Reference number: S26786; MUID:92111632; PMID:1730251  
A/Accession: S26793  
A/Status: preliminary  
A/Molecule type: mRNA

A/Residues: 1-74 <MOR>  
 A/Cross-references: UNIPARC:UPI0000115FCA; EMBL:X61019; NID:932787; PIDD:CAA43353.1; PIR  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 74;  
 Best Local Similarity 75.0%; Pred. No. 1.4;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
 |||:|:  
 Db 56 YYYGMDV 63

## RESULT 14

PH166  
 Ig heavy chain V region (clone 6C9) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
 C/Accession: PH1666  
 R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
 J. Exp. Med. 178, 331-336, 1993  
 A/Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphylo  
 A/Reference number: PH1642; MUID:93301610; PMID:8315388  
 A/Accession: PH1666  
 A/Molecule type: mRNA  
 A/Residues: 1-118 <HTL>  
 A/Cross-references: UNIPARC:UPI0000176BE7  
 A/Experimental source: B cell  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 42; DB 2; Length 118;  
 Best Local Similarity 75.0%; Pred. No. 2.2;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
 |||:|:  
 Db 100 YYYGMDV 107

## RESULT 15

PH0961  
 Ig heavy chain V region (G6+ T-L33) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-1996  
 C/Accession: PH0961  
 R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kippes, T.J.  
 J. Exp. Med. 175, 983-991, 1992  
 A/Title: Evidence for somatic selection of natural autoantibodies.  
 A/Reference number: PH0952; MUID:92202880; PMID:1552291  
 A/Accession: PH0961  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 1-119 <MAR>  
 A/Cross-references: UNIPARC:UPI0000176CE5  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/1-30/Region: framework 1  
 F/15-98/Domain: immunoglobulin homology <IMM>  
 F/31-35/Region: complementarity-determining 1  
 F/36-50/Region: framework 2  
 F/51-67/Region: complementarity-determining 2  
 F/68-98/Region: framework 3  
 F/99-107/Region: complementarity-determining 3

Query Match 70.0%; Score 42; DB 2; Length 119;  
 Best Local Similarity 75.0%; Pred. No. 2.2;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
 |||:|:

Db 101 YYYGMDV 108

Search completed: November 21, 2005, 12:22:14  
 Job time: 3.67949 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55, Search time 16.2784 Seconds  
(without alignments)  
476.756 Million cell updates/sec

Title: US-10-632-706-126  
Perfect score: 60  
Sequence: 1 LATYYPGLDV 11

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: UniProt\_05.80: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	44	73.3	Q4N9V2_THRPA	Q4N9V2 theileria p
2	44	73.3	Q4UPY8_THRAN	Q4UPY8 theileria a
3	43	71.7	O51659_BOBBU	O51659 borrelia bu
4	43	71.7	O660F6_BOBGA	O660F6 borrelia ga
5	43	71.7	O67072_AQJAE	O67072 aquifex ae
6	42	70.0	O7Y771_BOBPE	O7Y771 bordetella
7	42	70.0	O7W926_BOBPA	O7W926 bordetella
8	42	70.0	O7WKH1_BOBBA	O7WKH1 bordetella
9	42	70.0	O4QAL0_LEIMA	O4QAL0 leishmania
10	42	70.0	O89NT9_BRABA	O89NT9 bradyrhizob
11	42	70.0	O7AN07_NANEO	O7AN07 nanocarhaeu
12	42	70.0	O6GMY2_HUMAN	O6GMY2 homo sapien
13	42	70.0	O96X97_SULTOB	O96X97 sulfolobus
14	42	70.0	O4FWX4_LEIMA	O4FWX4 leishmania
15	41	68.3	O6A0Z1_DESPS	O6A0Z1 desulfohalob
16	41	66.7	O6F6N6_ACTAD	O6F6N6 acinetobact
17	40	66.7	O4ZUB1_PERSY	O4ZUB1 pseudomonas
18	40	66.7	O6D0Z3_ERECT	O6D0Z3 erwinia car
19	40	66.7	O8EU78_OCBIH	O8EU78 ocrenibacill
20	40	66.7	O8C3X8_MOCSH	O8C3X8 mus muscucu
21	40	66.7	O5AAV6_CANAL	O5AAV6 candida alb
22	40	66.7	O6WEO5_ARALY	O6WEO5 arabidopsis
23	40	66.7	O4OBV4_LEIMA	O4OBV4 leishmania
24	39.5	65.8	Y637_BRCHD	O9K494 bacillus ha
25	39	65.0	O52G31_MAGGR	O52G31 magnaporthe
26	39	65.0	O5YXQ2_NOCFA	O5YXQ2 nocardia fa
27	39	65.0	O97BK3_THRVO	O97BK3 thermoplasma
28	39	65.0	O9KDV6_BACDH	O9KDV6 bacillus ha
29	39	65.0	O82700_MEDTR	O82700 medicago tr
30	39	65.0	O95TA5_MEDTR	O95TA5 medicago tr
31	39	65.0	O6ZBX7_ORISA	O6ZBX7 oryza sativ

32	39	65.0	451	2	O6ZBX6_ORISA	O6ZBX6 oryza sativ
33	39	65.0	478	2	O6PI81_HUMAN	O6PI81 homo sapien
34	39	65.0	662	2	O88T15_LACPL	O88T15 lactobacill
35	39	65.0	701	1	LSP2_DROME	O24388 drosophila
36	39	65.0	779	2	O65S21_MANSW	O65S21 mantheimia
37	39	65.0	780	2	O7VQH6_CANBR	O7VQH6 candidatus
38	38	63.3	116	2	O7Z3Y6_HUMAN	O7Z3Y6 homo sapien
39	38	63.3	148	2	O5TWX6_HUMAN	O5TWX6 anopheles g
40	38	63.3	159	2	O96QSO_HUMAN	O96QSO homo sapien
41	38	63.3	239	2	O5X0G3_LEGPI	O5X0G3 legionella
42	38	63.3	243	2	O5Z2F4_LEGPI	O5Z2F4 legionella
43	38	63.3	307	2	O6NSD3_RHOPA	O6NSD3 rhodospendo
44	38	63.3	350	2	O8TVT5_METKA	O8TVT5 methanopyru
45	38	63.3	366	2	O9XTT1_CABEU	O9XTT1 caenorhabdi

## ALIGNMENTS

RESULT 1  
Q4N9V2\_THRPA  
ID Q4N9V2\_THRPA PRELIMINARY, PRT, 1348 AA.  
AC Q4N9V2:  
DT 13-SEP-2005 (TREMBLrel. 31, Created)  
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=TP01\_0021;  
OS Theileria parva.  
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;  
OC Theileria.  
OX NCBI\_TaxID=5875;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Muguga;  
RA Gardner M.J., Bishop R., Shah T., de Villiers B.P., Carlton J.M.,  
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,  
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J.,  
RA Jiang L., Lynn J., Weaver B., Shoib A., Wasawo D., Crabtree J.,  
RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,  
RA Silva J.C., Uteback T.R., Feldblyum T.V., Pertea M., Allen J.,  
RA Taracha B.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,  
RA Venter J.C., Fraser C.M., Nene V.,  
RT "Genome sequence of Theileria parva, a bovine pathogen that transforms  
lymphocytes.";  
RL Science 309:134-137(2005).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Muguga;  
RA Gardner M., Bishop R., Shah T., de Villiers B., Carlton J.M., Hall N.,  
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,  
RA Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J., Jiang L.,  
RA Lynn J., Weaver B., Shoib A., Wasawo D., Crabtree J., Wortman J.R.,  
RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,  
RA Uteback T., Feldblyum T., Pertea M., Allen J., Taracha B.L.,  
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,  
RA Fraser C.M., Nene V.,  
RL Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an  
EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
CC EMBL; AAGK0100001; EMBL3265.1; -; Genomic\_DNA.  
DR Hypothetical protein.  
SQ SEQUENCE 1348 AA; 155635 MW; 474C3A40C23B8C5F CRC64;  
Query Match 73.3%; Score 44; DB 2; Length 1348;  
Best Local Similarity 87.5%; Pred. No. 60;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

## RESULT 2

Q4UFY8\_THEAN PRELIMINARY; PRT; 2262 AA.  
 ID Q4UFY8\_THEAN PRELIMINARY; PRT; 2262 AA.  
 AC Q4UFY8; 13-SBP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SBP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SBP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=TA19710;  
 OS Theileria annulata.  
 OC Eukaryote; Alveolata; Apicomplexa; Piroplasmida; Theileridae;  
 OC Theileria.  
 NCBI\_TaxID=5874;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Ankara isolate clone C9;  
 RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Beriman M.,  
 RA Hall N., Barrell B.G.;  
 RT "The chromosome 1 sequence of Theileria annulata."  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 RM EMBL; CR940347; CA174001.1; -; Genomic\_DNA.  
 DR Hypothetical protein.  
 KW SEQUENCE 2262 AA; 262068 MW; FD9E8915243EF512 CRC64;

Query Match 73.3%; Score 44; DB 2; Length 2262;  
 Best Local Similarity 87.5%; Pred. No. 1e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYVFGLD 10  
 Db 1244 STYYFGLD 1251

## RESULT 3

051659\_BORBU PRELIMINARY; PRT; 160 AA.  
 ID 051659\_BORBU PRELIMINARY; PRT; 160 AA.  
 AC 051659;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DE Conserved hypothetical integral membrane protein.  
 GN OrderedLocustNames=BB0717;  
 OS Borrelia burgdorferi (Lyme disease spirochete).  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
 OC Borrelia burgdorferi group.  
 NCBI\_TaxID=139;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 35210 / B31;  
 RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;  
 RA Frazer C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,  
 RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,  
 RA Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,  
 RA Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,  
 RA Salzberg S.L., Hanson M., Van Vugt R., Palmer N., Adams M.D.,  
 RA Gocayne J.D., Weidman J.F., Ueteyback T.R., Matthey L., McDonald L.A.,  
 RA Atliach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,  
 RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;  
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia  
 burgdorferi."  
 RL Nature 390:580-586(1997).  
 DR EMBL; AF001171; AAC67057.1; -; Genomic\_DNA.  
 DR PIR; D70189; D70189.  
 DR TIGR; BB0717; -.  
 KM Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 160 AA; 19300 MW; 9DB28A497C0F5737 CRC64;

Query Match 71.7%; Score 43; DB 2; Length 160;  
 Best Local Similarity 60.0%; Pred. No. 11;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 ATYYVFGLDV 11

Db 23 ATYFYSIDI 32

## RESULT 4

Q660F6\_BORGA PRELIMINARY; PRT; 160 AA.  
 ID Q660F6\_BORGA PRELIMINARY; PRT; 160 AA.  
 AC Q660F6;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Conserved hypothetical integral membrane protein.  
 GN OrderedLocustNames=BG0739;  
 OS Borrelia garinii.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
 OC Borrelia burgdorferi group.  
 NCBI\_TaxID=29519;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PRI;  
 RA Gloeckner G., Lehmann R., Romualdi A., Pradelja S.,  
 RA Schulte-Spechtel U., Wilske B., Suenkel J., Plazzer M.;  
 RT "Comparative analysis of the Borrelia garinii genome."  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CP000013; AA07565.1; -; Genomic\_DNA.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 160 AA; 19293 MW; B5B15C5197BF89 CRC64;

Query Match 71.7%; Score 43; DB 2; Length 160;  
 Best Local Similarity 60.0%; Pred. No. 11;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYVFGLDV 11  
 Db 23 ATYFYSIDI 32

## RESULT 5

067072\_AQUAE PRELIMINARY; PRT; 408 AA.  
 ID 067072\_AQUAE PRELIMINARY; PRT; 408 AA.  
 AC 067072;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Na(+)/H(+) antiporter.  
 GN Name=napA2; OrderedLocustNames=AQ\_929;  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.  
 NCBI\_TaxID=63363;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=VF5;  
 RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;  
 RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 aeolicus."  
 RL Nature 392:353-358(1998).  
 DR EMBL; AF000714; AAC07034.1; -; Genomic\_DNA.  
 DR PIR; E70380; E70380.  
 DR GO; GO:0016021; C:Integral to membrane; IEA.  
 DR GO; GO:0015299; F:enzyme:hydrogen antiporter activity; IEA.  
 DR GO; GO:0006885; P:regulation of pH; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR006153; Na\_H\_porter.  
 DR Pfam; PF00999; Na\_H\_Exchange; 1.  
 KM Complete proteome; Transmembrane; Transport.  
 SQ SEQUENCE 408 AA; 43582 MW; 7E05B4B387A6C506 CRC64;

Query Match 71.7%; Score 43; DB 2; Length 408;  
 Best Local Similarity 54.5%; Pred. No. 28;  
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 LATYFFGIDV 11  
:|||||:  
Db 116 IVSYFFGIDL 126

## RESULT 6

Q7VY71 BORPE PRELIMINARY; PRT; 364 AA.  
ID Q7VY71 BORPE PRELIMINARY; PRT; 364 AA.  
AC Q7VY71  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Putative periplasmic solute-binding protein.  
GN Name=smow; OrderedLocuNames=BPI487;  
OS Bordetella pertussis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Alcaligenaceae; Bordetella.  
NCBI\_TaxID=520;  
[1]

## NUCLEOTIDE SEQUENCE.

RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;  
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;  
RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,  
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,  
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,  
RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
RT Bordetella parapertussis and Bordetella bronchiseptica."  
RL Nat. Genet. 35:32-40(2003).  
DR EMBL; BX640415; CAB41776.1; -; Genomic DNA.  
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR006311; Tat.  
DR InterPro; IPR004682; TRAP\_transpdtcp.  
DR Pfam; PF03480; SBP\_bac\_7; 1.  
DR TIGRFAMs; TIGR01409; TAT\_signal\_seq; 1.  
KW Complete proteome.  
SQ SEQUENCE 364 AA; 40021 MW; 03F1C2B6FC51D502 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;  
Best Local Similarity 77.8%; Pred. No. 38;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 ATYFFGID 10  
:|||||:  
Db 98 ASYFFGKD 106

Q7W926 BORPA PRELIMINARY; PRT; 364 AA.  
ID Q7W926 BORPA PRELIMINARY; PRT; 364 AA.  
AC Q7W926;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Putative periplasmic solute-binding protein.  
GN Name=smow; OrderedLocuNames=BPI1948;  
OS Bordetella parapertussis.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Alcaligenaceae; Bordetella.  
NCBI\_TaxID=519;  
[1]

## NUCLEOTIDE SEQUENCE.

RC STRAIN=12822 / ATCC BAA-587;  
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;  
RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,  
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,  
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,  
RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
RT Bordetella parapertussis and Bordetella bronchiseptica."  
RL Nat. Genet. 35:32-40(2003).  
DR EMBL; BX640443; CAB32632.1; -; Genomic DNA.  
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR006311; Tat.  
DR InterPro; IPR004682; TRAP\_transpdtcp.  
DR Pfam; PF03480; SBP\_bac\_7; 1.  
DR TIGRFAMs; TIGR01409; TAT\_signal\_seq; 1.  
KW Complete proteome.  
SQ SEQUENCE 364 AA; 39997 MW; 8AB672BA3BF09AD CRC64;

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,  
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,  
RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
RT Bordetella parapertussis and Bordetella bronchiseptica."  
RL Nat. Genet. 35:32-40(2003).  
DR EMBL; BX640428; CAB37248.1; -; Genomic DNA.  
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR006311; Tat.  
DR InterPro; IPR004682; TRAP\_transpdtcp.  
DR Pfam; PF03480; SBP\_bac\_7; 1.  
DR TIGRFAMs; TIGR01409; TAT\_signal\_seq; 1.  
KW Complete proteome.  
SQ SEQUENCE 364 AA; 39967 MW; 970BC4608CF1D88 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;  
Best Local Similarity 77.8%; Pred. No. 38;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 ATYFFGID 10  
:|||||:  
Db 98 ASYFFGKD 106

RESULT 8  
Q7W926 BORPE PRELIMINARY; PRT; 364 AA.  
ID Q7W926 BORPE PRELIMINARY; PRT; 364 AA.  
AC Q7W926;  
DT 01-OCT-2003 (TREMBLrel. 25, Created)  
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Putative periplasmic solute-binding protein.  
GN Name=smow; OrderedLocuNames=BPI2136;  
OS Bordetella bronchiseptica (Alcaligenes bronchiseptica).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Alcaligenaceae; Bordetella.  
NCBI\_TaxID=518;  
[1]

NUCLEOTIDE SEQUENCE.  
RC STRAIN=RB50 / ATCC BAA-589;  
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;  
RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,  
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,  
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,  
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,  
RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
RT Bordetella parapertussis and Bordetella bronchiseptica."  
RL Nat. Genet. 35:32-40(2003).  
DR EMBL; BX640443; CAB32632.1; -; Genomic DNA.  
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR006311; Tat.  
DR InterPro; IPR004682; TRAP\_transpdtcp.  
DR Pfam; PF03480; SBP\_bac\_7; 1.  
DR TIGRFAMs; TIGR01409; TAT\_signal\_seq; 1.  
KW Complete proteome.  
SQ SEQUENCE 364 AA; 39997 MW; 8AB672BA3BF09AD CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;  
Best Local Similarity 77.8%; Pred. No. 38;

Matches 7, Conservative 1, Mismatches 1, Indels 0, Gaps 0,

Qy 2 ATYYFGLD 10  
Db 98 ASYYFGKD 106

## RESULT 9

Q4QA10\_LEIMA PRELIMINARY; PRT; 378 AA.

AC Q4QA10; 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DE Hypothetical protein.  
GN ORFNames=LmjP25.0840;  
OS Leishmania major.  
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_TaxID=5664;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Fieldlin.  
RA Peacock C.S., Murphy L., Ivens A.C., Bertman M., Blackwell J.,  
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,  
RA Saunders D., Seeger K., Warren T., Rajadream M., and Barrell B.G.;  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; C7005264; CAJ04989.1; -; Genomic\_DNA.  
KM Hypothetical protein.  
SQ SEQUENCE 378 AA; 41605 MW; 9E3E7C7C1F04839 CRC64;

Query Match Best Local Similarity 70.0%; Score 42; DB 2; Length 378;

Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

Qy 3 TTYTFFGL 9  
Db 112 TTYTFFGL 118

## RESULT 10

Q89NT9\_BRAJA PRELIMINARY; PRT; 382 AA.

AC Q89NT9;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Orisplasmic mannitol-binding protein.  
GN OrderedLocustNames=bl3745;  
OS Bradyrhizobium japonicum.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae; Bradyrhizobium.  
OX NCBI\_TaxID=375;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=USDA 110;

RX MEDLINE=2248498; PubMed=12597275;

RA Kaneko T., Nakanura Y., Sato S., Minamisawa K., Uchiumi T.,

RA Sasamoto S., Watanabe A., Idegawa K., Iriyuchi M., Kawashima K.,

RA Kohara M., Matsumoto M., Shimpo S., Tsunoda H., Wada T., Yamada M.,

RA Tabata S.;

RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium

RT DNA Res. 9:189-197(2002).

DR EMBL; BA000040; BAC9010.1; -; Genomic\_DNA.

DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.

DR InterPro; IPR006311; Tat.

DR InterPro; IPR004682; TRAP transpDcP.

DR Pfam; PF03480; SBP\_bac\_7; 1.

DR TIGRFAMs; TIGR01403; TAT\_signal\_seg; 1.

DR Complete proteome.

Qy SEQUENCE 382 AA; 42090 MW; 23C264980A9F98BD CRC64;

Query Match Best Local Similarity 70.0%; Score 42; DB 2; Length 382;

Matches 7, Conservative 1, Mismatches 1, Indels 0, Gaps 0,

Qy 2 ATYYFGLD 10  
Db 117 ASYYFGKD 125

## RESULT 11

Q74N07\_NANEO PRELIMINARY; PRT; 594 AA.

AC Q74N07;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DE NEQ353.  
GN OrderedLocustNames=NEQ353;  
OS Nanoarchaeum equitans.  
OC Archaea; Nanoarchaeota; Nanoarchaeum.  
OX NCBI\_TaxID=160232;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=K14-M;  
RX PubMed=14566062; DOI=10.1073/pnas.1735403100;  
RA Waters E., Hohn M.J., Abel I., Graham D.E., Adams M.D., Barnstead M.,  
RA Beeson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X.,  
RA Mathur E., Ni J., Podar M., Richardson T., Sutton G.G., Simon M.,  
RA Scell D., Stetter K.O., Short J.M., Wooldraver M.;  
RT "The genome of Nanoarchaeum equitans: Insights into early archaeal  
evolution and derived parasitism."  
RL Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988(2003).  
DR EMBL; AE017199; AAR3202.1; -; Genomic\_DNA.  
KM Complete proteome.  
SQ SEQUENCE 594 AA; 69673 MW; FD2E60ACF00CD9F4 CRC64;

Query Match Best Local Similarity 70.0%; Score 42; DB 2; Length 594;

Matches 6, Conservative 4, Mismatches 1, Indels 0, Gaps 0,

Qy 1 LATYYFGLDV 11  
Db 569 LSRHYFGVDI 579

## RESULT 12

Q6GM72\_HUMAN PRELIMINARY; PRT; 606 AA.

AC Q6GM72;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE IGHM protein.

GN Name=IGHM;

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,

RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,

RA Bosek S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywiński M.I., Skalska U., Smallus D.B.,  
 RA Schermer A., Schein J.B., Jones S.U.M., Maira M.A.,  
 RT "generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RG NIH NCI Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073758; AAH73758.1; -, mRNA.  
 DR SMR; O6GMV2; 20-256.  
 DR InterPro; IPR003599; IG-like.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG-v.  
 DR Pfam; PF07654; C1-set; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
 SQ SEQUENCE 606 AA; 66185 MW; B6B3B5114FAC5 CRC64;  
 Query Match 70.0%; Score 42; DB 2; Length 606;  
 Best Local Similarity 75.0%; Pred. No. 63;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 YYYRGDV 11  
 Db 135 YYYGYMDV 142  
 RESULT 13  
 ID 096X97\_SUITO PRELIMINARY; PRT; 1062 AA.  
 AC 096X97;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DN 1062aa long hypothetical thermoprotein.  
 OS OrderedLocustNames=ST2615;  
 OC Sulfolobus tokodaii.  
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
 OC Sulfolobus.  
 CX NCBI\_TaxID=111955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=JCM 10545 / 7;  
 RX MEDLINE=21456156; PubMed=11572479;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,  
 RA Sekine M., Baba S.-I., Ankel A., Kosugi H., Hoshoyama A., Fukui S.,  
 RA Nagai Y., Nishijima K., Otuka R., Nakazawa H., Takamiya M., Kato Y.,  
 RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,  
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,  
 RA Oshima T., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic thermophilic  
 RT Crenarchaeon, Sulfolobus tokodaii strain7.";  
 RL DNA Res. 8:123-140(2001).  
 DR EMBL; BA000023; BAB67731.1; -, Genomic-DNA.  
 DR InterPro; IPR007981; Peptidase\_A5.  
 DR Pfam; PF05317; Thermopsin; 1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 1062 AA; 118024 MW; 166F4ED60A040BD4 CRC64;  
 Query Match 70.0%; Score 42; DB 2; Length 1062;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 TTYTFFGL 9  
 Db 623 TTYTFFGL 629  
 RESULT 14  
 ID 04FWX4\_LEIMA PRELIMINARY; PRT; 3212 AA.  
 AC 04FWX4;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=LMO\_1075;  
 OS Leishmania major.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 CX NCBI\_TaxID=5664;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Friedlin;  
 RX PubMed=16020728; DOI=10.1126/science.1112680;  
 RA Ivans A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,  
 RA Berriman M., Sisk B., Rajandream M.A., Adlem E., Aert R., Anupama A.,  
 RA Apostolou Z., Attipoe P., Baeson N., Bauser C., Beck A., Beverley S.M.,  
 RA Blanchard G., Borzym K., Bothe G., Brusch C.V., Collins M.,  
 RA Cadag B., Charlont L., Clayton C., Coulson R.M., Cronin A., Cruz A.K.,  
 RA Davies R.M., De Gaudenzi J., Dobson D.B., Duesterhoeft A.,  
 RA Farelina G., Foeker N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,  
 RA Goble A., Goffeau A., Harris D., Hertz-Powder C., Hilbert H., Horn D.,  
 RA Huang Y., Klages S., Knights A., Kube M., Larke N., Litvin L.,  
 RA Lord A., Louie T., Marra M., Maury D., Matthews K., Michael S.,  
 RA Mottacott J.C., Muller-Auer S., Munden H., Nelson S., Nordertczak H.,  
 RA Oliver K., O'Neill S., Pentony M., Pohl T.M., Price C., Purnelle B.,  
 RA Quail M.A., Rabinowitch B., Reinhardt R., Rieger M., Rinta J.,  
 RA Robben J., Robertson L., Ruiz J.C., Rutter S., Saunders D.,  
 RA Schaefer M., Schein U., Schwartz D.C., Seeger K., Seyler A., Sharp S.,  
 RA Shin H., Sivam D., Squares R., Squares S., Tosato V., Vogt C.,  
 RA Voickaert G., Wambut R., Warren T., Wedler R., Woodward J., Zhou S.,  
 RA Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.,  
 RA Myler P.J.;  
 RT "The genome of the kinetoplastid Parasite, Leishmania major.";  
 RL Science 309:436-442(2005).  
 DR EMBL; CP000081; AAZ14369.1; -, Genomic-DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 3212 AA; 342958 MW; E26BA125060F8A6B CRC64;  
 Query Match 70.0%; Score 42; DB 2; Length 3212;  
 Best Local Similarity 70.0%; Pred. No. 3.3e+02;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 LATYYFGLD 10  
 Db 164 LAGTYTFCVE 173  
 RESULT 15  
 ID 06AQZ1\_DESPS PRELIMINARY; PRT; 716 AA.  
 AC 06AQZ1;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Related to mercuric reductase.  
 GN OrderedLocustNames=DP0504;  
 OS Desulfotalea psychrophila.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;  
 OC Desulfobulbaceae; Desulfotalea.  
 CX NCBI\_TaxID=84980;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=LSv54 / DSM 12343;

RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;  
RA Rabus R., Ruepp A., Frickey T., Rattei T., Partmann B., Stark M.,  
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann U., Gellner K.,  
RA Teeling H., Leuchner W.D., Gloeckner F.-O., Lupas A.N., Amann K.,  
RA Klenk H.-P.;  
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium  
from permanently cold Arctic sediments.";  
RL Environ. Microbiol. 6:887-902(2004).  
DR EMBL: CR522870; CAG35233.1; -; Genomic\_DNA.  
DR GO: GO:0005377; C:cytoplasm; IEA.  
DR GO: GO:0015036; F:disulfide oxidoreductase activity; IEA.  
DR GO: GO:0050660; F:PAD binding; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR InterPro: IPR001327; FAD\_Pyr\_redox.  
DR InterPro: IPR000815; Hg\_reductase.  
DR InterPro: IPR005162; pAntne\_S.  
DR InterPro: IPR01100; Pyr\_redox.  
DR InterPro: IPR04099; Pyr\_redox\_dim.  
DR Pfam: PF00070; Pyr\_redox; 2.  
DR Pfam: PF02852; Pyr\_redox\_dim; 1.  
DR PRINTS: PR00368; FAD\_PNR.  
DR PRINTS: PR00945; HGRDTRSE.  
DR PRINTS: PR00411; PNDROTASEI.  
DR PRODOM: PD000139; FAD\_Pyr\_redox; 1.  
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN\_1.  
DR PROSITE: PS00076; PYRIDINE\_REDOX\_1; 1.  
KW Complete proteome.  
SQ SEQUENCE 716 AA; 78725 MW; 68EFC0600DE44094 CRC64;

Query Match 68.3%; Score 41; DB 2; Length 716;  
Best local similarity 60.0%; Pred. NO. 1.le+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LATYYFGLD 10  
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Db 14 VSAYYFRLD 23

Search completed: November 21, 2005, 12:04:09  
Job time : 19.2784 secs



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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:31 / Search time 4.15018 Seconds  
(without alignments)  
219.131 Million cell updates/sec

Title: US-10-632-706-126  
Perfect score: 60  
Sequence: 1 IATYYPGLDV 11

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA:  
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3: /cgn2\_6/ptodata/1/1aa/H-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PCTUS-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RE-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	71.7	33	1	US-08-053-131-78 Sequence 78, Appl
2	43	71.7	33	1	US-08-645-641-78 Sequence 78, Appl
3	43	71.7	33	1	US-07-853-408B-78 Sequence 78, Appl
4	43	71.7	33	1	US-08-096-762-78 Sequence 78, Appl
5	43	71.7	33	1	US-08-308-865-78 Sequence 78, Appl
6	43	71.7	33	2	US-09-042-353-275 Sequence 275, App
7	43	71.7	33	2	US-08-758-417A-123 Sequence 123, App
8	43	71.7	33	4	PCT-US92-10983-78 Sequence 78, Appl
9	43	71.7	125	2	US-09-840-459-84 Sequence 84, Appl
10	43	71.7	125	2	US-09-497-625A-84 Sequence 84, Appl
11	42	70.0	29	1	US-08-053-131-73 Sequence 73, Appl
12	42	70.0	29	1	US-08-645-641-73 Sequence 73, Appl
13	42	70.0	29	1	US-07-853-408B-73 Sequence 73, Appl
14	42	70.0	29	1	US-08-096-762-73 Sequence 73, Appl
15	42	70.0	29	1	US-08-308-865-73 Sequence 73, Appl
16	42	70.0	29	2	US-09-042-353-270 Sequence 270, App
17	42	70.0	29	2	US-08-758-417A-118 Sequence 118, App
18	42	70.0	29	4	PCT-US92-10983-73 Sequence 73, Appl
19	42	70.0	31	1	US-08-053-131-83 Sequence 83, Appl
20	42	70.0	31	1	US-08-645-641-83 Sequence 83, Appl
21	42	70.0	31	1	US-07-853-408B-83 Sequence 83, Appl
22	42	70.0	31	1	US-08-096-762-83 Sequence 83, Appl
23	42	70.0	31	1	US-08-308-865-83 Sequence 83, Appl
24	42	70.0	31	2	US-09-042-353-280 Sequence 280, App
25	42	70.0	31	2	US-08-758-417A-128 Sequence 128, App
26	42	70.0	31	4	PCT-US92-10983-83 Sequence 83, Appl
27	42	70.0	36	1	US-08-053-131-84 Sequence 84, Appl

28	42	70.0	36	1	US-08-645-641-84 Sequence 84, Appl
29	42	70.0	36	1	US-07-853-408B-84 Sequence 84, Appl
30	42	70.0	36	1	US-08-096-762-84 Sequence 84, Appl
31	42	70.0	36	1	US-08-308-865-84 Sequence 84, Appl
32	42	70.0	36	2	US-09-042-353-281 Sequence 281, App
33	42	70.0	36	2	US-08-758-417A-129 Sequence 129, App
34	42	70.0	36	4	PCT-US92-10983-84 Sequence 84, Appl
35	42	70.0	119	2	US-09-840-459-88 Sequence 88, Appl
36	42	70.0	119	2	US-09-497-625A-88 Sequence 77, Appl
37	42	70.0	128	2	US-09-840-459-77 Sequence 79, Appl
38	42	70.0	128	2	US-09-840-459-79 Sequence 77, Appl
39	42	70.0	128	2	US-09-497-625A-77 Sequence 79, Appl
40	42	70.0	128	2	US-09-497-625A-79 Sequence 80, Appl
41	42	70.0	167	2	US-09-472-087-80 Sequence 64, Appl
42	42	70.0	236	2	US-09-456-090A-64 Sequence 104, Appl
43	42	70.0	236	2	US-09-456-090A-104 Sequence 64, Appl
44	42	70.0	236	2	US-09-453-234-64 Sequence 104, App
45	42	70.0	236	2	US-09-453-234-104 Sequence 104, App

## ALIGNMENTS

RESULT 1  
US-08-053-131-78  
Sequence 78, Application US/08053131  
Patent No. 5661016  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for  
NUMBER OF INVENTION: Producing Heterologous Antibodies  
TITER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Townsend and Townsend Knott and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 200  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/053.131  
FILING DATE: 26-APR-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/910,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-053-131-78

Query Match 71.7%; Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11  
:||||:|  
Db 10 SYYYGMDV 18

## RESULT 2

US-08-645-641-78  
Sequence 78, Application US/08645641  
Patent No. 5719032  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for  
Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/645,641  
FILING DATE: 20-MAY-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-000913  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-645-641-78

Query Match 71.7%; Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11  
:||||:|  
Db 10 SYYYGMDV 18

## RESULT 3

US-07-853-408B-78  
Sequence 78, Application US/07853408B  
Patent No. 5789650  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for  
Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/853,408B  
FILING DATE: 19920318  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-853-408B-78

Query Match 71.7%; Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11  
:||||:|  
Db 10 SYYYGMDV 18

## RESULT 4

US-08-096-762-78  
Sequence 78, Application US/08096762  
Patent No. 5814318  
GENERAL INFORMATION:  
APPLICANT: Lomborg, Nils  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for  
Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 210  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Knoutle and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 200  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/096,762  
FILING DATE: 22-JUL-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860

FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-096-762-78

Query Match 71.7%; Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 3 TTYTGGDGV 11  
:||||:|  
Db 10 SYYTGGMDV 18

RESULT 5  
US-08-308-865-78  
Sequence 78, Application US/08308865  
Patent No. 5877397  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSER: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,865  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/145,707  
FILING DATE:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-308-865-78

Query Match 71.7%; Score 43; DB 1; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGGDGV 11  
:||||:|  
Db 10 SYYTGGMDV 18

RESULT 6  
US-09-042-353-275  
Sequence 275, Application US/09042353  
Patent No. 6255458  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 421  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,353  
FILING DATE: 13-MAR-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/209,741

FILING DATE: 09-MAR-1994  
PRIOR APPLICATION DATA: US 08/352,322  
FILING DATE: 07-DEC-1994  
PRIOR APPLICATION DATA: US 08/544,404  
FILING DATE: 10-OCT-1995  
PRIOR APPLICATION DATA: US 08/728,463  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA: WO PCT/US96/16433  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA: US 08/758,417  
FILING DATE: 02-DEC-1996  
PRIOR APPLICATION DATA: WO PCT/US97/21803  
FILING DATE: 01-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 014643-009040US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 275:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-042-353-275

Query Match 71.7%; Score 43; DB 2; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYRGLDV 11  
:|:|:|:|:  
Db 10 SYYYGMDV 18

RESULT 7  
US-08-758-417A-123  
Sequence 123, Application US/08758417A  
Patent No. 6300129  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 417  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,417A  
FILING DATE: 02-DEC-1996  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996

APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Serafini, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-009030US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 123:  
US-08-758-417A-123

Query Match 71.7%; Score 43; DB 2; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYRGLDV 11  
:|:|:|:|:  
Db 10 SYYYGMDV 18

RESULT 8  
PCT-US92-10983-78  
Sequence 78, Application PC/TUS9210983  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
Kay, Robert M.  
TITLE OF INVENTION: Transgenic Non-Human Animals for  
Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10983  
FILING DATE: 19921217  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US92-10983-78

Query Match 71.7%; Score 43; DB 4; Length 33;  
Best Local Similarity 66.7%; Pred. No. 1.6;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYRFGLDV 11  
Db 10 STYYGMDV 18

RESULT 9  
US-09-840-459-84  
Sequence 84, Application US/09840459  
Patent No. 6696550  
GENERAL INFORMATION:  
APPLICANT: Larosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1998-07-23  
PRIOR APPLICATION NUMBER: 09/121,781  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 84  
LENGTH: 125  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-840-459-84

Query Match 71.7%; Score 43; DB 2; Length 125;  
Best Local Similarity 66.7%; Pred. No. 6.4;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYRFGLDV 11  
Db 106 STYYGMDV 114

RESULT 10  
US-09-497-625A-84  
Sequence 84, Application US/09497625A  
Patent No. 6727349  
GENERAL INFORMATION:  
APPLICANT: Larosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-004  
CURRENT APPLICATION NUMBER: US/09/497,625A  
CURRENT FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 84  
LENGTH: 125  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-497-625A-84

Query Match 71.7%; Score 43; DB 2; Length 125;  
Best Local Similarity 66.7%; Pred. No. 6.4;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYRFGLDV 11  
Db 106 STYYGMDV 114

RESULT 11  
US-08-053-131-73  
Sequence 73, Application US/08053131  
Patent No. 5661016  
GENERAL INFORMATION:  
APPLICANT: Londerg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 200  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/053,131  
FILING DATE: 26-APR-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-053-131-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
Db 7 YYYGMDV 14

## RESULT 12

US-08-645-641-73  
Sequence 73, Application US/08645641  
Patent No. 5719032  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/645,641  
FILING DATE: 20-MAY-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-000913  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-645-641-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
Db 7 YYYGMDV 14

## RESULT 13

US-07-853-408B-73  
Sequence 73, Application US/07853408B  
Patent No. 5789650  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils

APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: William M. Smith  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/853,408B  
FILING DATE: 19920318  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-853-408B-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11  
Db 7 YYYGMDV 14

## RESULT 14

US-08-096-762-73  
Sequence 73, Application US/08096762  
Patent No. 5814318  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 210  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourtie and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 200  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/096,762  
FILING DATE: 22-JUL-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131

FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO.: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-096-762-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGGLDV 11  
|||:|:  
Db 7 YYFGMDV 14

RESULT 15  
US-08-308-865-73  
Sequence 73, Application US/08308865  
Patent No. 5877397  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nile  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 150  
CORRESPONDENCE ADDRESS:  
ADDRESSER: William M. Smith  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,865  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/145,707  
FILING DATE:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 14643-9-1-1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-308-865-73

Query Match 70.0%; Score 42; DB 1; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.1;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGGLDV 11  
|||:|:  
Db 7 YYFGMDV 14

Search completed: November 21, 2005, 12:07:38  
Job time : 5.15018 secs

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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:50:51 ; Search time 13.619 Seconds  
(without alignments)  
337.478 Million cell updates/sec

Title: US-10-632-706-126  
Perfect score: 60  
Sequence: 1 LATYYFGGLDV 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications RA-Main:  
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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	60	100.0	11 4 US-10-632-706-126	Sequence 126, App
2	60	100.0	11 4 US-10-632-706-127	Sequence 127, App
3	48	80.0	122 6 US-11-031-485-116	Sequence 116, App
4	47	78.3	129 4 US-10-364-743-101	Sequence 101, App
5	47	78.3	129 5 US-10-452-593-101	Sequence 101, App
6	47	78.3	134 4 US-10-364-743-15	Sequence 15, App1
7	47	78.3	134 5 US-10-452-593-15	Sequence 15, App1
8	47	78.3	468 6 US-11-031-485-56	Sequence 56, App1
9	47	78.3	469 6 US-11-031-485-18	Sequence 18, App1
10	46	76.7	13 4 US-10-632-706-114	Sequence 114, App
11	46	76.7	21 5 US-10-783-311-141	Sequence 141, App
12	46	76.7	140 5 US-10-783-311-135	Sequence 135, App
13	45	75.0	16 5 US-10-783-311-277	Sequence 277, App
14	45	75.0	21 3 US-09-880-748-3068	Sequence 3068, App
15	45	75.0	21 4 US-10-293-418-3068	Sequence 3068, App
16	45	75.0	117 6 US-11-009-731-47	Sequence 47, App1
17	45	75.0	135 5 US-10-783-311-271	Sequence 271, App
18	45	75.0	256 3 US-09-880-748-1600	Sequence 1600, App
19	45	75.0	256 4 US-10-293-418-1600	Sequence 1600, App
20	44	73.3	16 3 US-09-880-748-2129	Sequence 2129, App
21	44	73.3	16 4 US-10-293-418-2129	Sequence 2129, App
22	44	73.3	17 3 US-09-880-748-2876	Sequence 2876, App
23	44	73.3	17 4 US-10-293-418-2876	Sequence 2876, App
24	44	73.3	18 5 US-10-984-960A-8	Sequence 8, App1
25	44	73.3	117 4 US-10-041-860-206	Sequence 206, App1
26	44	73.3	123 4 US-10-309-762-18	Sequence 18, App1
27	44	73.3	123 4 US-10-309-762-19	Sequence 19, App1

28	44	73.3	124 4 US-10-292-088-106	Sequence 106, App
29	44	73.3	127 4 US-10-041-860-31	Sequence 31, App1
30	44	73.3	127 4 US-10-041-860-243	Sequence 243, App
31	44	73.3	127 4 US-10-041-860-325	Sequence 325, App
32	44	73.3	127 4 US-10-665-383-42	Sequence 42, App1
33	44	73.3	127 4 US-10-466-242-53	Sequence 53, App1
34	44	73.3	127 5 US-10-984-960A-2	Sequence 2, App1
35	44	73.3	129 4 US-10-292-088-10	Sequence 10, App1
36	44	73.3	124 4 US-10-364-743-16	Sequence 16, App1
37	44	73.3	134 4 US-10-364-743-109	Sequence 109, App
38	44	73.3	134 4 US-10-364-743-110	Sequence 110, App
39	44	73.3	134 5 US-10-452-593-16	Sequence 16, App1
40	44	73.3	134 5 US-10-452-593-109	Sequence 109, App
41	44	73.3	134 5 US-10-452-593-110	Sequence 110, App
42	44	73.3	145 5 US-10-644-277-146	Sequence 146, App
43	44	73.3	157 5 US-10-473-287-34	Sequence 34, App1
44	44	73.3	157 5 US-10-473-287-63	Sequence 63, App1
45	44	73.3	249 5 US-10-935-290-61	Sequence 61, App1

## ALIGNMENTS

```
RESULT 1
US-10-632-706-126
Sequence 126, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 126
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-126
Query Match 100.0%; Score 60; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LATYYFGGLDV 11
Db 1 LATYYFGGLDV 11
RESULT 2
US-10-632-706-127
Sequence 127, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
```

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/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 127
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-127

Query Match          100.0%; Score 60; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
Db 1 LATYYFGLDV 11

RESULT 3
US-11-031-485-116
/ Sequence 116, Application US/11031485
/ Publication No. US20050232917A1
/ GENERAL INFORMATION:
/ APPLICANT: PULEN, NICHOLAS
/ APPLICANT: MOLLOY, ELIZABETH
/ APPLICANT: KELLERMAN, SIRID-AIMEE
/ APPLICANT: GREEN, LARRY L.
/ APPLICANT: HAAK-FREDSCHIO, MARY
/ TITLE OF INVENTION: ANTIBODIES TO MADCAM
/ FILE REFERENCE: ABX-DF6
/ CURRENT APPLICATION NUMBER: US/11/031,485
/ PRIOR FILING DATE: 2005-01-07
/ PRIOR APPLICATION NUMBER: 60/535,490
/ PRIOR FILING DATE: 2004-01-09
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 116
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-031-485-116

Query Match          80.0%; Score 48; DB 6; Length 122;
Best Local Similarity 63.6%; Pred. No. 2.8;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
Db 100 VTTYGGMDV 110

RESULT 4
US-10-364-743-101
/ Sequence 101, Application US/10364743
/ Publication No. US20040009178A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowdish, Katherine S.
/ APPLICANT: Frederickson, Shana
/ APPLICANT: Wild, Martha A.
/ APPLICANT: Maruyama, Toshiaki
/ APPLICANT: NO. US20040009178A1an, Mary Jean
/ TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
/ FILE REFERENCE: 84 (1087-73)
/ CURRENT APPLICATION NUMBER: US/10/364,743
/ PRIOR FILING DATE: 2003-02-11
/ PRIOR APPLICATION NUMBER: US 60/428,807
/ PRIOR FILING DATE: 2002-11-25
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 101
/ LENGTH: 129
/ TYPE: PRT
```

```
/ TYPE: PRT
/ ORGANISM: human
US-10-364-743-101

Query Match          78.3%; Score 47; DB 4; Length 129;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11
Db 105 TTYYGMDV 113

RESULT 5
US-10-452-593-101
/ Sequence 101, Application US/10452593
/ Publication No. US2004025899A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowdish, Katherine S.
/ APPLICANT: Frederickson, Shana
/ APPLICANT: Wild, Martha A.
/ APPLICANT: Maruyama, Toshiaki
/ APPLICANT: Nolan, Mary Jean
/ TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
/ FILE REFERENCE: 98 CIP (1087-73 CIP)
/ CURRENT APPLICATION NUMBER: US/10/452,593
/ PRIOR FILING DATE: 2003-06-02
/ PRIOR APPLICATION NUMBER: US 10/364,743
/ PRIOR FILING DATE: 2003-02-11
/ PRIOR APPLICATION NUMBER: US 60/356,086
/ PRIOR FILING DATE: 2002-02-11
/ PRIOR APPLICATION NUMBER: US 60/376,408
/ PRIOR FILING DATE: 2002-04-29
/ PRIOR APPLICATION NUMBER: US 60/428,807
/ PRIOR FILING DATE: 2002-11-25
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 101
/ LENGTH: 129
/ TYPE: PRT
/ ORGANISM: human
US-10-452-593-101

Query Match          78.3%; Score 47; DB 5; Length 129;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11
Db 105 TTYYGMDV 113

RESULT 6
US-10-364-743-15
/ Sequence 15, Application US/10364743
/ Publication No. US20040009178A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowdish, Katherine S.
/ APPLICANT: Frederickson, Shana
/ APPLICANT: Wild, Martha A.
/ APPLICANT: Maruyama, Toshiaki
/ APPLICANT: NO. US20040009178A1an, Mary Jean
/ TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
/ FILE REFERENCE: 84 (1087-73)
/ CURRENT APPLICATION NUMBER: US/10/364,743
/ PRIOR FILING DATE: 2003-02-11
/ PRIOR APPLICATION NUMBER: US 60/428,807
/ PRIOR FILING DATE: 2002-11-25
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 15
/ LENGTH: 134
/ TYPE: PRT
```

ORGANISM: human  
US-10-364-743-15

Query Match 78.3%; Score 47; DB 4; Length 134;  
Best Local Similarity 77.8%; Pred. No. 4.5;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
DB 110 TTYTFFGLDV 118

## RESULT 7

US-10-452-593-15  
Sequence 15, Application US/10452593  
Publication No. US20040258699A1  
GENERAL INFORMATION:  
APPLICANT: Bowdlen, Katherine S.  
APPLICANT: Frederickson, Shana  
APPLICANT: Wild, Martha A..  
APPLICANT: Maruyama, Toshiaki  
APPLICANT: Nolan, Mary Jean  
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE  
FILE REFERENCE: 98 CIP (1087-73 CIP)  
CURRENT FILING DATE: 2003-06-02  
PRIOR APPLICATION NUMBER: US/10/364,743  
PRIOR FILING DATE: 2003-02-11  
PRIOR APPLICATION NUMBER: US 60/356,086  
PRIOR FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: US 60/376,408  
PRIOR FILING DATE: 2002-04-29  
PRIOR APPLICATION NUMBER: US 60/428,807  
PRIOR FILING DATE: 2002-11-25  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 15  
LENGTH: 134  
TYPE: PRT  
ORGANISM: human  
US-10-452-593-15

Query Match 78.3%; Score 47; DB 5; Length 134;  
Best Local Similarity 77.8%; Pred. No. 4.5;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
DB 110 TTYTFFGLDV 118

## RESULT 8

US-11-031-485-56  
Sequence 56, Application US/11031485  
Publication No. US20050232917A1  
GENERAL INFORMATION:  
APPLICANT: PULLEN, NICHOLAS  
APPLICANT: MOLLOY, ELIZABETH  
APPLICANT: KELLERMANN, STRID-AIMEE  
APPLICANT: GREEN, LARRY L.  
APPLICANT: HAAR-FRENDSCHO, MARY  
TITLE OF INVENTION: ANTIBODIES TO MADCAM  
FILE REFERENCE: ABX-PF6  
CURRENT APPLICATION NUMBER: US/11/031,485  
CURRENT FILING DATE: 2005-01-07  
PRIOR APPLICATION NUMBER: 60/535,490  
PRIOR FILING DATE: 2004-01-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 56  
LENGTH: 468  
TYPE: PRT  
ORGANISM: Homo sapiens

US-11-031-485-56

Query Match 78.3%; Score 47; DB 6; Length 468;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
DB 123 TTYTFFGLDV 131

## RESULT 9

US-11-031-485-18  
Sequence 18, Application US/11031485  
Publication No. US20050232917A1  
GENERAL INFORMATION:  
APPLICANT: PULLEN, NICHOLAS  
APPLICANT: MOLLOY, ELIZABETH  
APPLICANT: KELLERMANN, STRID-AIMEE  
APPLICANT: GREEN, LARRY L.  
APPLICANT: HAAR-FRENDSCHO, MARY  
TITLE OF INVENTION: ANTIBODIES TO MADCAM  
FILE REFERENCE: ABX-PF6  
CURRENT APPLICATION NUMBER: US/11/031,485  
CURRENT FILING DATE: 2005-01-07  
PRIOR APPLICATION NUMBER: 60/535,490  
PRIOR FILING DATE: 2004-01-09  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 18  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-031-485-18

Query Match 78.3%; Score 47; DB 6; Length 469;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11  
DB 123 TTYTFFGLDV 131

## RESULT 10

US-10-632-706-114  
Sequence 114, Application US/10632706  
Publication No. US20040175385A1  
GENERAL INFORMATION:  
APPLICANT: MARKS, JAMES D.  
APPLICANT: AMERSDORFER, PETER  
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
FILE REFERENCE: 407T-895120US  
CURRENT APPLICATION NUMBER: US/10/632,706  
CURRENT FILING DATE: 2003-08-01  
PRIOR APPLICATION NUMBER: US 60/400,721  
PRIOR FILING DATE: 2002-08-01  
PRIOR APPLICATION NUMBER: US 09/144,806  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 278  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 114  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial  
OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-114

Query Match 76.7%; Score 46; DB 4; Length 13;  
Best Local Similarity 70.0%; Pred. No. 0.64;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYFGLDV 11  
| | | | |  
Db 4 ANYYGMDV 13

RESULT 11  
US-10-783-311-141  
; Sequence 141, Application US/10783311  
; Publication No. US20050009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; TITLE OF INVENTION: PAP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 141  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Heavy Chain amino acid sequence  
US-10-783-311-141

Query Match 76.7%; Score 46; DB 5; Length 21;  
Best Local Similarity 63.6%; Pred. No. 1;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11  
| | | | |  
Db 11 LGNYYYGMDV 21

RESULT 12  
US-10-783-311-135  
; Sequence 135, Application US/10783311  
; Publication No. US20050009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; TITLE OF INVENTION: PAP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 135  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Heavy Chain amino acid sequence  
US-10-783-311-135

Query Match 76.7%; Score 46; DB 5; Length 140;  
Best Local Similarity 63.6%; Pred. No. 6.9;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11  
| | | | |  
Db 109 LGNYYYGMDV 119

RESULT 13  
US-10-783-311-277  
; Sequence 277, Application US/10783311

; Publication No. US20050009136A1  
; GENERAL INFORMATION:  
; APPLICANT: Nixon, Andrew  
; TITLE OF INVENTION: PAP-A LIGANDS  
; FILE REFERENCE: 10280-059001  
; CURRENT APPLICATION NUMBER: US/10/783,311  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/448,515  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 394  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 277  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Heavy Chain amino acid sequence  
US-10-783-311-277

Query Match 75.0%; Score 45; DB 5; Length 16;  
Best Local Similarity 63.6%; Pred. No. 1.2;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11  
| | | | |  
Db 6 VAGYYYGMDV 16

RESULT 14  
US-09-880-748-3068  
; Sequence 3068, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3068  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-3068

Query Match 75.0%; Score 45; DB 3; Length 21;  
Best Local Similarity 70.0%; Pred. No. 1.5;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYFGLDV 11  
| | | | |  
Db 12 APYYYGMDV 21

RESULT 15  
US-10-293-418-3068  
; Sequence 3068, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

```

FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3068
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-3068

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Query Match 75.0% Score 45 DB 4 Length 21
Best Local Similarity 70.0% Pred. No. 1.5
Matches 7 Conservative 2 Mismatches 1 Indels 0 Gaps 0

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QY 2 ATYYFGLDV 11
DB 12 APYYGMDV 21

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Search completed: November 21, 2005, 12:33:36  
 Job time : 14.619 secs

**This Page Blank (usp10)**



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/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-8

Query Match      70.0%; Score 42; DB 7; Length 124;
Best Local Similarity 75.0%; Pred. No. 0.092;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
DB 106 YYYGMDV 113

RESULT 3
US-11-144-248-16
/ Sequence 16, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 125
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-16

Query Match      70.0%; Score 42; DB 7; Length 125;
Best Local Similarity 75.0%; Pred. No. 0.092;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 174
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-4

Query Match      70.0%; Score 42; DB 7; Length 174;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
DB 99 YYYGMDV 106

RESULT 5
US-11-144-248-45
/ Sequence 45, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 45
/ LENGTH: 470
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-45

Query Match      70.0%; Score 42; DB 7; Length 470;
Best Local Similarity 75.0%; Pred. No. 0.35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
DB 126 YYYGMDV 133

RESULT 6
US-11-144-248-46
/ Sequence 46, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
```



```

; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-46
```

```
Query Match
Best Local Similarity 70.0%; Score 42; DB 7; Length 470;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 4 YYYFGLDV 11
|||:|:|
Db 126 YYYGMDV 133
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```

RESULT 7
US-11-144-248-49
; Sequence 49, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-49
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Query Match
Best Local Similarity 70.0%; Score 42; DB 7; Length 470;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 4 YYYFGLDV 11
|||:|:|
Db 126 YYYGMDV 133
```

```

RESULT 8
US-11-144-248-50
; Sequence 50, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-50
```

```

; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-50
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```
Query Match
Best Local Similarity 70.0%; Score 42; DB 7; Length 473;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 4 YYYFGLDV 11
|||:|:|
Db 129 YYYGMDV 136
```

```

RESULT 9
US-11-144-248-20
; Sequence 20, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-20
```

```
Query Match
Best Local Similarity 66.7%; Score 40; DB 7; Length 113;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 2 ATYYRGLDV 11
::|:|:|
Db 93 SSFYRGMDV 102
```

```

RESULT 10
US-11-017-550-42
; Sequence 42, Application US/11017550
; Publication No. US20050250183A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Schultz, Peter G
; APPLICANT: Wang, Lei
```

APPLICANT: Anderson, John C  
APPLICANT: Chiu, Jason  
APPLICANT: Liu, David R  
APPLICANT: Magliery, Thomas  
APPLICANT: Meggers, Eric L  
APPLICANT: Muhl, Ryan A  
APPLICANT: Pastinak, Miro  
APPLICANT: Santoro, Stephen W  
APPLICANT: Zhang, Zhilwen  
TITLE OF INVENTION: In vivo incorporation of unnatural amino acids  
FILE REFERENCE: 34-000120US  
CURRENT APPLICATION NUMBER: US/11/017,550  
CURRENT FILING DATE: 2004-12-17  
PRIORITY APPLICATION NUMBER: US/10/126,927  
PRIORITY FILING DATE: 2002-04-19  
PRIORITY APPLICATION NUMBER: US 60/285,030  
PRIORITY FILING DATE: 2001-04-19  
PRIORITY APPLICATION NUMBER: US 60/355,514  
PRIORITY FILING DATE: 2002-02-06  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 42  
LENGTH: 306  
TYPE: PRT  
ORGANISM: Methanococcus jannaschii  
US-11-017-550-42

Query Match 60.0%; Score 36; DB 7; Length 306;  
Best Local Similarity 66.7%; Pred. No. 2.4;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 TYYFGLDV 11  
DB 158 TYYHAGVDV 166

RESULT 11  
US-10-839-799-112  
Sequence 112, Application US/10839799  
Publication No. US20050249726A1  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
SATO, Koh  
TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/839,799  
FILING DATE: 06-May-2004  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,265  
FILING DATE: 09-SEP-1996  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 87 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 112:  
US-10-839-799-112

Query Match 58.3%; Score 35; DB 1; Length 87;  
Best Local Similarity 75.0%; Pred. No. 1;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYFG 8  
DB 72 LATYYCFG 79

RESULT 12  
US-10-721-763-29  
Sequence 29, Application US/10721763  
Publication No. US20050249729A1  
GENERAL INFORMATION:  
APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY  
FILE REFERENCE: PH-1573-PCT  
CURRENT APPLICATION NUMBER: US/10/721,763  
CURRENT FILING DATE: 2003-11-26  
PRIORITY APPLICATION NUMBER: JP2001-150213  
PRIORITY FILING DATE: 2001-05-18  
PRIORITY APPLICATION NUMBER: JP2001-243040  
PRIORITY FILING DATE: 2001-08-09  
PRIORITY APPLICATION NUMBER: JP2001-314489  
PRIORITY FILING DATE: 2001-10-11  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 29  
LENGTH: 145  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-721-763-29

Query Match 58.3%; Score 35; DB 1; Length 145;  
Best Local Similarity 71.4%; Pred. No. 1.7;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 YYFGLDV 11  
DB 128 YYYGMDV 134

RESULT 13  
US-10-721-763-25  
Sequence 25, Application US/10721763  
Publication No. US20050249729A1  
GENERAL INFORMATION:  
APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY  
FILE REFERENCE: PH-1573-PCT  
CURRENT APPLICATION NUMBER: US/10/721,763  
CURRENT FILING DATE: 2003-11-26  
PRIORITY APPLICATION NUMBER: JP2001-150213  
PRIORITY FILING DATE: 2001-05-18  
PRIORITY APPLICATION NUMBER: JP2001-243040  
PRIORITY FILING DATE: 2001-08-09  
PRIORITY APPLICATION NUMBER: JP2001-314489  
PRIORITY FILING DATE: 2001-10-11  
NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 154  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-721-763-25

Query Match 58.3%; Score 35; DB 1; Length 154;  
Best Local Similarity 71.4%; Pred. No. 1.8;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 5 YYYFGLDV 11  
||:|:|  
Db 135 YYYGMDV 141

RESULT 14  
US-11-017-550-37  
; Sequence 37, Application US/11017550  
; Publication No. US20050250183A1  
; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute  
; APPLICANT: Schultz, Peter G  
; APPLICANT: Wang, Lei  
; APPLICANT: Anderson, John C  
; APPLICANT: Chin, Jason  
; APPLICANT: Liu, David R  
; APPLICANT: Magliery, Thomas  
; APPLICANT: Meggers, Eric L  
; APPLICANT: Mehl, Ryan A  
; APPLICANT: Pastinak, Miro  
; APPLICANT: Santoro, Stephen W  
; APPLICANT: Zhang, Zhiwen  
; TITLE OF INVENTION: In Vivo Incorporation of Unnatural Amino Acids  
; FILE REFERENCE: 54-000120US  
; CURRENT APPLICATION NUMBER: US/11/017,550  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: US/10/126,927  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/285,030  
; PRIOR FILING DATE: 2001-04-19  
; PRIOR APPLICATION NUMBER: US 60/355,514  
; PRIOR FILING DATE: 2002-02-06  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 306  
; TYPE: PRT  
; ORGANISM: Mechanococcus jannaschii  
US-11-017-550-37

Query Match 55.0%; Score 33; DB 7; Length 306;  
Best Local Similarity 62.5%; Pred. No. 8;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 4 YYYFGLDV 11  
||:|:|  
Db 159 YYYGMDV 166

RESULT 15  
US-11-022-562-211  
; Sequence 211, Application US/11022562  
; Publication No. US20050249742A1  
; GENERAL INFORMATION:  
; APPLICANT: Rupprecht, Ruth M.  
; APPLICANT: Shieong, Jiang  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE  
; FILE REFERENCE: DFN-043CN  
; CURRENT APPLICATION NUMBER: US/11/022,562  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: PCT/US03/20322

; PRIOR FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: 60/392718  
; PRIOR FILING DATE: 2002-06-27  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 211  
; LENGTH: 2280  
; TYPE: PRT  
; ORGANISM: Hepatitis C Virus  
US-11-022-562-211

Query Match 55.0%; Score 33; DB 7; Length 2280;  
Best Local Similarity 70.0%; Pred. No. 60;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 ATYYFGLDV 11  
||:|:|  
Db 1414 AVAYYRGLDV 1423

Search completed: November 21, 2005, 12:33:51  
Job time : 0.301465 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:32 ; Search time 18.7436 Seconds  
(without alignments)  
328.182 Million cell updates/sec

Title: US-10-632-706-156  
Perfect score: 81  
Sequence: 1 WVRQAPGKLEWVA 14

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseqp21:\*  
2: Geneseqp1980s:\*  
3: Geneseqp1990s:\*  
4: Geneseqp2000s:\*  
5: Geneseqp2001s:\*  
6: Geneseqp2002s:\*  
7: Geneseqp2003as:\*  
8: Geneseqp2003bs:\*  
9: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	14	2	AAR97326 Humanised
2	81	100.0	14	5	Aa017610 Human PAP
3	81	100.0	14	7	AB033890 Anti-GPI-
4	81	100.0	14	7	AD120633 HPR2 prot
5	81	100.0	14	8	ADR38742 Mouse hea
6	81	100.0	14	8	ADR38754 Mouse hea
7	81	100.0	14	8	ADR38738 Mouse hea
8	81	100.0	14	8	ADR38762 Mouse hea
9	81	100.0	14	8	ADR38766 Mouse hea
10	81	100.0	14	8	ADR38766 Mouse hea
11	81	100.0	14	8	ADR38758 Mouse hea
12	81	100.0	14	8	ADR38750 Mouse hea
13	81	100.0	14	9	ADW96736 Anti-EGFR
14	81	100.0	14	9	ADW96723 Anti-EGFR
15	81	100.0	14	9	ADW80308 Human ant
16	81	100.0	14	9	ADW80325 Human ant
17	81	100.0	14	9	ADY31370 Human ant
18	81	100.0	14	9	ADY31373 Human ant
19	81	100.0	14	9	ADY31400 Human ant
20	81	100.0	14	9	ADZ35836 Anti-gluc
21	81	100.0	14	9	AB21477 Human ant
22	81	100.0	17	9	ADY31505 Human ant
23	81	100.0	17	9	ADY31532 Human ant
24	81	100.0	17	9	ADY31502 Human ant

25	81	100.0	19	2	AAW94736 Anti-Strap
26	81	100.0	44	8	ADU87725 Human hea
27	81	100.0	58	9	AEC20858 Human var
28	81	100.0	61	2	AAR76975 HSV-neutr
29	81	100.0	62	2	AAR76976 BONT/A HC
30	81	100.0	66	6	ABU56837 BONT/A HC
31	81	100.0	66	6	ABU56866 BONT/A HC
32	81	100.0	82	8	ADL35113 Humanised
33	81	100.0	82	8	ADL35115 Humanised
34	81	100.0	82	8	ADL35112 Murine an
35	81	100.0	82	8	ADL35114 Humanised
36	81	100.0	82	8	ADL35117 Humanised
37	81	100.0	82	8	ADL35116 Humanised
38	81	100.0	82	9	AB21573 Human Ig
39	81	100.0	87	8	ADU87732 Amino aci
40	81	100.0	89	6	AAE35911 Human DP5
41	81	100.0	91	9	ADW97148 Human IL-
42	81	100.0	92	9	ADW97150 Human IL-
43	81	100.0	93	6	ABO27274 Human Hum
44	81	100.0	93	9	ADW97147 Human IL-
45	81	100.0	93	9	ADW97179 Human IL-

#### ALIGNMENTS

RESULT 1  
AAR97326  
ID AAR97326 standard; peptide, 14 AA.

AC AAR97326;  
DT 15-OCT-1996 (first entry)

DE Humanised monoclonal antibody heavy chain framework region.

KM Monoclonal antibody; humanised; mouse; framework region; FR; CDR;  
KW Complementary determining region; anti-carcinoma/embryonic antigen; CEA;  
KM diagnosis; imaging; therapy; immune response.

OS Homo sapiens.

XX W09611013-AL.

PD 18-APR-1996.

PF 28-SEP-1995; 95WO-US011964.

PR 05-OCT-1994; 94US-00318157.

XX (IMMU-) IMMUNOMEDICS INC.

XX Hansen HJ, Armour KL;

XX WPI, 1996-209653/21.

PT New humanised anti-CEA monoclonal antibody - having engrafted murine

CDRE, used for diagnosis, imaging and therapy of CEA-producing cancers.

Claim 7; Page 39; 62pp; English.

New humanised monoclonal antibodies (MAbs) comprising the complementary determining regions (CDRs) of a parental murine class III anti-carcinoma/embryonic (CEA) Mab engrafted to the framework regions (FRs) of a heterologous antibody which can be derived from any species including human, retain the anti-CEA binding specificity of the parental murine Mab but are less immunogenic in a human subject than the parental Mab. The humanised antibodies can be used in diagnosis, imaging and therapy of CEA-producing cancers and patients receiving the humanised antibodies and conjugates show improved therapeutic results, decreased immune responses and decreased immune-mediated adverse effects compared to the parent antibody. This sequence corresponds to the second framework region of the heavy chain of the humanised Mab. See AAR97313-97333

XX  
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLSEWVA 14  
Db 1 WVRQAPGKGLSEWVA 14

RESULT 2  
AA017610  
ID AA017610 standard; peptide; 14 AA.

AC AA017610;

DT 08-AUG-2002 (first entry)

DE Human PAPalpa specific VL region from VH50 FR2 peptide.

KM Human; PAPalpa; fibroblast activating protein alpha; antibody; Ab;  
KW gene therapy; cancer; wound healing; inflammation; cytostatic.

OS Homo sapiens.

PN NC000168708-A2.

PD 20-SEP-2001.

PF 16-MAR-2001; 2001WO-EP004716.

PR 17-MAR-2000; 2000DR-01013286.

PR 11-SEP-2000; 2000GB-00022216.

XX (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.

PI Park J, Garin-Chesa P, Pfizenmaier K, Moosmayer D, Mersmann M;  
PI Schmidt A;

XX WPI; 2002-041180/05.

DR N-PSDB; AAL46555.

XX New human humanized antibody that specifically binds to fibroblasts

PT activating protein alpha, useful for treating cancer or tumor, and for  
PT imaging tumors associated with activated stromal fibroblasts, e.g. lung  
PT or breast cancer.

PS Disclosure; Fig 6C; 1099p; English.

XX The present invention relates to a human or humanised antibody (Ab) which  
CC specifically binds to fibroblast activating protein alpha (PAPalpa). The  
CC antibodies are useful for preparing a composition for the treatment of  
CC cancer, and for imaging tumours associated with activated stromal  
CC fibroblasts, such as colorectal cancer, non-small-cell lung cancer,  
CC breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder  
CC cancer, pancreatic cancer and metastatic brain cancer, and diseases  
CC associated with the same, such as inflammation and wound healing. The  
CC present sequence is a peptide described in the exemplification of the  
CC invention

XX Sequence 14 AA;

Query Match 100.0%; Score 81; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLSEWVA 14  
Db 1 WVRQAPGKGLSEWVA 14

RESULT 3  
AB033890  
ID AB033890 standard; peptide; 14 AA.

AC AB033890;

DT 18-SEP-2003 (first entry)

DE Anti-GPI-antibody heavy chain framework region #8.

KM Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;  
KW anti-GPI-antibody; GPI; glucose-6-phosphate isomerase;  
KW autoimmune disease; rheumatoid arthritis; heavy chain variable region;  
KW VH; framework region.

OS Homo sapiens.

PN US2002146753-A1.

PD 10-OCT-2002.

PF 06-APR-2001; 2001US-00828708;

PR 06-APR-2001; 2001US-00828708.

XX (DITZEL/) DITZEL H.

PA (BURTON/) BURTON D R.

PA (SCHALLER/) SCHALLER M.

PI Ditzel H, Burton DR, Schaller M;

DR WPI; 2003-521517/49.

XX Immunopolypeptide for diagnosis and treatment of human autoimmune  
PT disease, e.g., human rheumatoid arthritis; comprises a polypeptide that  
PT binds to human glucose-6-phosphate isomerase.

XX Claim 6; Fig 4B; 47pp; English.

XX The invention describes an immunopolypeptide comprising a polypeptide  
CC that binds to human glucose-6-phosphate isomerase (GPI). The methods and  
CC compositions are used for diagnosis and treatment of human autoimmune  
CC disease, e.g., human rheumatoid arthritis. This is the amino acid  
CC sequence of human anti-GPI-antibody heavy chain variable region framework  
CC region

XX Sequence 14 AA;

Query Match 100.0%; Score 81; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLSEWVA 14  
Db 1 WVRQAPGKGLSEWVA 14

RESULT 4

AD120633  
ID AD120633 standard; protein; 14 AA.

XX AD120633;

DT 22-APR-2004 (first entry)

DE HFR2 protein.

KM Immunoglobulin molecule; heavy chain framework region; HFR1; HFR2; HFR3;  
KW HFR4; tumour imaging; protein chips assay; light chain framework region;  
KW LFR.

XX Synthetic.

XX

PN WO2003025124-A2.  
 XX 27-MAR-2003.  
 PD  
 XX 13-SEP-2002, 2002WO-US029003.  
 PF  
 XX 14-SEP-2001, 2001US-0318904P.  
 PR  
 XX (FRAU-) FRAUNHOFER INST MOLEKULARBIOLOGIE & ANGE.  
 PA  
 XX Zhang MY, Schillberg S, Zimmermann S, Di Fiore S, Emans N;  
 PI Fischer R;  
 PI WPI: 2003-371805/35.  
 DR N-PSDB; ADI20654, ADI20663, ADI20672.  
 XX  
 PT New immunoglobulin molecule, useful in therapeutic or diagnostic assays  
 PT comprising ELISA, phage display, tumor imaging or protein chips assay or  
 PT in screening assays for detecting molecules that bind to the  
 PT immunoglobulin molecule.  
 XX  
 PS Claim 7; SEQ ID NO 2; 198pp; English.  
 CC  
 CC The present invention relates to an immunoglobulin molecule comprising of  
 CC one or more heavy chain framework regions comprising HFR1, HFR2, HFR3 or  
 CC HFR4 and one or more light chain framework regions comprising LFR1, LFR2,  
 CC LFR3 or LFR4; and complementarily determining regions (CDRs) comprising  
 CC CDR-H1, CDR-H2, CDR-H3 and/or CDR-L1, CDR-L2 or CDR-L3. The immunoglobulin  
 CC is useful in therapeutic or diagnostic assays comprising ELISA, phage  
 CC display, tumor imaging or protein chips assay. Further, the  
 CC immunoglobulin is useful in screening assays for detecting molecules that  
 CC bind to the immunoglobulin molecule. The present sequence represents a  
 CC chain framework region.  
 CC  
 CC Sequence 14 AA;  
 SO  
 Query Match 100.0%; Score 81; DB 7; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WVRQAPGKGLEWVA 14  
 DB 1 WVRQAPGKGLEWVA 14  
 RESULT 5  
 ADR38742  
 ID ADR38742 standard; peptide; 14 AA.  
 XX  
 XX ADR38742;  
 AC  
 XX  
 DT 02-DEC-2004 (first entry)  
 DE  
 XX Mouse heavy chain anti-BONT-antibody framework 2 seqid 144.  
 DE  
 XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
 KW framework 2.  
 KM  
 XX  
 XX Mus sp.  
 OS  
 XX US2004175385-A1.  
 PN  
 XX 09-SEP-2004.  
 PD  
 XX 01-AUG-2003, 2003US-00632706.  
 PF  
 XX 31-AUG-1998; 98US-00144886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX

PI Marks JD, Amersdorfer P;  
 XX  
 DR WPI: 2004-652009/63.  
 XX  
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 PT  
 XX  
 PS Example 4; SEQ ID NO 144; 110pp; English.  
 XX  
 CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC 825, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
 CC comprising BONT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain anti-BONT-antibody framework region 2.  
 CC  
 CC Sequence 14 AA;  
 SO  
 Query Match 100.0%; Score 81; DB 8; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WVRQAPGKGLEWVA 14  
 DB 1 WVRQAPGKGLEWVA 14  
 RESULT 6  
 ADR38754  
 ID ADR38754 standard; peptide; 14 AA.  
 XX  
 XX ADR38754;  
 AC  
 XX  
 DT 02-DEC-2004 (first entry)  
 DE  
 XX Mouse heavy chain anti-BONT-antibody framework 2 seqid 156.  
 DE  
 XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
 KW framework 2.  
 KM  
 XX  
 XX Mus sp.  
 OS  
 XX US2004175385-A1.  
 PN  
 XX 09-SEP-2004.  
 PD  
 XX 01-AUG-2003, 2003US-00632706.  
 PF  
 XX 31-AUG-1998; 98US-00144886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 PR  
 XX

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PA (RESC ) UNIV CALIFORNIA.
XX
XX PI Marks JD, Amersdorfer P;
XX
XX DR WPI, 2004-652009/63.
XX
XX PT New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
XX
XX PS Example 4; SEQ ID NO 156; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralizes botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC 525, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX
XX SQ Sequence 14 AA;
XX
XX Query Match 100.0%; Score 81; DB 8; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-05;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
QY 1 WYRQAPGKGLEWYA 14
DB 1 WYRQAPGKGLEWYA 14
XX
RESULT 7
XX ADR38738
XX ID ADR38738 standard; peptide; 14 AA.
XX AC ADR38738;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Mouse heavy chain anti-BoNT-antibody framework 2 seqid 140.
XX
XX KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX framework 2.
XX
XX OS Mus sp.
XX
XX PN US2004175385-A1.
XX
XX PD 09-SEP-2004.
XX
XX PF 01-AUG-2003; 2003US-00632706.
XX
XX PR 31-AUG-1998; 98US-00144886.
XX

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PR 01-AUG-2002; 2002US-0400721P.
XX
XX (RSGC ) UNIV CALIFORNIA.
XX
XX PA
XX PI Marks JD, Amersdorfer P;
XX
XX DR WPI; 2004-652009/63.
XX
XX PT New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
XX
XX PS Example 4; SEQ ID NO 140; 110pp; English.
XX
XX CC The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (I) binds to and neutralises botulinum neurotoxin type A
XX (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
XX specifically bound by an antibody expressed by a clone chosen from clone
XX S25, C25, C39, 1C6, 3D12, B4, 1F3, hUC25, A71, A72, WR1(V), WR1(T), 3-1,
XX 3-8, 3-10 and 1NG1, where (I) binds to and neutralizes botulinum
XX neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
XX comprising BoNT/A neutralising epitope having an epitope that is
XX specifically bound by an antibody expressed by clones as mentioned in (I)
XX ; producing (I); and a composition (III) comprising several anti-
XX botulinum neurotoxin antibodies, where each antibody is specific for a
XX different epitope of a botulinum neurotoxin and the combination of
XX antibodies shows greater toxin neutralisation than the single antibodies
XX in surplus. The following are disclosed: a pharmaceutical composition
XX comprising (I); and a kit comprising (I). (I) is useful for neutralising
XX BoNT/A antibody and for neutralising a botulinum neurotoxin which
XX involves contacting neurotoxin with (I) in surplus, where each of (I) is
XX specific for a different epitope of the botulinum neurotoxin and the
XX combination of antibodies shows greater toxin neutralisation than the
XX single antibodies in surplus. (I) is useful for diagnosing the botulism
XX or for treating pathologies associated with botulinum neurotoxin
XX poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
XX enables rapid detection or diagnosis of botulism. This is the amino acid
XX sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX
XX SQ Sequence 14 AA;
XX
XX Query Match 100.0%; Score 81; DB 8; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-05;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MYROAPGKGLEWVA 14
XX |||||
XX 1 WYROAPGKGLEWVA 14
XX
XX DB
XX
XX RESULT 8
XX ADR38762
XX ID ADR38762 standard; peptide; 14 AA.
XX
XX AC ADR38762;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Mouse heavy chain anti-BoNT-antibody framework 2 seqid 164.
XX
XX KM antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX framework 2.
XX
XX KM
XX OS Mus sp.
XX
XX PN US2004175385-A1.
XX
XX PD 09-SEP-2004.
XX
XX PF 01-AUG-2003; 2003US-00632706.
XX

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XX 31-AUG-1998; 98US-0014486.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA Marks JD, Amerdorter P;  
 PI WPI; 2004-652009/63.  
 XX  
 XX  
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 XX  
 XX  
 PS Example 4; SEQ ID NO 164; 110pp; English.  
 XX  
 CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI(V), WRI(T), 3-1,  
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 100.0%; Score 81; DB 8; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WVRQAPGKLEWVA 14  
 |||||  
 DB 1 WVRQAPGKLEWVA 14  
 |||||  
 RESULT 9  
 ADR38746  
 ID ADR38746 standard; peptide; 14 AA.  
 XX  
 AC ADR38746;  
 DT 02-DEC-2004 (first entry)  
 XX  
 DB Mouse heavy chain anti-BoNT-antibody framework 2 seqid 148.  
 XX  
 XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
 KW framework 2.  
 XX  
 OS Mus sp.  
 XX  
 PN US2004175385-A1.  
 XX  
 PD 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.  
 PF  
 XX 31-AUG-1998; 98US-0014486.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA Marks JD, Amerdorter P;  
 PI WPI; 2004-652009/63.  
 XX  
 XX  
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 XX  
 XX  
 PS Example 4; SEQ ID NO 148; 110pp; English.  
 XX  
 CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI(V), WRI(T), 3-1,  
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 100.0%; Score 81; DB 8; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 WVRQAPGKLEWVA 14  
 |||||  
 DB 1 WVRQAPGKLEWVA 14  
 |||||  
 RESULT 10  
 ADR38766  
 ID ADR38766 standard; peptide; 14 AA.  
 XX  
 AC ADR38766;  
 DT 02-DEC-2004 (first entry)  
 XX  
 DB Mouse heavy chain anti-BoNT-antibody framework 2 seqid 168.  
 XX  
 XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
 KW framework 2.  
 XX  
 OS Mus sp.  
 XX  
 PN US2004175385-A1.

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XX PD 09-SEP-2004.
XX PF 01-AUG-2003; 2003US-00632706.
XX PR 31-AUG-1998; 98US-00144886.
XX PR 01-AUG-2002; 2002US-0400721P.
XX (REGC ) UNIV CALIFORNIA.
XX PA Marks JD, Amersdorfer P;
XX PI WPI; 2004-652009/63.
XX DR
XX PT New isolated antibody that neutralizes botulinum neurotoxin type A,
XX PT useful for diagnosing botulism or for treating pathologies associated
XX PT with botulinum neurotoxin poisoning.
XX PS Example 4; SEQ ID NO 168; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC 525, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WRI(V), WRI(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 81; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVRQAPGKGLWVA 14
DB 1 WVRQAPGKGLWVA 14

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XX XX US2004175385-A1.
XX PN
XX PD 09-SEP-2004.
XX PF 01-AUG-2003; 2003US-00632706.
XX PR 31-AUG-1998; 98US-00144886.
XX PR 01-AUG-2002; 2002US-0400721P.
XX (REGC ) UNIV CALIFORNIA.
XX PA Marks JD, Amersdorfer P;
XX PI WPI; 2004-652009/63.
XX DR
XX PT New isolated antibody that neutralizes botulinum neurotoxin type A,
XX PT useful for diagnosing botulism or for treating pathologies associated
XX PT with botulinum neurotoxin poisoning.
XX PS Example 4; SEQ ID NO 160; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC 525, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WRI(V), WRI(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 81; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVRQAPGKGLWVA 14
DB 1 WVRQAPGKGLWVA 14

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RESULT 11
ADR38758
ID ADR38758 standard; peptide; 14 AA.
XX
XX ADR38758;
XX AC
XX DT 02-DEC-2004 (first entry)
XX DE Mouse heavy chain anti-BoNT-antibody framework 2 segid 160.
XX
XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX framework 2.
XX
XX Mus sp.
XX

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RESULT 12
ADR38750
ID ADR38750 standard; peptide; 14 AA.
XX
XX ADR38750;
XX AC
XX DT 02-DEC-2004 (first entry)
XX DE Mouse heavy chain anti-BoNT-antibody framework 2 segid 152.
XX
XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX framework 2.
XX

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XX Mus sp.  
 XX US2004175385-A1.  
 XX 09-SEP-2004.  
 XX 01-AUG-2003; 2003US-00632706.  
 XX 31-AUG-1998; 98US-00144886.  
 XX 01-AUG-2002; 2002US-0400721P.  
 XX (RSGC ) UNIV CALIFORNIA.  
 XX Marks JD, Amersdorfer P;  
 XX WPI; 2004-652009/63.  
 XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
 XX useful for diagnosing botulism or for treating pathologies associated  
 XX with botulinum neurotoxin poisoning.  
 XX Example 4, SEQ ID NO 152; 110pp; English.  
 XX The invention describes an isolated antibody (I) that specifically binds  
 XX to an epitope specifically bound by an antibody expressed by a specific  
 XX clone where (I) binds to and neutralizes botulinum neurotoxin type A  
 XX (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
 XX specifically bound by an antibody expressed by a clone chosen from clone  
 XX 525, C35, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1 (V), WR1 (T), 3-1,  
 XX 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum  
 XX neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
 XX comprising BONT/A neutralising epitope having an epitope that is  
 XX specifically bound by an antibody expressed by clones as mentioned in (I)  
 XX ; producing (I); and a composition (III) comprising several anti-  
 XX botulinum neurotoxin antibodies, where each antibody is specific for a  
 XX different epitope of a botulinum neurotoxin and the combination of  
 XX antibodies shows greater toxin neutralisation than the single antibodies  
 XX in surplus. The following are disclosed: a pharmaceutical composition  
 XX comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 XX BONT/A antibody and for neutralising a botulinum neurotoxin which (I)  
 XX involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 XX specific for a different epitope of the botulinum neurotoxin and the  
 XX combination of antibodies shows greater toxin neutralisation than the  
 XX single antibodies in surplus. (I) is useful for diagnosing the botulism  
 XX or for treating pathologies associated with botulinum neurotoxin  
 XX poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
 XX enables rapid detection or diagnosis of botulism. This is the amino acid  
 XX sequence of mouse heavy chain anti-BONT-antibody framework region 2.  
 XX Sequence 14 AA;  
 XX Query Match 100.0%; Score 81; DB 8; Length 14;  
 XX Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX QY 1 WYRQAPGKGLIEWYA 14  
 XX 1 WYRQAPGKGLIEWYA 14  
 XX DB 1 WYRQAPGKGLIEWYA 14  
 XX RESULT 13  
 XX ADM96736  
 XX ID ADM96736 standard; peptide; 14 AA.  
 XX AC ADM96736;  
 XX DT 21-APR-2005 (first entry)  
 XX DE Anti-EGFRvIII antibody 13.1.2 VH peptide #3.  
 XX XX Monoclonal antibody; diagnosis; therapy; cancer; tumor; carcinoma;  
 XX KM glioma; neoplasm; cytostatic; epidermal growth factor receptor;

KM heavy chain variable region.  
 XX Homo sapiens.  
 XX WO2005012479-A2.  
 XX 10-FEB-2005.  
 XX 25-JUN-2004; 2004WO-US020564.  
 XX 27-JUN-2003; 2003US-0483145P.  
 XX 26-NOV-2003; 2003US-0525570P.  
 XX 15-APR-2004; 2004US-0562453P.  
 XX (ABGE-) ABGENIX INC.  
 XX Weber R, Feng X, Foord O, Green L, Gudas J, Keyt B, Liu Y;  
 XX Rathnaswami P, Raya R, Yang XD, Corvalan J, Foltz I, Jia X;  
 XX Kang J, King CT, Katakamp SL, Su QY;  
 XX WPI; 2005-142884/15.  
 XX New human monoclonal antibodies directed against type III deletion  
 XX mutants of epidermal growth factor receptor (EGFRvIII), useful for  
 XX diagnosing, preventing or treating diseases associated with EGFRvIII  
 XX expression, e.g. cancer.  
 XX Example 17, SEQ ID NO 122; 207pp; English.  
 XX The invention relates to an isolated human monoclonal antibody, or its  
 XX variant, directed against deletion mutants of epidermal growth factor  
 XX receptor, particularly to the type III deletion mutant (EGFRvIII). Also  
 XX included are a hybridoma cell line producing the above antibody, a  
 XX transformed cell comprising a gene encoding the antibody, an isolated  
 XX polynucleotide molecule comprising a nucleotide sequence encoding a heavy  
 XX or light chain amino acid sequence (or its fragment), an article of  
 XX manufacture (comprising a container, a composition contained in the  
 XX container, and a package insert or label indicating that the composition  
 XX can be used to treat cancer characterized by the expression of EGFRvIII,  
 XX where the composition comprises the antibody cited above), an assay kit  
 XX for the detection of EGFRvIII in mammalian tissues or cells (to screen  
 XX for lung, colon, gastric, renal, prostate or ovarian carcinomas, the  
 XX EGFRvIII being an antigen expressed by epithelial cancers, the kit  
 XX comprising an antibody that binds the antigen protein and means for  
 XX indicating the reaction of the antibody with the antigen, if present), a  
 XX purified protein variant of EGFRvIII, selecting variants of antibodies to  
 XX EGFRvIII, making antibody variants to EGFRvIII and killing a targeted  
 XX cell. The composition and methods are useful for diagnosing, preventing  
 XX or treating diseases associated with the expression of EGFRvIII, such as  
 XX cancer, gliomas, tumors and carcinomas. The present sequence is a peptide  
 XX derived from a VH region of an anti-EGFRvIII antibody of the invention  
 XX used to determine the antibody structure.  
 XX Sequence 14 AA;  
 XX Query Match 100.0%; Score 81; DB 9; Length 14;  
 XX Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX QY 1 WYRQAPGKGLIEWYA 14  
 XX 1 WYRQAPGKGLIEWYA 14  
 XX DB 1 WYRQAPGKGLIEWYA 14  
 XX RESULT 14  
 XX ADM96723  
 XX ID ADM96723 standard; peptide; 14 AA.  
 XX AC ADM96723;  
 XX DT 21-APR-2005 (first entry)

DE Anti-EGFRvIII antibody 131 VH peptide #3.  
XX Monoclonal antibody; diagnosis; therapy; cancer; tumor; carcinoma;  
KM glioma; neoplasm; cytostatic; epidermal growth factor receptor;  
XX heavy chain variable region.  
XX Homo sapiens.  
PN NC005012479-A2.  
XX  
XX 10-FEB-2005.  
PD  
PF 25-JUN-2004; 2004MO-US020564.  
XX  
XX 27-JUN-2003; 2003JUS-0483145P.  
PR 26-NOV-2003; 2003JUS-0525570P.  
PR 15-APR-2004; 2004US-0562453P.  
XX  
XX (ABGE-) ABGENIX INC.  
PA  
PI Weber R, Feng X, Foord O, Green L, Gudas J, Keyt B, Liu Y;  
PI Rathanaswami P, Raya R, Yang XD, Corvatan J, Foltz I, Jia X;  
PI Kang J, King CT, Klakamp SL, Su QJ;  
XX WPI; 2005-142884/15.  
DR  
XX  
XX New human monoclonal antibodies directed against type III deletion  
PT mutants of epidermal growth factor receptor (EGFRvIII), useful for  
PT diagnosing, preventing or treating diseases associated with EGFRvIII  
PT expression, e.g. cancer.  
XX  
XX  
XX Example 16; SEQ ID NO 109; 207pp; English.  
XX  
XX The invention relates to an isolated human monoclonal antibody, or its  
CC variant, directed against deletion mutants of epidermal growth factor  
CC receptor, particularly to the type III deletion mutant (EGFRvIII). Also  
CC included are a hybridoma cell line producing the above antibody, a  
CC transformed cell comprising a gene encoding the antibody, inhibiting cell  
CC proliferation associated with the expression of EGFRvIII, an isolated  
CC polynucleotide molecule comprising a nucleotide sequence encoding a heavy  
CC or light chain amino acid sequence (or its fragment), an article of  
CC manufacture (comprising a container, a composition contained in the  
CC container, and a package insert or label indicating that the composition  
CC can be used to treat cancer characterized by the expression of EGFRvIII,  
CC where the composition comprises the antibody cited above), an assay kit  
CC for the detection of EGFRvIII in mammalian tissues or cells (to screen  
CC for lung, colon, gastric, renal, prostate or ovarian carcinomas, the  
CC EGFRvIII being an antigen expressed by epithelial cancers, the kit  
CC comprising an antibody that binds the antigen protein and means for  
CC indicating the reaction of the antibody with the antigen, if present), a  
CC purified protein variant of EGFRvIII, selecting variants of antibodies to  
CC EGFRvIII, making antibody variants to EGFRvIII and killing a targeted  
CC cell. The composition and methods are useful for diagnosing, preventing  
CC or treating diseases associated with the expression of EGFRvIII, such as  
CC cancer, gliomas, tumors and carcinomas. The present sequence is a peptide  
CC derived from a VH region of an anti-EGFRvIII antibody of the invention  
CC used to determine the antibody structure.  
XX  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 81; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKGLWVA 14  
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|  
Db 1 WVRQAPGKGLWVA 14

RESULT 15  
ADM80308  
ID ADM80308 standard; peptide; 14 AA.  
XX

AC ADM80308;  
XX  
XX 21-APR-2005 (first entry)  
XX  
XX Human anti-EGFRvIII antibody 13.1.2 VH peptide - SEQ ID 122.  
DE  
XX cell death; monoclonal antibody; toxin; cytostatic; cancer; neoplasm;  
KM lung tumor; colon tumor; stomach tumor; renal tumor; prostatic cancer;  
KM breast tumor; ovary tumor; epidermal growth factor receptor; EGFRvIII;  
XX heavy chain variable region.  
XX  
XX Homo sapiens.  
OS  
XX  
XX NC005010151-A2.  
PN  
XX  
XX 03-FEB-2005.  
PD  
PF 25-JUN-2004; 2004MO-US020295.  
XX  
XX 27-JUN-2003; 2003JUS-0483145P.  
PR 26-NOV-2003; 2003JUS-0525570P.  
PR 15-APR-2004; 2004US-0562453P.  
XX  
XX (ABGE-) ABGENIX INC.  
PA  
PI Weber R, Feng X, Foord O, Green L, Gudas J, Keyt B, Liu Y;  
PI Rathanaswami P, Raya R, Yang XD, Corvatan J, Foltz I, Jia X;  
PI Kang J, King CT, Klakamp SL, Su QJ;  
XX WPI; 2005-123139/13.  
DR  
XX  
XX New isolated antibody that binds to epidermal growth factor receptor type  
PT III mutant EGFRvIII and being conjugated to therapeutic agent such as  
PT toxin, useful for inhibiting cell proliferation associated with  
PT expression of EGFRvIII.  
XX  
XX Example 18; SEQ ID NO 122; 233pp; English.  
XX  
XX The invention relates to a novel method for killing a target cell. The  
CC method comprises contacting the cell with an isolated antibody or its  
CC fragment that binds to epidermal growth factor receptor type III deletion  
CC mutant (EGFRvIII), the antibody being conjugated to a therapeutic agent,  
CC which is a toxin chosen from ABPP, MMAE, AURISTATIN B, DM-1 and ZAP, and  
CC where the antibody comprises a heavy chain amino acid sequence chosen  
CC from antibodies 13.1.2, 131, 170, 150, 085, 250. EGFR variants are caused  
CC by gene rearrangement accompanied by gene amplification. Eight major  
CC variants of EGFR are known. EGFRvIII, which is the most commonly  
CC occurring variant of EGFR in human cancers, comprises a 267 aa in-frame  
CC deletion in the extracellular domain. The method of the invention  
CC demonstrates cytostatic activity and may be useful for inhibiting cell  
CC proliferation associated with the expression of EGFRvIII or for  
CC inhibiting cell proliferation of cells expressing EGFRvIII. As such the  
CC method may be utilized, in vivo, on a mammal e.g. human, suffering from  
CC an epithelial cell cancer such as lung, colon, gastric, renal, prostate,  
CC breast, glioblastoma or ovarian carcinoma. The current sequence is that  
CC of a human anti-epidermal growth factor receptor type III variant  
CC (EGFRvIII) antibody 13.1.2 heavy chain variable region peptide of the  
CC invention.  
XX  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 81; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKGLWVA 14  
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Db 1 WVRQAPGKGLWVA 14

Search completed: November 21, 2005, 12:20:01  
Job time : 19.7436 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:36 / Search time 3.41026 Seconds  
(without alignments)  
394.995 Million cell updates/sec

Title: US-10-632-706-156  
Perfect score: 81  
Sequence: 1 WVRQAPGKLEWVA 14

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	94	2	PL0120
2	81	100.0	96	2	PH0873
3	81	100.0	97	2	S44115
4	81	100.0	97	2	PH0872
5	81	100.0	98	2	PL0116
6	81	100.0	98	2	S29543
7	81	100.0	98	2	PL0123
8	81	100.0	98	2	S29546
9	81	100.0	99	2	S20765
10	81	100.0	100	2	S26462
11	81	100.0	101	2	B42572
12	81	100.0	108	2	PH1642
13	81	100.0	109	2	PH1646
14	81	100.0	109	2	PH1644
15	81	100.0	110	2	PH1655
16	81	100.0	110	2	PH1092
17	81	100.0	110	2	PH1091
18	81	100.0	111	2	PH1643
19	81	100.0	111	2	PH1645
20	81	100.0	113	2	S57410
21	81	100.0	113	2	S57441
22	81	100.0	113	2	S38490
23	81	100.0	114	2	PH1658
24	81	100.0	114	2	PH1657
25	81	100.0	114	2	S46390
26	81	100.0	114	2	S46391
27	81	100.0	114	2	S46392
28	81	100.0	114	2	S36280
29	81	100.0	115	2	S36284

30	81	100.0	115	2	S57445	Ig heavy chain V-I
31	81	100.0	115	2	S36267	Ig heavy chain V-I
32	81	100.0	116	1	M3H0CL	Ig heavy chain V-I
33	81	100.0	117	1	G1H0WS	Ig heavy chain V-I
34	81	100.0	117	2	S17079	Ig heavy chain V-I
35	81	100.0	117	2	S36270	Ig heavy chain V-I
36	81	100.0	117	2	S78486	Ig heavy chain V-I
37	81	100.0	118	2	S31677	Ig heavy chain V-I
38	81	100.0	118	2	PH1660	Ig heavy chain V-I
39	81	100.0	118	2	PH1662	Ig heavy chain V-I
40	81	100.0	118	2	S31116	Ig heavy chain V-I
41	81	100.0	119	1	G1H0N1	Ig heavy chain V-I
42	81	100.0	119	1	M3H0UX	Ig heavy chain V-I
43	81	100.0	119	1	M3H0PM	Ig heavy chain V-I
44	81	100.0	119	2	S31111	Ig heavy chain V-I
45	81	100.0	119	2	A27630	Ig heavy chain pre

## ALIGNMENTS

## RESULT 1

PL0120  
Ig heavy chain V-III region (TD-Vo) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 31-Dec-2004  
C/Accession: PL0120  
R/Bird, J.; Galli, N.; Link, M.; Stiles, D.; Sklar, J.  
J. Exp. Med. 168, 229-245, 1988  
A/Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A/Reference number: PL0116, MUID:88286083, PMID:2840480  
A/Accession: PL0120  
A/Molecule type: mRNA  
A/Residues: 1-94 <BIR>  
A/Cross-references: UNIPROT:Q8WUK1, UNIPROT:Q9UN93, UNIPARC:UPI0000176A2C  
A/Note: Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL  
C/Suprafamily: Immunoglobulin homology  
C/Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin  
F/31-35/Region: complementarity-determining 1  
F/49-65/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 94;  
Best Local Similarity 100.0%; Pred. NO. 4.6e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 WVRQAPGKLEWVA 14  
DB 36 WVRQAPGKLEWVA 49

## RESULT 2

PH0873  
Ig heavy chain V region (anti-DNA, I-2a) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 16-Aug-1996  
C/Accession: PH0873  
J. Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.  
R. Exp. Med. 174, 1639-1652, 1991  
A/Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.  
A/Reference number: PH0862; MUID:92078875; PMID:1660528  
A/Accession: PH0873  
A/Molecule type: DNA  
A/Residues: 1-96 <MAN>  
A/Cross-references: UNIPARC:UPI0000176C02  
C/Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/14-96/Domain: immunoglobulin homology <IMM>  
F/30-35/Region: complementarity-determining 1  
F/49-66/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 96;

Best Local Similarity 100.0%; Pred. No. 4.7e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWYA 14  
|||||  
Db 35 WVRQAPGKGLWYA 48

## RESULT 3

S24115

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence\_rev1sion 13-Jan-1995 #text\_change 24-May-2001

C/Accession: S24115

R/Hawkins, R.B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

Submitted to the EMBL Data Library, March 1994

A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r

A/Reference number: S24105

A/Accession: S24115

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-97 &lt;HAM&gt;

A/Cross-references: UNIPARC:UPI000011662B; EMBL:Z31384; NID:G472969; PIDN:CAA83559.1; PI

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 81; DB 2; Length 97;

Best Local Similarity 100.0%; Pred. No. 4.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWYA 14  
|||||  
Db 36 WVRQAPGKGLWYA 49

## RESULT 4

PH0872

Ig heavy chain V region (anti-DNA, III-3R) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 09-Oct-1992 #sequence\_rev1sion 09-Oct-1992 #text\_change 09-Jul-2004

C/Accession: PH0872

R/Mahleimer-Lory, A.; Katz, J.B.; Pillingner, M.; Ghoseain, C.; Smith, A.; Diamond, B.

J. Exp. Med. 174, 1639-1652, 1991

A/Title: Molecular characterization of antibodies bearing an anti-DNA-associated idiotypic

A/Reference number: PH0862; MUID:92078875; PMID:1660528

A/Accession: PH0872

A/Molecule type: DNA

A/Residues: 1-97 &lt;MAN&gt;

A/Cross-references: UNIPROT:Q9ULB6; UNIPARC:UPI0000176C04

A/Note: a "G" was inserted at the position of between 72nd and 73rd of the DNA sequence

C/Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/14-97/Domain: immunoglobulin homology &lt;IMM&gt;

F/30-35/Region: complementarity-determining 1

F/49-66/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 97;

Best Local Similarity 100.0%; Pred. No. 4.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWYA 14  
|||||  
Db 35 WVRQAPGKGLWYA 48

## RESULT 5

Ig heavy chain V-III region (AW-Vx) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-Jun-1990 #sequence\_rev1sion 07-Jun-1990 #text\_change 23-Jul-1999

C/Accession: PL0116; S26892

R/Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A/Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin

A/Reference number: PL0116; MUID:88286083; PMID:2840480

A/Accession: PL0116

A/Molecule type: mRNA

A/Residues: 1-98 &lt;BIR&gt;

A/Cross-references: UNIPARC:UPI0000031F3A

A/Experimental source: B cells from patient AW with acute lymphoblastic leukemia, ALL

A/Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement fr

R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A/Reference number: S26885; MUID:93021117; PMID:1404388

A/Accession: S26892

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-98 &lt;TOM&gt;

A/Cross-references: UNIPARC:UPI0000031F3A; EMBL:Z12349; NID:G32918; PIDN:CAA78219.1; PID:

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology &lt;IMM&gt;

F/31-35/Region: complementarity-determining 1

F/49-65/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 4.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWYA 14  
|||||  
Db 36 WVRQAPGKGLWYA 49

## RESULT 6

S29543

Ig heavy chain V region (COS 3) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-Jan-1994 #sequence\_rev1sion 17-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S29543

R/Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.

Submitted to the EMBL Data Library, October 1992

A/Reference number: S29543

A/Accession: S29543

A/Molecule type: DNA

A/Residues: 1-98 &lt;TOM&gt;

A/Cross-references: UNIPARC:UPI000011649C; EMBL:Z17389; NID:G32835; PIDN:CAA78994.1; PID:

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 100.0%; Score 81; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 4.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWYA 14  
|||||  
Db 36 WVRQAPGKGLWYA 49

## RESULT 7

PL0123

Ig heavy chain V-III region (TD-Vr) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-Jun-1990 #sequence\_rev1sion 07-Jun-1990 #text\_change 23-Jul-1999

C/Accession: PL0123; S26897

R/Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A/Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin

A/Reference number: PL0116; MUID:88286083; PMID:2840480

A/Accession: PL0123

A/Molecule type: mRNA

A/Residues: 1-98 &lt;BIR&gt;

A/Cross-references: UNIPARC:UPI0000116413

A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL  
 A:Note: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement  
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
 J. Mol. Biol. 227, 776-798, 1992  
 A:Title: The repertoire of human germ-line V(H) sequences reveals about fifty groups of V  
 A:Reference number: S26885; MUID:93021117; PMID:1404388  
 A:Accession: S26897  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-98 <TOM>  
 A:Cross-references: UNIPARC:UPI0000116413; EMBL:Z12354; NID:G32930; PIDN:CAA78224.1; PID  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>  
 F:31-35/Region: complementarity-determining 1  
 F:49-65/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14  
 |||||  
 Db 36 WVRQAPGKGLWVA 49

## RESULT 8

S29546  
 Ig heavy chain V region (COS-8 / DP-46) - human (fragment)

C:Species: Homo sapiens (man)  
 C:Date: 07-Jan-1994 #sequence\_revision 17-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S29546; S26888  
 R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.  
 submitted to the EMBL Data Library, October 1992  
 A:Reference number: S29543  
 A:Accession: S29546  
 A:Molecule type: DNA  
 A:Residues: 1-98 <TOM>  
 A:Cross-references: UNIPARC:UPI000002DD16; EMBL:Z17394; NID:G32843; PIDN:CAA78997.1; PID  
 A:Note: designated COS-8  
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.  
 J. Mol. Biol. 227, 776-798, 1992  
 A:Title: The repertoire of human germ-line V(H) sequences reveals about fifty groups of V  
 A:Reference number: S26885; MUID:93021117; PMID:1404388  
 A:Accession: S26888  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-98 <TOM>  
 A:Cross-references: UNIPARC:UPI000002DD16; EMBL:Z12346; NID:G32912; PIDN:CAA78216.1; PID  
 A:Note: designated DP-46  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14  
 |||||  
 Db 36 WVRQAPGKGLWVA 49

## RESULT 9

S20765  
 Ig heavy chain V region - human

C:Species: Homo sapiens (man)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 C:Accession: S20765  
 R:Mortari, F.; Wang, J.; Schroeder, H.W.  
 submitted to the EMBL Data Library, April 1992  
 A:Description: Analysis of human cord blood Ig heavy chain IGA and IGC repertoire.  
 A:Reference number: S20764

A:Accession: S20765  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-99 <MOR>  
 A:Cross-references: UNIPARC:UPI0000116387; EMBL:Z11943; NID:G33858; PIDN:CAA78000.1; PID:  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 81; DB 2; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14  
 |||||  
 Db 12 WVRQAPGKGLWVA 25

## RESULT 10

S26462  
 Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Sep-1997  
 C:Accession: S26462  
 R:Kavaler, J.  
 submitted to the EMBL Data Library, April 1991  
 A:Reference number: S26459  
 A:Accession: S26462  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-100 <KAN>  
 A:Cross-references: UNIPARC:UPI000017685E; EMBL:X59104; NID:G51920; PID:G51921  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:7-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 100;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14  
 |||||  
 Db 28 WVRQAPGKGLWVA 41

## RESULT 11

B42575  
 Ig heavy chain V region (anti-angiotensin II) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
 C:Accession: B42575  
 R:Garcia, K.C.; Desiderio, S.V.; Ronco, P.M.; Verroust, P.J.; Amzel, L.M.  
 Science 257, 528-531, 1992  
 A:Title: Recognition of angiotensin II antibodies at different levels of an idiotypic re  
 A:Reference number: B42575; MUID:92342952; PMID:1636087  
 A:Accession: B42575  
 A:Molecule type: mRNA  
 A:Residues: 1-101 <GAR>  
 A:Cross-references: UNIPARC:UPI0000115389; GJ:S40679; NID:G252098; PIDN:AAB32669.1; PID:G  
 A:Experimental source: BALB/c mice, myeloma cell line NS-1  
 A:Note: sequence extracted from NCBI backbone (NCBIN:109337, NCBIR:109338)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:7-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14  
 |||||  
 Db 28 WVRQAPGKGLWVA 41



## RESULT 12

PH1642  
Ig heavy chain V region (clone 5A10) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 31-Dec-2004  
C/Accession: PH1642  
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A  
A/Reference number: PH1642; MUID:93301610; PMID:8315388  
A/Accession: PH1642  
A/Molecule type: mRNA  
A/Residues: 1-108 <HIL>  
A/Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176B78  
C/Superfamily: immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKGLWYA 14  
|||||

DB 28 WVRQAPGKGLWYA 41  
|||||

## RESULT 13

PH1646  
Ig heavy chain V region (clone 6H12) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 31-Dec-2004  
C/Accession: PH1646  
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A  
A/Reference number: PH1642; MUID:93301610; PMID:8315388  
A/Accession: PH1646  
A/Molecule type: mRNA  
A/Residues: 1-109 <HIL>  
A/Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176B7C  
C/Superfamily: immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKGLWYA 14  
|||||

DB 28 WVRQAPGKGLWYA 41  
|||||

## RESULT 14

PH1644  
Ig heavy chain V region (clone 5D11) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 31-Dec-2004  
C/Accession: PH1644  
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A  
A/Reference number: PH1642; MUID:93301610; PMID:8315388  
A/Accession: PH1644  
A/Molecule type: mRNA  
A/Residues: 1-109 <HIL>  
A/Cross-references: UNIPROT:Q9UTL93; UNIPARC:UPI0000176B7A  
C/Superfamily: immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 5.4e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKGLWYA 14  
|||||

DB 28 WVRQAPGKGLWYA 41  
|||||

## RESULT 15

PH1655  
Ig heavy chain V region (clone 2B8) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 16-Aug-1996  
C/Accession: PH1655  
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.  
J. Exp. Med. 178, 331-336, 1993  
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A  
A/Reference number: PH1642; MUID:93301610; PMID:8315388  
A/Accession: PH1655  
A/Molecule type: mRNA  
A/Residues: 1-110 <HIL>  
A/Cross-references: UNIPARC:UPI0000176BDC  
A/Experimental source: B cell  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 5.4e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKGLWYA 14  
|||||

DB 28 WVRQAPGKGLWYA 41  
|||||

Search completed: November 21, 2005, 12:22:15  
Job time : 4.41026 secs





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RESULT 2
Q9UL90 HUMAN PRELIMINARY, PRT, 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NCBIOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NCBIOTIDE SEQUENCE.
RX Rasphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RX PubMed=1730252;
DR HSSP; P01772; 2FB4.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 100.0%; Score 81; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLNWVA 14
Db 36 WVRQAPGKGLNWVA 49

RESULT 3
HV3T HUMAN STANDARD, PRT, 116 AA.
AC P01781;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region GAL.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=75059123; PubMed=4803843;
RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT "The primary structure of a monoclonal Igm-immunoglobulin
RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT type), subgroup H III. Architecture of the complete Igm-molecule.";

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RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [2]
RP SEQUENCE REVISION TO 28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
CC -1- MISCELLANEOUS: This mu chain was isolated from a Waldenström's
CC macroglobulin.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A02064; M3HUL.
DR HSSP; P01772; 2FB4.
DR SMR; P01781; 1-116.
DR GO; GO:0005576; Extracellular region; NAS.
DR GO; GO:0003823; Antigen binding; NAS.
DR GO; GO:0006955; P-immune response; NAS.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin domain;
KV Immunoglobulin V region.
FT DOMAIN 1
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12731 MW; 2C67CA9A9AAA1282 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLNWVA 14
Db 36 WVRQAPGKGLNWVA 49

RESULT 4
Q9UL93 HUMAN PRELIMINARY, PRT, 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NCBIOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NCBIOTIDE SEQUENCE.
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA Hillson J.L., Karr N.S., Opliger I.R., Mannik M., Sasso E.H.;
RT "The structural basis of germ-line-encoded VH3 immunoglobulin binding
RT to staphylococcal protein A.";
RL J. Exp. Med. 178:331-336(1993).
RN [3]
RP NCBIOTIDE SEQUENCE.
RX PubMed=2840480;
RA Bird J., Gallili N., Link M., Stites D., Sklar J.;

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RT "Continuing rearrangement but absence of somatic hypermutation in  
 RT immunoglobulin genes of human B cell precursor leukemia.";  
 RL J. Exp. Med. 168:229-245 (1988).  
 DR EMBL; AF035021; AAC56257.1; -, mRNA.  
 DR PIR; PH1644; PH1644.  
 DR PIR; P0120; P0120.  
 DR HSSP; P01772; 2FB4.  
 DR SMR; Q9UL93; 1-116.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON TER 1 116  
 FT NON TER 1 116  
 SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKLEWVA 14  
 |||||  
 DB 35 WVRQAPGKLEWVA 48

RESULT 5  
 HV30 HUMAN STANDARD; PRT; 117 AA.  
 AC P01776;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig heavy chain V-II region WAS.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=74142702; PubMed=4522793;  
 RA Capra J.D., Kehoe J.M.;  
 RT "Variable region sequences of five human immunoglobulin heavy chains  
 RT of the VH3 subgroup: definitive identification of four heavy chain  
 RT hypervariable regions."  
 RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).  
 CC -1- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma  
 CC protein.  
 CC -1- SIMILARITY: Contains 1 Ig-1like (immunoglobulin-like) domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC PIR; A02059; G1H0WS.  
 DR HSSP; P01772; 2FB4.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 112  
 FT NON TER 1 117  
 FT NON TER 1 112  
 SQ SEQUENCE 117 AA; 13091 MW; 201DEF0E1E53D9BF CRC64;

Query Match 100.0%; Score 81; DB 1; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKLEWVA 14  
 |||||  
 DB 36 WVRQAPGKLEWVA 49

RESULT 6  
 HV31 HUMAN STANDARD; PRT; 119 AA.  
 ID HV31 HUMAN  
 AC P01770;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig heavy chain V-II region NIE.  
 DE Homo sapiens (Human).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=77070269; PubMed=826475;  
 RA Ponstingl H., Hilschmann N.;  
 RT "The rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic  
 RT peptides of the H-chain, alignment of the tryptic peptides and  
 RT discussion of the complete structure."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
 RN [2]  
 RP DISULFIDE BOND.  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Drexler L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein NIE). I: purification and  
 RT characterization of the protein, the L- and H-chains, the cyanogen  
 RT bromide cleavage products, and the disulfide bridges."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 CC -1- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma  
 CC protein.  
 CC -1- SIMILARITY: Contains 1 Ig-1like (immunoglobulin-like) domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
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 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC PIR; A91668; G1H0NI.  
 DR HSSP; P01772; 2FB4.  
 DR SMR; P01770; 1-119.  
 DR GO; GO:0005576; C:extracellular region; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin domain;  
 KW Immunoglobulin V region; Pyroliodon carboxylic acid.  
 FT DOMAIN 1 112  
 FT MOD RES 1 112  
 FT DISULFID 22 96  
 FT NON TER 119 119  
 FT NON TER 119 119  
 SQ SEQUENCE 119 AA; 13243 MW; C96935A6B5B165B CRC64;

Query Match 100.0%; Score 81; DB 1; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKLEWVA 14  
 |||||  
 DB 36 WVRQAPGKLEWVA 49

```

RESULT 7
HV3M_HUMAN STANDARD; PRT; 119 AA.
ID HV3M_HUMAN
AC P01774;
DT 21-JUL-1986 (Rel. 01, Created)
RT "Structure of antibodies with shared idiotypic: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins."
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 112
FT VARIANT 54 54
FT NON TER 119 119
FT SEQUENCE 119 AA; 12954 MW; 2R018AFADCEB2610 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 119;
Best local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 WVRQAPGKGLWVA 14
36 WVRQAPGKGLWVA 49

RESULT 8
HV3M_HUMAN STANDARD; PRT; 119 AA.
ID HV3M_HUMAN
AC P01775;
DT 21-JUL-1986 (Rel. 01, Created)
RT "Structure of antibodies with shared idiotypic: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins."
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 112
FT VARIANT 54 54
FT NON TER 119 119
FT SEQUENCE 119 AA; 12954 MW; 2R018AFADCEB2610 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 119;
Best local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 WVRQAPGKGLWVA 14
36 WVRQAPGKGLWVA 49

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OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypic: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins."
DR Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
DR MISCBLANEOUS: This chain was isolated from IGM with anti-gamma globulin activity.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC
CC PIR; A02058; MJHUY.
DR HSP; P01820; 1G7J.
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 112
FT NON TER 119 119
FT SEQUENCE 119 AA; 12858 MW; D6338098794DCFE5B CRC64;

Query Match 100.0%; Score 81; DB 1; Length 119;
Best local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 WVRQAPGKGLWVA 14
36 WVRQAPGKGLWVA 49

RESULT 9
HV3J_HUMAN STANDARD; PRT; 121 AA.
ID HV3J_HUMAN
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
RT "Structure of antibodies with shared idiotypic: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins."
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 112
FT NON TER 119 119
FT SEQUENCE 119 AA; 12858 MW; D6338098794DCFE5B CRC64;

Query Match 100.0%; Score 81; DB 1; Length 119;
Best local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 WVRQAPGKGLWVA 14
36 WVRQAPGKGLWVA 49

```

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DR PIR; A02054; GIHUKL.
DR HSSP; P01772; 2PB4.
DR SMR; P01771; 2-121.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; Ig_v.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin domain;
FT Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 112
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 100.0%; Score 81; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYRQAPGKLEWVA 14
DB 36 WYRQAPGKLEWVA 49

RESULT 10
Q9UL84_HUMAN PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TREMBLrel. 13; Created)
DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01772; 2PB4.
DR EMBL; AF035030; AAD56266.1; -; mRNA.
DR SMR; Q9UL84; 1-122.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; Ig_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 122
FT NON_TER 121 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D4136545B8 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYRQAPGKLEWVA 14
DB 36 WYRQAPGKLEWVA 49

RESULT 11
HVK_HUMAN STANDARD; PRT; 126 AA.
ID HVK_HUMAN STANDARD; PRT; 126 AA.
AC P01772;

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DT 21-JUL-1986 (Rel. 01; Created)
DT 21-JUL-1986 (Rel. 01; Last sequence update)
DT 10-MAY-2005 (Rel. 47; Last annotation update)
DE Ig heavy chain V-II region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marguerat M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A02055; GIHUKL.
DR PDB; 2PB4; X-ray; H=2-126.
DR PDB; 2IG2; X-ray; H=2-126.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; Ig_v.
DR PROSITE; PS50835; IG_LIKE; 1.
KM 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KM Immunoglobulin V region; Pyrrolidone carboxylic acid.
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1
FT DISULFID 22 96
FT DISULFID 105 110
FT NON_TER 126 126
FT STRAND 3 7
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FT TURN 14 15
FT STRAND 18 25
FT STRAND 29 31
FT HELIX 34 39
FT STRAND 41 42
FT TURN 45 51
FT STRAND 53 54
FT TURN 58 60
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FT STRAND 65 65
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FT STRAND 74 77
FT TURN 78 83
FT STRAND 88 90
FT HELIX 92 99
FT STRAND 106 106
FT TURN 107 108
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FT STRAND 113 116
FT STRAND 120 124
SQ SEQUENCE 126 AA; 13718 MW; E4D7B52B16F8776 CRC64;

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Query Match 100.0%; Score 81; DB 1; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14  
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 Db 36 WVRQAPGKGLEWVA 49

## RESULT 12

HV01 RAT STANDARD; PRT; 142 AA.  
 AC P01805;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig heavy chain V region IR2 precursor.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=83064537; PubMed=6292865;  
 RA Hellman U., Petersson U., Engstrom A., Karlsson T., Bennich H.;  
 RT "Structure and evolution of the heavy chain from rat immunoglobulin  
 E.";  
 RL Nucleic Acids Res. 10:6041-6049 (1982).  
 CC -1- MISCELLANEOUS: The mRNA was isolated from an IGE-secreting  
 immunocytoma that arises spontaneously in LOU/C/Mel rats.  
 CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC -----  
 DR PIR; A02075; EVRTR2.  
 DR HSP; P01789; IMCP.  
 DR SMR; P01805; 20-141.  
 DR Ensembl; ENSNR000000031589; Rattus norvegicus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IG\_1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KM Immunoglobulin domain; Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 142 Ig heavy chain V region IR2.  
 FT DOMAIN 20 133 Ig-like.  
 FT NON TER 142 142  
 SQ SEQUENCE 142 AA; 16024 MW; D82956CFE745DF3B CRC64;

Query Match 100.0%; Score 81; DB 1; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14  
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 Db 55 WVRQAPGKGLEWVA 68

## RESULT 13

0652C9 HUMAN PRELIMINARY; PRT; 240 AA.  
 AC 0652C9;  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Single-chain Fv (Fragment).  
 GN Name=scfv;

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C1q/7;  
 RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;  
 RA Kontermann R.E., Wing M.G., Winter G.;  
 RT "Complement recruitment using bispecific diabodies.";  
 RL Nat. Biotechnol. 15:629-631 (1997).  
 DR EMBL; Y13056; CAA73499.1; -; mRNA.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00409; IG\_2.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 FT NON TER 1 1  
 FT NON TER 240 240  
 SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645FE4B373 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14  
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 Db 36 WVRQAPGKGLEWVA 49

## RESULT 14

06N093 HUMAN PRELIMINARY; PRT; 417 AA.  
 ID 06N093;  
 AC 06N093;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp666I04196 (Fragment).  
 GN Name=DKFZp666I04196;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Human esophagus tumor;  
 RG The German Human cDNA Consortium;  
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oanger A.,  
 RA Fodor G., Han W., Wiemann S.;  
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX640623; CAA5777.1; -; mRNA.  
 DR HSP; P01861; IADQ.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; C1-set; 3.  
 DR SMART; SM00409; IG\_2.  
 DR SMART; SM00407; IG1; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KM Hypothetical protein.  
 FT NON TER 1 1  
 FT NON TER 417 417  
 SQ SEQUENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64;

Query Match 100.0%; Score 81; DB 2; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKGLEWVA 14  
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DB 8 WVRQAPGKGLEWVA 21

Search completed: November 21, 2005, 12:04:10  
Job time : 21.7179 secs

## RESULT 15

06P6C4 HUMAN  
ID 06P6C4 HUMAN PRELIMINARY; PRT; 465 AA.  
AC 06P6C4  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uebin T.B., Toshitoki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Farley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC062335; AAH62335.1; -, mRNA.  
DR HSSP; P01661; IADQ.  
DR SMR; 06P6C4; 20-465.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-1like.  
DR InterPro; IPR003597; IG\_C1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-sect; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG\_C1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 465 AA; 51325 MW; FDD89348ADC37E6D CRC64;

Query Match 100.0%; Score 81; DB 2; Length 465;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKGLEWVA 14  
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DB 55 WVRQAPGKGLEWVA 68

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:31 ; Search time 5.28205 Seconds  
(without alignments)  
219.131 Million cell updates/sec

Title: US-10-632-706-156

Perfect score: 81

Sequence: 1 WVRQAPGKGLWVA 14

Scoring table: BLOSUM62

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	81	100.0	14 1 US-08-318-157B-33	Sequence 33, Appl
2	81	100.0	14 2 US-09-534-717-645	Sequence 33, Appl
3	81	100.0	89 2 US-09-534-717-646	Sequence 72, Appl
4	81	100.0	95 2 US-09-534-717-653	Sequence 653, Appl
5	81	100.0	98 1 US-08-211-202-118	Sequence 118, Appl
6	81	100.0	98 1 US-07-942-245-37	Sequence 37, Appl
7	81	100.0	98 2 US-10-194-975-15	Sequence 15, Appl
8	81	100.0	98 2 US-10-194-975-23	Sequence 23, Appl
9	81	100.0	98 2 US-10-194-975-24	Sequence 24, Appl
10	81	100.0	98 2 US-10-194-975-25	Sequence 25, Appl
11	81	100.0	98 2 US-10-194-975-26	Sequence 26, Appl
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18	81	100.0	98 2 US-09-534-717-630	Sequence 630, Appl
19	81	100.0	98 2 US-09-534-717-631	Sequence 631, Appl
20	81	100.0	98 2 US-09-534-717-632	Sequence 632, Appl
21	81	100.0	98 2 US-09-534-717-633	Sequence 633, Appl
22	81	100.0	98 2 US-09-534-717-636	Sequence 636, Appl
23	81	100.0	98 2 US-09-534-717-637	Sequence 637, Appl
24	81	100.0	98 2 US-09-534-717-640	Sequence 640, Appl
25	81	100.0	98 2 US-09-534-717-641	Sequence 641, Appl
26	81	100.0	98 2 US-09-534-717-642	Sequence 642, Appl
27	81	100.0	98 2 US-09-534-717-643	Sequence 643, Appl

#### ALIGNMENTS

28	81	100.0	98 2 US-09-534-717-644	Sequence 644, Appl
29	81	100.0	98 2 US-09-534-717-645	Sequence 645, Appl
30	81	100.0	98 2 US-09-534-717-646	Sequence 646, Appl
31	81	100.0	98 2 US-09-534-717-647	Sequence 647, Appl
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35	81	100.0	98 2 US-09-534-717-651	Sequence 651, Appl
36	81	100.0	98 2 US-09-534-717-652	Sequence 652, Appl
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42	81	100.0	98 2 US-10-330-613A-61	Sequence 61, Appl
43	81	100.0	98 2 US-10-330-613A-62	Sequence 62, Appl
44	81	100.0	100 2 US-09-840-459-35	Sequence 35, Appl
45	81	100.0	100 2 US-09-497-625A-35	Sequence 35, Appl

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RESULT 1
US-08-318-157B-33
; Sequence 33, Application US/08318157B
; Patent No. 5874540
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: AMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,157B
; FILING DATE: 05-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-318-157B-33

Query Match 100.0%; Score 81; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVRQAPGKGLWVA 14
DB 1 WVRQAPGKGLWVA 14
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RESULT 2
US-09-253-794-33
; Sequence 33, Application US/09253794
; Patent No. 6676924
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CER HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-253-794-33

Query Match 100.0%; Score 81; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2,9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
DB 1 WVRQAPGKGLWVA 14

RESULT 3
US-09-472-087-72
; Sequence 72, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSEN, DOUGLAS C.
; APPLICANT: NEYEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALLAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PPI
; CURRENT APPLICATION NUMBER: US/09/472,087
```

```
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 72
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-72

Query Match 100.0%; Score 81; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2,2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
DB 27 WVRQAPGKGLWVA 40

RESULT 4
US-09-534-717-653
; Sequence 653, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 653
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-653

Query Match 100.0%; Score 81; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 2,4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
DB 36 WVRQAPGKGLWVA 49

RESULT 5
US-08-211-202-118
; Sequence 118, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Reneus Jacobus Matheus
; APPLICANT: BAIER, Michael
; APPLICANT: JESPEERS, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/211,202  
FILING DATE: 23-SEP-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9120252.3  
FILING DATE: 23-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9120377.8  
FILING DATE: 25-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206372.6  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/00883  
FILING DATE: 15-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/31960  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-211-202-118

Query Match 100.0%; Score 81; DB 1; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 WVRQAPGKGLWVA 14  
|||||  
Db 36 WVRQAPGKGLWVA 49

## RESULT 6

US-07-942-245-37  
Sequence 37, Application US/07942245  
Patent No. 5639641

GENERAL INFORMATION:  
APPLICANT: PEDERSEN, Jan T.  
APPLICANT: SEARLE, Stephen M.J.  
APPLICANT: REES, Anthony R.  
APPLICANT: ROGUSKA, Michael A.  
APPLICANT: GUILD, Braydon C.  
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT  
NUMBER OF SEQUENCES: 522  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sughrie, Mion, Zinn, Macpeak & Seas  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: HP 9000/700 workstation  
OPERATING SYSTEM: UNIX  
SOFTWARE: In house  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/942,245  
FILING DATE: 09-SEP-1992

CLASSIFICATION: 530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-942-245-37

Query Match 100.0%; Score 81; DB 1; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 WVRQAPGKGLWVA 14  
|||||  
Db 36 WVRQAPGKGLWVA 49

## RESULT 7

US-10-194-975-15  
Sequence 15, Application US/10194975  
Patent No. 6881557

GENERAL INFORMATION:  
APPLICANT: Foote, Jefferson  
TITLE OF INVENTION: Super Humanized Antibodies  
FILE REFERENCE: 501231.01  
CURRENT FILING DATE: 2002-10-10/194,975  
PRIOR APPLICATION NUMBER: US/10/194,975  
PRIOR FILING DATE: 2001-07-12  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 15  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-194-975-15

Query Match 100.0%; Score 81; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 WVRQAPGKGLWVA 14  
|||||  
Db 36 WVRQAPGKGLWVA 49

RESULT 8  
US-10-194-975-23  
Sequence 23, Application US/10194975  
Patent No. 6881557

GENERAL INFORMATION:  
APPLICANT: Foote, Jefferson  
TITLE OF INVENTION: Super Humanized Antibodies  
FILE REFERENCE: 501231.01  
CURRENT FILING DATE: 2002-10-10/194,975  
PRIOR APPLICATION NUMBER: US/10/194,975  
PRIOR FILING DATE: 2001-07-12  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 23  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-194-975-23

Query Match 100.0%; Score 81; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVRQAPGKGLWVA 14
| | | | | | | | | | | | | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 9
US-10-194-975-24
; Sequence 24, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Focce, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-24

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | | | | | | | | | | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 10
US-10-194-975-25
; Sequence 25, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Focce, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-25

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | | | | | | | | | | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 11
US-10-194-975-26
; Sequence 26, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Focce, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | | | | | | | | | | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 12
US-09-534-717-624
; Sequence 624, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 624
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-624

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | | | | | | | | | | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 13
US-09-534-717-625
; Sequence 625, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 625
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-625

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 WVRQAPGKGLEWVA 14  
 |||||  
 Db 36 WVRQAPGKGLEWVA 49

## RESULT 14

US-09-534-717-626  
 ; Sequence 626, Application US/09534717  
 ; Patent No. 6914128  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jochen, Salfeid et al.  
 ; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing  
 ; FILE REFERENCE: BBI-093CP  
 ; CURRENT APPLICATION NUMBER: US/09/534,717  
 ; CURRENT FILING DATE: 2000-03-24  
 ; EARLIER APPLICATION NUMBER: 60/126,603  
 ; EARLIER FILING DATE: March 25, 1999  
 ; NUMBER OF SEQ ID NOS: 675  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 626  
 ; LENGTH: 98  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-534-717-626

Query Match 100.0%; Score 81; DB 2; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLEWVA 14  
 |||||  
 Db 36 WVRQAPGKGLEWVA 49

## RESULT 15

US-09-534-717-627  
 ; Sequence 627, Application US/09534717  
 ; Patent No. 6914128  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jochen, Salfeid et al.  
 ; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing  
 ; FILE REFERENCE: BBI-093CP  
 ; CURRENT APPLICATION NUMBER: US/09/534,717  
 ; CURRENT FILING DATE: 2000-03-24  
 ; EARLIER APPLICATION NUMBER: 60/126,603  
 ; EARLIER FILING DATE: March 25, 1999  
 ; NUMBER OF SEQ ID NOS: 675  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 627  
 ; LENGTH: 98  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-534-717-627

Query Match 100.0%; Score 81; DB 2; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLEWVA 14  
 |||||  
 Db 36 WVRQAPGKGLEWVA 49

Search completed: November 21, 2005, 12:07:38  
 Job time : 5.28205 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:50:51 ; Search time 17.3333 Seconds  
(without alignments)  
337.478 Million cell updates/sec

Title: US-10-632-706-156  
Perfect score: 81  
Sequence: 1 WVRQAPKGLMWVA 14

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA\_Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	14	3	US-09-253-794-33 Sequence 33, App1
2	81	100.0	14	3	US-09-828-708-64 Sequence 64, App1
3	81	100.0	14	4	US-10-632-706-140 Sequence 140, App
4	81	100.0	14	4	US-10-632-706-144 Sequence 144, App
5	81	100.0	14	4	US-10-632-706-148 Sequence 148, App
6	81	100.0	14	4	US-10-632-706-152 Sequence 152, App
7	81	100.0	14	4	US-10-632-706-156 Sequence 156, App
8	81	100.0	14	4	US-10-632-706-160 Sequence 160, App
9	81	100.0	14	4	US-10-632-706-164 Sequence 164, App
10	81	100.0	14	4	US-10-632-706-168 Sequence 168, App
11	81	100.0	14	5	US-10-788-625-6 Sequence 6, App11
12	81	100.0	14	5	US-10-489-328-2 Sequence 2, App11
13	81	100.0	14	5	US-10-923-068-202 Sequence 202, App
14	81	100.0	14	5	US-10-923-068-205 Sequence 205, App
15	81	100.0	14	5	US-10-923-068-232 Sequence 232, App
16	81	100.0	14	5	US-10-877-773-109 Sequence 109, App
17	81	100.0	14	5	US-10-877-773-122 Sequence 122, App
18	81	100.0	14	5	US-10-877-774-109 Sequence 109, App
19	81	100.0	14	5	US-10-877-774-122 Sequence 122, App
20	81	100.0	14	5	US-10-630-009-64 Sequence 64, App1
21	81	100.0	14	5	US-10-755-382-33 Sequence 33, App1
22	81	100.0	14	5	US-10-984-960A-41 Sequence 41, App1
23	81	100.0	14	5	US-10-923-068-334 Sequence 334, App
24	81	100.0	17	5	US-10-923-068-337 Sequence 337, App
25	81	100.0	17	5	US-10-923-068-364 Sequence 364, App
26	81	100.0	44	5	US-10-842-011-39 Sequence 39, App1
27	81	100.0	82	4	US-10-230-880-118 Sequence 118, App

28	81	100.0	82	4	US-10-230-880-119 Sequence 119, App
29	81	100.0	82	4	US-10-230-880-120 Sequence 120, App
30	81	100.0	82	4	US-10-230-880-121 Sequence 121, App
31	81	100.0	82	4	US-10-230-880-122 Sequence 122, App
32	81	100.0	82	4	US-10-230-880-123 Sequence 123, App
33	81	100.0	87	5	US-10-788-625-90 Sequence 90, App1
34	81	100.0	87	5	US-10-842-011-45 Sequence 45, App1
35	81	100.0	89	5	US-10-612-497-72 Sequence 72, App1
36	81	100.0	89	5	US-10-776-649-72 Sequence 72, App1
37	81	100.0	93	3	US-09-910-483-39 Sequence 39, App1
38	81	100.0	93	3	US-09-910-483-45 Sequence 45, App1
39	81	100.0	95	4	US-10-363-204-89 Sequence 89, App1
40	81	100.0	95	4	US-10-363-204-91 Sequence 91, App1
41	81	100.0	95	5	US-10-884-830-653 Sequence 653, App
42	81	100.0	98	3	US-09-948-939-15 Sequence 15, App1
43	81	100.0	98	3	US-09-948-939-21 Sequence 21, App1
44	81	100.0	98	4	US-10-194-975-15 Sequence 15, App1
45	81	100.0	98	4	US-10-194-975-23 Sequence 23, App1

#### ALIGNMENTS

```
RESULT 1
US-09-253-794-33
Sequence 33, Application US/09253794
Patent No. US20020018750A1
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
ARMOUR, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,794
FILING DATE: 22-Feb-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,157
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-253-794-33
Query Match 100.0%; Score 81; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 WVRQAPGKGLEWVA 14  
Db 1 WVRQAPGKGLEWVA 14

## RESULT 2

US-09-828-708-64  
Sequence 64, Application US/09828708  
Patent No. US20020146753A1  
GENERAL INFORMATION:  
APPLICANT: Ditzel, H.  
APPLICANT: Burton, D.  
APPLICANT: Schaller, M.  
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl  
TITLE OF INVENTION: Autoimmune disease  
FILE REFERENCE: 1361.005US1  
CURRENT APPLICATION NUMBER: US/09/828,708  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 64  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-828-708-64

Query Match 100.0%; Score 81; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLEWVA 14  
Db 1 WVRQAPGKGLEWVA 14

## RESULT 3

US-10-632-706-140  
Sequence 140, Application US/10632706  
Publication No. US20040175385A1  
GENERAL INFORMATION:  
APPLICANT: MARKS, JAMES D.  
APPLICANT: AMERSDORFER, PETER  
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
TITLE OF INVENTION: NEUROTOXINS  
FILE REFERENCE: 407T-895120US  
CURRENT APPLICATION NUMBER: US/10/632,706  
CURRENT FILING DATE: 2003-08-01  
PRIOR APPLICATION NUMBER: US 60/400,721  
PRIOR FILING DATE: 2002-08-01  
PRIOR APPLICATION NUMBER: US 09/144,806  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 278  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 140  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-140

Query Match 100.0%; Score 81; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLEWVA 14  
Db 1 WVRQAPGKGLEWVA 14

RESULT 4  
US-10-632-706-144

Sequence 144, Application US/10632706  
Publication No. US20040175385A1  
GENERAL INFORMATION:  
APPLICANT: MARKS, JAMES D.  
APPLICANT: AMERSDORFER, PETER  
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
TITLE OF INVENTION: NEUROTOXINS  
FILE REFERENCE: 407T-895120US  
CURRENT APPLICATION NUMBER: US/10/632,706  
CURRENT FILING DATE: 2003-08-01  
PRIOR APPLICATION NUMBER: US 60/400,721  
PRIOR FILING DATE: 2002-08-01  
PRIOR APPLICATION NUMBER: US 09/144,806  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 278  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 144  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-144

Query Match 100.0%; Score 81; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLEWVA 14  
Db 1 WVRQAPGKGLEWVA 14

## RESULT 5

US-10-632-706-148  
Sequence 148, Application US/10632706  
Publication No. US20040175385A1  
GENERAL INFORMATION:  
APPLICANT: MARKS, JAMES D.  
APPLICANT: AMERSDORFER, PETER  
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
TITLE OF INVENTION: NEUROTOXINS  
FILE REFERENCE: 407T-895120US  
CURRENT APPLICATION NUMBER: US/10/632,706  
CURRENT FILING DATE: 2003-08-01  
PRIOR APPLICATION NUMBER: US 60/400,721  
PRIOR FILING DATE: 2002-08-01  
PRIOR APPLICATION NUMBER: US 09/144,806  
PRIOR FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 278  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 148  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-148

Query Match 100.0%; Score 81; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLEWVA 14  
Db 1 WVRQAPGKGLEWVA 14

RESULT 6  
US-10-632-706-152  
Sequence 152, Application US/10632706  
Publication No. US20040175385A1  
GENERAL INFORMATION:



```
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
TITLE OF INVENTION: NEUROTOXINS
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 152
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-152
```

```
Query Match          100.0%; Score 81; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 WVRQAPGKGLFWVA 14
        |||||
Db      1 WVRQAPGKGLFWVA 14
```

```
RESULT 7
US-10-632-706-156
; Sequence 156, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 156
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-156
```

```
Query Match          100.0%; Score 81; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 WVRQAPGKGLFWVA 14
        |||||
Db      1 WVRQAPGKGLFWVA 14
```

```
RESULT 8
US-10-632-706-160
; Sequence 160, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
```

```
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 160
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-160
```

```
Query Match          100.0%; Score 81; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 WVRQAPGKGLFWVA 14
        |||||
Db      1 WVRQAPGKGLFWVA 14
```

```
RESULT 9
US-10-632-706-164
; Sequence 164, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 164
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-164
```

```
Query Match          100.0%; Score 81; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 WVRQAPGKGLFWVA 14
        |||||
Db      1 WVRQAPGKGLFWVA 14
```

```
RESULT 10
US-10-632-706-168
; Sequence 168, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
```

```

CURRENT FILING DATE: 2003-08-01
PRIORITY APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 168
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-168

Query Match          100.0%; Score 81; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 WYROAPGKGLEWVA 14
|||||
Db 1 WYROAPGKGLEWVA 14

RESULT 11
US-10-788-625-6
Sequence 6, Application US/10788625
Publication No. US20040260068A1
GENERAL INFORMATION:
APPLICANT: Teunushita, Naoya
APPLICANT: Kumar, Shankar
APPLICANT: Vasquez, Maximiliano
TITLE OF INVENTION: Humanized Chicken Antibodies
FILE REFERENCE: 05882.0044.NPUS02
CURRENT APPLICATION NUMBER: US/10/788,625
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-788-625-6

Query Match          100.0%; Score 81; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 WYROAPGKGLEWVA 14
|||||
Db 1 WYROAPGKGLEWVA 14

RESULT 12
US-10-489-328-2
Sequence 2, Application US/10489328
Publication No. US20050037420A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer -Gesellschaft zur Forderung der angewandten
APPLICANT: Forschung e.V.
APPLICANT: ZHANG, Mei Yun
APPLICANT: SCHILLBERG, Stefan
APPLICANT: ZIMMERMANN, Sabine
APPLICANT: DI FIORE, Stefano
APPLICANT: EMANS, Neil
APPLICANT: FISCHER, Rainer
TITLE OF INVENTION: Immunoglobulin having Particular Framework Scaffold and Methods
FILE REFERENCE: FRAU-202.1US
CURRENT APPLICATION NUMBER: US/10/489,328
CURRENT FILING DATE: 2004-03-11
PRIORITY APPLICATION NUMBER: PCT/US02/29003
PRIOR FILING DATE: 2002-09-13

```

```

; PRIOR APPLICATION NUMBER: 60/318,904
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This is a heavy chain framework region 2 (HFR2)
US-10-489-328-2

Query Match                100.0%; Score 81; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. NO. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1  WVRQAPGKGLEWVA 14
      |||||
      1  WVRQAPGKGLEWVA 14

Db
      1  WVRQAPGKGLEWVA 14

RESULT 13
US-10-923-068-202
; Sequence 202, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Aquila, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AB600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-202

Query Match                100.0%; Score 81; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. NO. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1  WVRQAPGKGLEWVA 14
      |||||
      1  WVRQAPGKGLEWVA 14

Db
      1  WVRQAPGKGLEWVA 14

RESULT 14
US-10-923-068-205
; Sequence 205, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Aquila, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AB600US
; CURRENT APPLICATION NUMBER: US/10/923,068
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-923-068-205

Query Match                100.0%; Score 81; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. NO. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1  WVRQAPGKGLEWVA 14
      |||||
      1  WVRQAPGKGLEWVA 14

Db
      1  WVRQAPGKGLEWVA 14

Query Match                100.0%; Score 81; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. NO. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1  WVRQAPGKGLEWVA 14
      |||||
      1  WVRQAPGKGLEWVA 14

Db
      1  WVRQAPGKGLEWVA 14

```

OY 1 WVRQAPGKLEWVA 14  
 |||||  
 DB 1 WVRQAPGKLEWVA 14

RESULT 15  
 US-10-923-068-232  
 ; Sequence 232, Application US/10923068  
 ; Publication No. US20050042664A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wu, Heren  
 ; APPLICANT: Dai, Acqua, William  
 ; APPLICANT: Damschroder, Melissa  
 ; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES  
 ; FILE REFERENCE: A66005  
 ; CURRENT APPLICATION NUMBER: US/10/923,068  
 ; CURRENT FILING DATE: 2004-08-20  
 ; NUMBER OF SEQ ID NOS: 518  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 232  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-923-068-232

Query Match 100.0%; Score 81; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 WVRQAPGKLEWVA 14  
 |||||  
 DB 1 WVRQAPGKLEWVA 14

Search completed: November 21, 2005, 12:33:36  
 Job time : 17.3333 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 21, 2005, 12:04:27 ; Search time 0.25641 Seconds  
(without alignments)  
61.686 Million cell updates/sec

Title: US-10-632-706-156  
Perfect score: 81  
Sequence: 1 WVRQAPGKLEWVA 14

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	120	7	US-11-077-978-7
2	81	100.0	121	7	US-11-077-978-2
3	81	100.0	121	7	US-11-077-978-3
4	81	100.0	138	1	US-10-789-273-8
5	81	100.0	138	1	US-10-789-273-12
6	81	100.0	250	1	US-10-512-184-27
7	81	100.0	261	1	US-10-512-184-35
8	81	100.0	313	1	US-10-512-184-72
9	79	97.5	252	1	US-10-512-184-28
10	78	96.3	98	1	US-10-789-273-10
11	78	96.3	98	1	US-11-144-248-32
12	78	96.3	121	1	US-10-789-273-9
13	78	96.3	122	7	US-11-144-248-24
14	78	96.3	124	7	US-11-144-248-8
15	78	96.3	125	7	US-11-144-248-16
16	78	96.3	139	1	US-10-721-763-33
17	78	96.3	444	7	US-11-172-320-6
18	78	96.3	470	7	US-11-144-248-45
19	78	96.3	470	7	US-11-144-248-46
20	77	95.1	98	7	US-11-144-248-30
21	77	95.1	102	1	US-10-997-201A-6
22	77	95.1	118	1	US-10-648-816-9
23	77	95.1	118	1	US-10-648-816-10
24	77	95.1	118	1	US-10-648-816-11
25	77	95.1	118	1	US-10-648-816-12

26	77	95.1	118	1	US-10-648-816-13	Sequence 13, Appl
27	77	95.1	118	1	US-10-648-816-14	Sequence 14, Appl
28	77	95.1	121	1	US-10-648-816-15	Sequence 15, Appl
29	77	95.1	121	1	US-10-648-816-16	Sequence 16, Appl
30	77	95.1	174	7	US-11-144-248-4	Sequence 4, Appl
31	77	95.1	470	7	US-11-144-248-49	Sequence 49, Appl
32	77	95.1	473	7	US-11-144-248-50	Sequence 50, Appl
33	77	95.1	116	7	US-11-174-186-17	Sequence 17, Appl
34	77	91.4	116	7	US-11-144-248-34	Sequence 34, Appl
35	71	87.7	98	7	US-10-726-554-8	Sequence 8, Appl
36	71	87.7	119	1	US-10-502-145-25	Sequence 25, Appl
37	71	87.7	154	1	US-10-721-763-25	Sequence 25, Appl
38	71	87.7	258	1	US-10-512-184-26	Sequence 26, Appl
39	71	87.7	327	1	US-10-512-184-62	Sequence 62, Appl
40	71	87.7	327	1	US-10-512-184-64	Sequence 64, Appl
41	71	87.7	328	1	US-10-512-184-63	Sequence 63, Appl
42	71	87.7	576	1	US-10-512-184-65	Sequence 65, Appl
43	71	87.7	625	1	US-10-512-184-47	Sequence 47, Appl
44	70	86.4	14	1	US-10-839-799-127	Sequence 127, App
45	70	86.4	76	1	US-10-839-799-113	Sequence 113, App

## ALIGNMENTS

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RESULT 1
US-11-077-978-7
; Sequence 7, Application US/11077978
; Publication No. US20050244333A1
; GENERAL INFORMATION:
; APPLICANT: Yazaki, Paul J.
; APPLICANT: Sherman, Mark A.
; APPLICANT: Shively, John E.
; APPLICANT: Raubitschek, Andrew A.
; APPLICANT: Wu, Anna M.
; TITLE OF INVENTION: A Humanized Anti-CEA T84.66 Antibody and Uses Thereof
; FILE REFERENCE: 54435.8012.US01
; CURRENT APPLICATION NUMBER: US/11/077,978
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Variable heavy chain of humanized anti-p185HER2 antibody 4D5,
; US-11-077-978-7
;
Query Match          100.0%; Score 81; DB 7; Length 120;
Best Local Similarity 100.0%; Pred. NO. 1.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WVRQAPGKLEWVA 14
Db      36 WVRQAPGKLEWVA 49

RESULT 2
US-11-077-978-2
; Sequence 2, Application US/11077978
; Publication No. US20050244333A1
; GENERAL INFORMATION:
; APPLICANT: Yazaki, Paul J.
; APPLICANT: Sherman, Mark A.
; APPLICANT: Shively, John E.
; APPLICANT: Raubitschek, Andrew A.
; APPLICANT: Wu, Anna M.
; TITLE OF INVENTION: A Humanized Anti-CEA T84.66 Antibody and Uses Thereof
; FILE REFERENCE: 54435.8012.US01
; CURRENT APPLICATION NUMBER: US/11/077,978
; CURRENT FILING DATE: 2005-03-11
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/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 121
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Artificially constructed variable heavy chain of M5A humanized
US-11-077-978-2
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Query Match          100.0%; Score 81; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WVRQAPGKGLEWVA 14
         |||
Db       36 WVRQAPGKGLEWVA 49
```

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RESULT 3
US-11-077-978-3
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/ Sequence 3, Application US/11077978
/ Publication No. US2005024433A1
/ GENERAL INFORMATION:
/ APPLICANT: Yazaki, Paul J.
/ APPLICANT: Sherman, Mark A.
/ APPLICANT: Shively, John R.
/ APPLICANT: Raubitschek, Andrew A.
/ APPLICANT: Wu, Anna M.
/ TITLE OF INVENTION: A Humanized Anti-CEA T84.66 Antibody and Uses Thereof
/ FILE REFERENCE: 54435.8012.US01
/ CURRENT APPLICATION NUMBER: US/11/077,978
/ CURRENT FILING DATE: 2005-03-11
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3
/ LENGTH: 121
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Artificially constructed variable heavy chain of M5B humanized
US-11-077-978-3
```

```
Query Match          100.0%; Score 81; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WVRQAPGKGLEWVA 14
         |||
Db       36 WVRQAPGKGLEWVA 49
```

```
RESULT 4
US-10-789-273-8
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/ Sequence 8, Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Baei, Gurig
/ APPLICANT: Saldanha, Jose
/ APPLICANT: Yednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
/ TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
/ FILE REFERENCE: ELN-002CP
/ CURRENT APPLICATION NUMBER: US/10/789,273
/ CURRENT FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: US/10/388,389
/ PRIOR FILING DATE: 2003-03-12
/ PRIOR APPLICATION NUMBER: US 10/010,942
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US 60/251,892
/ PRIOR FILING DATE: 2000-12-06
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/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 138
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanized 3D6 heavy chain variable region
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(19)
US-10-789-273-8
```

```
Query Match          100.0%; Score 81; DB 1; Length 138;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WVRQAPGKGLEWVA 14
         |||
Db       55 WVRQAPGKGLEWVA 68
```

```
RESULT 5
US-10-789-273-12
```

```
/ Sequence 12, Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Baei, Gurig
/ APPLICANT: Saldanha, Jose
/ APPLICANT: Yednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
/ TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
/ FILE REFERENCE: ELN-002CP
/ CURRENT APPLICATION NUMBER: US/10/789,273
/ CURRENT FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: US/10/388,389
/ PRIOR FILING DATE: 2003-03-12
/ PRIOR APPLICATION NUMBER: US 10/010,942
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US 60/251,892
/ PRIOR FILING DATE: 2000-12-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 138
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanized 3D6 light chain variable region
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(19)
US-10-789-273-12
```

```
Query Match          100.0%; Score 81; DB 1; Length 138;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WVRQAPGKGLEWVA 14
         |||
Db       55 WVRQAPGKGLEWVA 68
```

```
RESULT 6
US-10-512-184-27
```

```
/ Sequence 27, Application US/10512184
/ Publication No. US20050244901A1
/ GENERAL INFORMATION:
/ APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
/ TITLE OF INVENTION: Antibodies, recombinant antibodies, fragments and fusions mediated plant disease
/ TITLE OF INVENTION: resistance against fungi
/ FILE REFERENCE: 3581.01US01
```

```
;; CURRENT APPLICATION NUMBER: US/10/512,184
;; CURRENT FILING DATE: 2004-10-22
;; NUMBER OF SEQ ID NOS: 72
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 27
;; LENGTH: 250
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: scFv SGB3 with
;; OTHER INFORMATION: specificity against Fusarium ssp.; originates from
;; OTHER INFORMATION: Gallus gallus.
US-10-512-184-27

Query Match          100.0%; Score 81; DB 1; Length 250;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 WVRQAPGKGLWVA 14
        |||||
        38 WVRQAPGKGLWVA 51

RESULT 7
US-10-512-184-35
; Sequence 35, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv P1P9 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-35

Query Match          100.0%; Score 81; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 WVRQAPGKGLWVA 14
        |||||
        38 WVRQAPGKGLWVA 51

RESULT 8
US-10-512-184-72
; Sequence 72, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 313
; TYPE: PRT
```

```
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: precursor
;; OTHER INFORMATION: fusion protein comprising MBP - linker -
;; OTHER INFORMATION: scFv P1P9.
US-10-512-184-72

Query Match          100.0%; Score 81; DB 1; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 WVRQAPGKGLWVA 14
        |||||
        90 WVRQAPGKGLWVA 103

RESULT 9
US-10-512-184-28
; Sequence 28, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv FPQWPA5
; OTHER INFORMATION: with specificity against Fusarium ssp.; originates
; OTHER INFORMATION: from Gallus gallus.
US-10-512-184-28

Query Match          97.5%; Score 79; DB 1; Length 252;
Best Local Similarity 92.9%; Pred. No. 4.4e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy      1 WVRQAPGKGLWVA 14
        |||||
        38 WVRQAPGKGLWVA 51

RESULT 10
US-10-789-273-10
; Sequence 10, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basl, Gurid
; APPLICANT: Saldana, Jose
; APPLICANT: Vedhock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 98
; TYPE: PRT
```

ORGANISM: Homo sapiens  
US-10-789-273-10

Query Match 96.3%; Score 78; DB 1; Length 98;  
Best Local Similarity 92.9%; Pred. No. 2.8e-06;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14  
| | | | | | | | | | | | | | | | | |  
Db 36 WVRQAPGKGLWVS 49

RESULT 11

US-11-144-248-32  
Sequence 32, Application US/11144248  
Publication No. US20050244408A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce D.  
APPLICANT: Beebe, Jean  
APPLICANT: Miller, Penelope E.  
APPLICANT: Moyer, James D.  
APPLICANT: Cortalan, Jose R.  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
FILE REFERENCE: ABX-PF2  
CURRENT APPLICATION NUMBER: US/11/144,248  
CURRENT FILING DATE: 2005-06-02  
PRIOR APPLICATION NUMBER: US/10/038,591  
PRIOR FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: 60/259,927  
PRIOR FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 32  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-144-248-32

Query Match 96.3%; Score 78; DB 7; Length 98;  
Best Local Similarity 92.9%; Pred. No. 2.8e-06;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14  
| | | | | | | | | | | | | | | | | |  
Db 36 WVRQAPGKGLWVS 49

RESULT 12

US-10-789-273-9  
Sequence 9, Application US/10789273  
Publication No. US20050249725A1  
GENERAL INFORMATION:  
APPLICANT: Basi, Gurjit  
APPLICANT: Saldanha, Jose  
APPLICANT: Yednock, Ted  
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
FILE REFERENCE: EAM-002CP  
CURRENT APPLICATION NUMBER: US/10/789,273  
CURRENT FILING DATE: 2004-02-27  
PRIOR APPLICATION NUMBER: US/10/388,389  
PRIOR FILING DATE: 2003-03-12  
PRIOR APPLICATION NUMBER: US/10/010,942  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: US 60/251,892  
PRIOR FILING DATE: 2000-12-06  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Homo sapiens

US-10-789-273-9

Query Match 96.3%; Score 78; DB 1; Length 121;  
Best Local Similarity 92.9%; Pred. No. 3.4e-06;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14  
| | | | | | | | | | | | | | | | | |  
Db 36 WVRQAPGKGLWVS 49

RESULT 13

US-11-144-248-24  
Sequence 24, Application US/11144248  
Publication No. US20050244408A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce D.  
APPLICANT: Beebe, Jean  
APPLICANT: Miller, Penelope E.  
APPLICANT: Moyer, James D.  
APPLICANT: Cortalan, Jose R.  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
FILE REFERENCE: ABX-PF2  
CURRENT APPLICATION NUMBER: US/11/144,248  
CURRENT FILING DATE: 2005-06-02  
PRIOR APPLICATION NUMBER: US/10/038,591  
PRIOR FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: 60/259,927  
PRIOR FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 24  
LENGTH: 122  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-144-248-24

Query Match 96.3%; Score 78; DB 7; Length 122;  
Best Local Similarity 92.9%; Pred. No. 3.4e-06;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14  
| | | | | | | | | | | | | | | | | |  
Db 36 WVRQAPGKGLWVS 49

RESULT 14

US-11-144-248-8  
Sequence 8, Application US/11144248  
Publication No. US20050244408A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce D.  
APPLICANT: Beebe, Jean  
APPLICANT: Miller, Penelope E.  
APPLICANT: Moyer, James D.  
APPLICANT: Cortalan, Jose R.  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
FILE REFERENCE: ABX-PF2  
CURRENT APPLICATION NUMBER: US/11/144,248  
CURRENT FILING DATE: 2005-06-02  
PRIOR APPLICATION NUMBER: US/10/038,591  
PRIOR FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: 60/259,927  
PRIOR FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 124  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-144-248-8



Query Match 96.3%; Score 78; DB 7; Length 124;  
 Best Local Similarity 92.9%; Pred. No. 3.4e-06;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLEWVA 14  
 |||||  
 Db 35 WVRQAPGKGLEWVS 48

## RESULT 15

US-11-144-248-16  
 ; Sequence 16, Application US/11144248  
 ; Publication No. US20050244408A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cohen, Bruce D.  
 ; APPLICANT: Beebe, Jean  
 ; APPLICANT: Miller, Penelope B.  
 ; APPLICANT: Moyer, James D.  
 ; APPLICANT: Corvalan, Jose R.  
 ; APPLICANT: Gallo, Michael  
 ; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
 ; FILE REFERENCE: ABX-PP2  
 ; CURRENT APPLICATION NUMBER: US/11/144,248  
 ; CURRENT FILING DATE: 2005-06-02  
 ; PRIOR APPLICATION NUMBER: US/10/038,591  
 ; PRIOR FILING DATE: 2002-01-04  
 ; PRIOR APPLICATION NUMBER: 60/259,927  
 ; PRIOR FILING DATE: 2001-01-05  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 16  
 ; LENGTH: 125  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-11-144-248-16

Query Match 96.3%; Score 78; DB 7; Length 125;  
 Best Local Similarity 92.9%; Pred. No. 3.5e-06;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLEWVA 14  
 |||||  
 Db 36 WVRQAPGKGLEWVS 49

Search completed: November 21, 2005, 12:33:51  
 Job time : 0.35641 secs

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CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I); and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (II) exhibits specificity and affinity towards BONT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain anti-BONT-antibody CDR2.  
XX  
SQ Sequence 17 AA;  
XX  
Query Match 100.0%; Score 93; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TISDGGSYTYPPDSVKG 17  
Db 1 TISDGGSYTYPPDSVKG 17  
XX  
RESULT 2  
ADR38743  
ID ADR38743 standard; peptide; 17 AA.  
XX  
AC ADR38743;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Mouse heavy chain anti-BONT-antibody CD2 seqid 145.  
XX  
XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
KM CDR2; complementarity determining region 2.  
XX  
OS Mus sp.  
XX  
PN US2004175385-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 01-AUG-2003; 2003US-00632706.  
XX  
PR 31-AUG-1998; 98US-00144886.  
PR 01-AUG-2002; 2002US-0400721P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Marke JD, Amerdorfer P;  
XX  
DR WPI; 2004-652009/63.  
XX  
PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
XX  
XX Example 4; SEQ ID NO 145; 110pp; English.  
XX  
CC The invention describes an isolated antibody (I) that specifically binds  
CC to an epitope specifically bound by an antibody expressed by a specific  
CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone  
CC 855, C25, C39, 1C6, 3D12, B4, 1F3, huc25, A1, A12, WRI(V), WRI(T), 3-1,  
CC 3-8, 3-10 and INGI, where (I) binds to and neutralises botulinum

CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
CC comprising BONT/A neutralising epitope having an epitope that is  
CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I); and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (II) exhibits specificity and affinity towards BONT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain anti-BONT-antibody CDR2.  
XX  
SQ Sequence 17 AA;  
XX  
Query Match 100.0%; Score 93; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TISDGGSYTYPPDSVKG 17  
Db 1 TISDGGSYTYPPDSVKG 17  
XX  
RESULT 3  
ADR38739  
ID ADR38739 standard; peptide; 17 AA.  
XX  
AC ADR38739;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Mouse heavy chain anti-BONT-antibody CD2 seqid 141.  
XX  
XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
KM CDR2; complementarity determining region 2.  
XX  
OS Mus sp.  
XX  
PN US2004175385-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 01-AUG-2003; 2003US-00632706.  
XX  
PR 31-AUG-1998; 98US-00144886.  
PR 01-AUG-2002; 2002US-0400721P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Marke JD, Amerdorfer P;  
XX  
DR WPI; 2004-652009/63.  
XX  
PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
XX  
XX Example 4; SEQ ID NO 141; 110pp; English.  
XX  
CC The invention describes an isolated antibody (I) that specifically binds  
CC to an epitope specifically bound by an antibody expressed by a specific  
CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone

CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
CC 3-8, 3-10 and INGI1, where (I) binds to and neutralizes botulinum  
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
CC comprising BoNT/A neutralising epitope having an epitope that is  
CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I); and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising a botulinum neurotoxin which  
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain anti-BoNT-antibody CDR2.

XX Sequence 17 AA;

SO Query Match 100.0%; Score 93; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TISDGSSTYYPDSVKG 17  
1 TISDGSSTYYPDSVKG 17

DB 1 TISDGSSTYYPDSVKG 17

RESULT 4

ADR38747 standard; peptide; 17 AA.

ADR38747;

02-DEC-2004 (first entry)

Mouse heavy chain anti-BoNT-antibody CD2 seqid 149.

antibacterial; antibody; botulinum neurotoxin type A; BoNT/A.

BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
KW CDR2; complementarity determining region 2.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC ) UNIV CALIFORNIA.

XX Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
XX useful for diagnosing botulism or for treating pathologies associated  
XX with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 149; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds  
XX to an epitope specifically bound by an antibody expressed by a specific  
XX clone where (I) binds to and neutralises botulinum neurotoxin type A.

CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone  
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
CC 3-8, 3-10 and INGI1, where (I) binds to and neutralizes botulinum  
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
CC comprising BoNT/A neutralising epitope having an epitope that is  
CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I); and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising a botulinum neurotoxin which  
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain anti-BoNT-antibody CDR2.

XX Sequence 17 AA;

SO Query Match 100.0%; Score 93; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TISDGSSTYYPDSVKG 17  
1 TISDGSSTYYPDSVKG 17

DB 1 TISDGSSTYYPDSVKG 17

RESULT 5

ADR38755 standard; peptide; 17 AA.

ADR38755;

02-DEC-2004 (first entry)

Mouse heavy chain anti-BoNT-antibody CD2 seqid 157.

antibacterial; antibody; botulinum neurotoxin type A; BoNT/A.

BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
KW CDR2; complementarity determining region 2.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC ) UNIV CALIFORNIA.

XX Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
XX useful for diagnosing botulism or for treating pathologies associated  
XX with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 157; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds  
XX to an epitope specifically bound by an antibody expressed by a specific  
XX clone where (I) binds to and neutralises botulinum neurotoxin type A.



CC clone S25, C35, C39, 1G6 and clone 1F3, where the antibody binds to and  
 CC neutralises botulinum neurotoxin type A (BoNT/A). Also included are a  
 CC polypeptide comprising BoNT/A neutralising epitope comprising an epitope  
 CC which is specifically bound by the antibody, where the polypeptide is not  
 CC a full-length botulinum neurotoxin H c fragment and making an anti-BoNT/A  
 CC antibody that neutralises BoNT/A (by contacting several antibodies with  
 CC an epitope specifically bound by an antibody expressed by any of the  
 CC novel clones and isolating an antibody that specifically binds to the  
 CC epitope). The antibody is useful for neutralising a BoNT/A, by contacting  
 CC botulinum neurotoxin type A with the antibody comprising VH CDR (heavy  
 CC chain variable region complementarily determining region) and with a  
 CC second anti-BoNT/A antibody which comprises a VH CDR, where the second  
 CC antibody binds to a different epitope than the first anti-BoNT/A  
 CC antibody. The antibody is useful in the treatment of pathologies  
 CC associated with botulinum neurotoxin poisoning, for rapid  
 CC detection/diagnosis of botulinum and in the detection and/or  
 CC quantification of BoNT/A in a biological sample obtained from an organism  
 CC which is indicative of a Clostridium botulinum infection of the organism.  
 CC The present sequence is a heavy chain variable region (VH) of a single  
 CC chain antibody (scFv) of the invention  
 CC  
 SQ Sequence 66 AA;

Query Match 100.0%; Score 93; DB 6; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSYKVG 17  
 |||||  
 DB 50 TISDGSYYTPDSYKVG 66

RESULT 8  
 ADR38657  
 ID ADR38657 standard; peptide; 118 AA.

AC ADR38657;  
 DT 02-DEC-2004 (first entry)  
 XX

DE Mouse heavy chain variable region scFv seqid 59.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
 XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 KW heavy chain variable region; single chain antibody; scFv.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

XX (REGC ) UNIV CALIFORNIA.

PA Marks JD, Amersdorfer P;

PI WPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.

XX Example 1; SEQ ID NO 59; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A

CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C35, 1G6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralises botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of a botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (II) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of a mouse heavy chain variable fragment anti-botulinum toxin  
 CC scFv.

SQ Sequence 118 AA;  
 Query Match 100.0%; Score 93; DB 8; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSYKVG 17  
 |||||  
 DB 50 TISDGSYYTPDSYKVG 66

RESULT 9  
 ADR38658  
 ID ADR38658 standard; peptide; 118 AA.

AC ADR38658;  
 DT 02-DEC-2004 (first entry)  
 XX

DE Mouse heavy chain variable region scFv seqid 60.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
 XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;  
 KW heavy chain variable region; single chain antibody; scFv.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

XX (REGC ) UNIV CALIFORNIA.

PA Marks JD, Amersdorfer P;

PI WPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.

XX Example 1; SEQ ID NO 60; 110pp; English.

PS

CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC 835, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Axi, A2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralises botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I) and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of a mouse heavy chain variable fragment anti-botulinum toxin  
 CC scfv.

SO Sequence 118 AA;

Query Match 100.0%; Score 93; DB 8; Length 118;

Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSSTYTPDSVKG 17  
 |||||  
 Db 50 TISDGSSTYTPDSVKG 66

RESULT 10

AAR54930 standard; peptide; 120 AA.

AC AAR54930;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 19-OCT-1994 (first entry)

XX Fc receptor humanized VH chain 022 KLVH.

XX Fc receptor; FcR; humanized antibody; hab; IgG; cancer; allergy;

KW autoimmune disease; heteroantibody; bifunctional antibody; immunotoxin;

KW CDR; complementarity determining region; VH; heavy chain variable region;

KW VK; kappa chain variable region; mononuclear phagocyte; PCR;

KW polymerase chain reaction; primer; site-directed mutagenesis; KLVH;

XX monoclonal antibody; Mab.

OS Homo sapiens.

OS Mus sp.

XX WO9410332-A1.

XX 11-MAY-1994.

XX 04-NOV-1993; 93WO-US010384.

XX 04-NOV-1992; 92GB-00023377.

XX (MEDA-) MEDAREX INC.

XX Tempest PR, Harris WJ, Carr FJ;

XX WPI; 1994-167486/20.

XX New humanised antibodies to Fc receptors - used for diagnosis or for  
 PT treatment of e.g. cancer, allergies and infectious and auto-immune  
 PT diseases.  
 XX Disclosure; Page 14-15; 36pp; English.

SO Sequence 120 AA;

Query Match 100.0%; Score 93; DB 2; Length 120;

Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSSTYTPDSVKG 17  
 |||||  
 Db 50 TISDGSSTYTPDSVKG 66

RESULT 11

AAR54929 standard; peptide; 120 AA.

AC AAR54929;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 19-OCT-1994 (first entry)

XX Fc receptor humanized VH chain 022 NMVH.

XX Fc receptor; FcR; humanized antibody; hab; IgG; cancer; allergy;

KW autoimmune disease; heteroantibody; bifunctional antibody; immunotoxin;

KW CDR; complementarity determining region; VH; heavy chain variable region;

KW VK; kappa chain variable region; mononuclear phagocyte; PCR;

KW polymerase chain reaction; primer; site-directed mutagenesis; NMVH;

XX monoclonal antibody; Mab.

OS Homo sapiens.

OS Mus sp.

XX WO9410332-A1.

XX 11-MAY-1994.

XX 04-NOV-1993; 93WO-US010384.

XX 04-NOV-1992; 92GB-00023377.

XX (MEDA-) MEDAREX INC.

XX Tempest PR, Harris WJ, Carr FJ;

XX WPI; 1994-167486/20.

XX New humanised antibodies to Fc receptors - used for diagnosis or for

PT treatment of e.g. cancer, allergies and infectious and auto-immune

PT diseases.

XX Disclosure; Page 14; 36pp; English.





XX 11-OCT-2002 (first entry)  
 DT Humanised murine CBE11 heavy chain variable domain #3.  
 XX  
 DE Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;  
 XX neoplasia; LT-beta-R; light chain; heavy chain; variable region.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN WO200230986-A2.  
 PD 18-APR-2002.  
 XX  
 PF 12-OCT-2001; 2001WO-US032140.  
 XX  
 PR 13-OCT-2000; 2000US-0240285P.  
 PR 13-MAR-2001; 2001US-0275289P.  
 PR 21-JUN-2001; 2001US-029987P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PI Garber E, Lyne P, Saldanha JW;  
 XX  
 DR WPI; 2002-583337/62.  
 DR N-PSDB; AAL48454.  
 XX  
 PT New humanized anti-lymphotoxin-beta receptor antibody, useful for  
 PT treating or reducing the advancement, severity or effects of neoplasia,  
 PT particularly solid tumors (i.e. carcinomas) including colorectal cancer  
 PT and breast cancer.  
 XX  
 PS Disclosure; Page 15; 41pp; English.  
 XX  
 CC The present invention relates to humanised anti-lymphotoxin beta receptor  
 CC (LT-beta-R) antibodies. These are derived from the murine LT-beta-R  
 CC binding antibody CBE11 and can be used to treat neoplasia in humans. The  
 CC present sequence is a humanised murine CBE11 heavy chain variable region  
 XX  
 SQ Sequence 120 AA;

Query Match 100.0%; Score 93; DB 5; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TISDGSYTYPPDSVKG 17  
 |||||  
 DB 50 TISDGSYTYPPDSVKG 66

RESULT 15  
 AAO18395  
 ID AAO18395 standard; protein; 120 AA.  
 XX  
 AC AAO18395;  
 XX  
 DT 11-OCT-2002 (first entry)  
 XX  
 DE Humanised murine CBE11 heavy chain variable domain #1.  
 XX  
 KM Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;  
 KM neoplasia; LT-beta-R; light chain; heavy chain; variable region.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN WO200230986-A2.  
 PD 18-APR-2002.  
 XX  
 PF 12-OCT-2001; 2001WO-US032140.  
 XX

PR 13-OCT-2000; 2000US-0240285P.  
 PR 13-MAR-2001; 2001US-0275289P.  
 PR 21-JUN-2001; 2001US-029987P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PI Garber E, Lyne P, Saldanha JW;  
 XX  
 DR WPI; 2002-583337/62.  
 DR N-PSDB; AAL48452.  
 XX  
 PT New humanized anti-lymphotoxin-beta receptor antibody, useful for  
 PT treating or reducing the advancement, severity or effects of neoplasia,  
 PT particularly solid tumors (i.e. carcinomas) including colorectal cancer  
 PT and breast cancer.  
 XX  
 PS Disclosure; Page 14; 41pp; English.  
 XX  
 CC The present invention relates to humanised anti-lymphotoxin beta receptor  
 CC (LT-beta-R) antibodies. These are derived from the murine LT-beta-R  
 CC binding antibody CBE11 and can be used to treat neoplasia in humans. The  
 CC present sequence is a humanised murine CBE11 heavy chain variable region  
 XX  
 SQ Sequence 120 AA;

Query Match 100.0%; Score 93; DB 5; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TISDGSYTYPPDSVKG 17  
 |||||  
 DB 50 TISDGSYTYPPDSVKG 66

Search completed: November 21, 2005, 12:20:02  
 Job time : 23.7601 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 / Search time 4.14103 Seconds  
(without alignments)  
394.995 Million cell updates/sec

Title: US-10-632-706-157

Perfect score: 93  
Sequence: 1 TISDGSSTYYPPDSVKG 17

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	98	1	HVMS96
2	93	100.0	101	2	C27889
3	93	100.0	119	2	B27889
4	93	100.0	152	2	B26471
5	87	93.5	83	2	C25913
6	87	93.5	94	2	S14580
7	87	93.5	102	2	S14581
8	87	93.5	108	2	PH1010
9	87	93.5	119	2	F27888
10	87	93.5	120	2	S55537
11	87	93.5	120	2	S55536
12	87	93.5	122	2	E27888
13	84	90.3	121	2	I27887
14	84	90.3	123	2	S63597
15	84	90.3	124	2	C27888
16	84	90.3	124	2	B31790
17	84	90.3	548	2	S38864
18	83	89.2	121	2	A27888
19	81	87.1	117	1	HVMS57
20	81	87.1	118	2	PH0096
21	81	87.1	120	2	S55539
22	78	83.9	119	2	D27889
23	78	83.9	120	2	S55538
24	78	83.9	121	2	B27888
25	77	82.8	121	2	H27887
26	77	82.8	121	2	D27888
27	77	82.8	136	2	S31615
28	75	80.6	119	2	B34353
29	74	79.6	108	2	PL0248

30	74	79.6	118	2	PH0097	Ig heavy chain V r
31	74	79.6	138	2	S09258	Ig heavy chain V r
32	73	78.5	114	2	PH1009	Ig heavy chain V r
33	73	78.5	117	1	HVMS39	Ig heavy chain pre
34	73	78.5	121	2	H27888	Ig heavy chain V r
35	72	77.4	112	2	A27889	Ig heavy chain V r
36	70	75.3	108	2	PH1006	Ig heavy chain V r
37	70	75.3	123	2	C27888	Ig heavy chain V r
38	69	74.2	111	2	PH1007	Ig heavy chain V r
39	69	74.2	118	2	S20641	Ig heavy chain V r
40	69	74.2	124	2	I27888	Ig heavy chain V r
41	67	72.0	117	1	HVMS84	Ig heavy chain pre
42	67	72.0	118	2	S00700	Ig heavy chain V r
43	67	72.0	119	2	A43413	Ig heavy chain V r
44	66	71.0	113	2	S26468	Ig heavy chain V r
45	66	71.0	117	1	HVMS34	Ig heavy chain pre

#### ALIGNMENTS

##### RESULT 1

HVMS96  
Ig heavy chain V region (6.96) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C/Accession: J0501  
R/Levy, N.S.; Malpietro, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A/Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary in  
A/Reference number: J0501, MUID:89279149; PMID:249654  
A/Accession: J0501  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-98 <LEAV>  
A/Cross-references: UNIPROT:P18528; UNIPARC:UPI0000278DB  
A/Experimental source: STRAIN BALB/cJ  
A/Note: This sequence belongs to the VH7183 subfamily  
C/Superfamily: Immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
P:15-98/Domain: immunoglobulin homology <IMM>  
P:122-96/Disulfide bonds: #status predicted

Query Match 100.0%; Score 93; DB 1; Length 98;  
Best Local Similarity 100.0%; Pred. No. 3.8e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSSTYYPPDSVKG 17  
DB 50 TISDGSSTYYPPDSVKG 66

##### RESULT 2

C27889  
Ig heavy chain V region (H220-25) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C/Accession: C27889  
R/Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986  
A/Title: Structural and functional implications of a restricted antibody response to a de  
A/Reference number: A91043; MUID:86300658; PMID:2427335  
A/Accession: C27889  
A/Molecule type: DNA  
A/Residues: 1-101 <CAT>  
A/Cross-references: UNIPARC:UPI0000176A0C  
A/Experimental source: strain Balb/c  
A/Note: This sequence was determined from the germ-line gene  
C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus he  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 93; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 3.9e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYTYPPDSVKG 17  
Db 32 TISDGSYTYPPDSVKG 48

## RESULT 3

B27889 Ig heavy chain V region (H146-24B3) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996

C/Accession: B27889

R/Author: A.J. Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A/Title: Structural and functional implications of a restricted antibody response to a

A/Reference number: A91043; MUID:86300658; PMID:2427335

A/Accession: B27889

A/Molecule type: DNA

A/Residues: 1-119 <CAT>

A/Cross-references: UNIPARC:UPI0000176B67

A/Experimental source: strain Balb/c

A/Note: this sequence was determined from the germ-line gene

C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus H

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 93; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 4.6e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYTYPPDSVKG 17  
Db 50 TISDGSYTYPPDSVKG 66

## RESULT 4

B26471 Ig heavy chain precursor V region (MAK33) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 23-Jul-1999

C/Accession: B26471; S70410

R/Buckle, P.; Hubner-Parfisz, C.; Matres, R.; Lenz, H.; Haug, H.; Beaucamp, K.

Gene 51, 13-19, 1987

A/Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine

A/Reference number: A91572; MUID:87248058; PMID:3110009

A/Accession: B26471

A/Molecule type: mRNA

A/Residues: 1-152 <BUC>

A/Cross-references: UNIPARC:UPI000011677B; GB:M16163; NID:G195405; PIDN:AAA38292.1; PID:

R/LeDeque, S.G.; Gearhart, P.U.

J. Exp. Med. 172, 1717-1727, 1990

A/Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary

A/Reference number: S70410; MUID:91079775; PMID:2258702

A/Accession: S70410

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-19 <LEB>

A/Cross-references: UNIPARC:UPI0000115B81; EMBL:X53776; NID:G52475; PIDN:CAA37792.1; PIT

C/Genetics: 16/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-19/Domain: signal sequence #status predicted <SIG>

F/20-15/Domain: Ig heavy chain V region MAK33 #status predicted <MAT>

F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 93; DB 2; Length 152;

Best Local Similarity 100.0%; Pred. No. 5.9e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYTYPPDSVKG 17  
Db 69 TISDGSYTYPPDSVKG 85

## RESULT 5

C25913

Ig heavy chain V region (BFL14) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 31-Dec-2004

C/Accession: C25913

R/Lawler, A.M.; Lin, P.S.; Gearhart, P.U.

Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987

A/Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes

A/Reference number: A9148; MUID:87175692; PMID:3104915

A/Accession: C25913

A/Molecule type: DNA

A/Residues: 1-83 <LAW>

A/Cross-references: UNIPROT:Q920E7; UNIPARC:UPI00001769E3

C/Superfamily: immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 93.5%; Score 87; DB 2; Length 83;  
Best Local Similarity 94.1%; Pred. No. 2.6e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TISDGSYTYPPDSVKG 17  
Db 35 TISDGSYTYPPDSVKG 51

## RESULT 6

S14580 Ig heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

C/Accession: S14580

R/Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.

submitted to the EMBL Data Library, March 1991

A/Description: Natural polyclonal antibodies differ from Ag-induced antibodies in VH CI

A/Reference number: S14484

A/Accession: S14580

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-94 <CHE>

A/Cross-references: UNIPARC:UPI0000115F39; EMBL:X58652; NID:G51293; PIDN:CAA41509.1; PID:

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 93.5%; Score 87; DB 2; Length 94;  
Best Local Similarity 94.1%; Pred. No. 3e-06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TISDGSYTYPPDSVKG 17  
Db 42 TISDGSYTYPPDSVKG 58

## RESULT 7

S14581

Ig heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

C/Accession: S14581

R/Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.

submitted to the EMBL Data Library, March 1991

A/Description: Natural polyclonal antibodies differ from Ag-induced antibodies in VH CI

A/Reference number: S14484

A/Accession: S14581

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-102 <CHE>

RESULT 10  
555537  
Ig heavy chain V region pe21 - mouse (fragment)  
C|Species: Mus musculus (house mouse)  
|Date: 27-Oct-1995 #sequence rev1:0n 03-Nov-1995 #text change 23-Jul-1999

C/Accession: S5537  
R/Boettger: V. J. Boettger, A. J. Lane, E. B. J. Spruce, B. A. J. Mol. Biol. 247, 932-946, 1995  
T/Mol. Biol. 247, 932-946, 1995  
T/Mol. Biol. 247, 932-946, 1995

Accession: S5537  
Reference number: S5528; MUID:9539763; PMID:7536850

A:Residues: 1-120 <BOB>  
 A:Cross-references:UPI00000116201; EMBL:X82590; NID:G854306; PIDD:CAA57926.1; PIR:J01492; SwissProt:J01492.1  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 D:Immunoglobulin V region; immunoglobulin homology

Query Match	93.5%	Score 87	DB 2	Length 120
Accession	U01811	Seed	NO	3.8e-06
F;14-97/Domain:immunoglobulin homology <IMM>				

Matches	16;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
1 m r e d o c a u v u v u d n i t w 17									

Db  
49 TISSGGSYTTYPDsvKG 65

## RESULT 11

ig heavy chain v region pe20 - mouse (fragment)  
CISpecies: Mus musculus (house mouse)  
Accession: AF000001  
Date Recd: 03 May 1995  
#cont: 27  
#seq: 1000

C:Accession: S5536  
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.  
J. Mol. Biol. 247, 932-946, 1995  
Title: Isolation of monoclonal anti- $\alpha$ -crystallin antibodies using

utations in the variable region genes.  
A:Reference number: S5528; MUID:95239763; PMID:7536850  
A:Accession: S5536

A;Molecule type: mRNA  
A;Residues: 1-120 <BO>  
MUTATED: mtr000011200. mtr1-vc0590. mtr2-c8c4304. btrn-c0b5925 1. btrp-

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
G:KeyWords: heterotrimer; immunoglobulin  
F14-97/Domain: immunoglobulin homology <Imm>

Query Match	93.5%	Score 87	DB 2	Length 120
Best Local Similarity	94.1%	Pred. No. 3	8e-06	
Matches	16	Conservative	0	Mismatches 1
				Indels 0
				Gaps 0

Qy 1 TIDGGSYTYPPDSVKG 17  
||| ||||||||  
||| ||||||||

E27888  
Ig heavy chain V region (H35-C6) - mouse

C/Accession: B27888  
R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986  
A title: Structural and functional implications of a restricted antibody response to a d  
A reference number: 101003 WITH SCIENCE. DMD-247215

A:Accession: E27888  
A:Molecule type: DNA  
A:Residues: 1-122 <CAT>  
ATTTTCTGTCATTGGAGCGC

A/Note: this sequence was determined from the germline gene  
C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus h  
C/Species: Mus musculus (house mouse)  
C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C/Accession: I27887  
C/KeyWords: heterotrimer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.5%; Score 87; DB 2; Length 122;  
Best Local Similarity 94.1%; Pred. No. 3,9e-06;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TISDGSYTYYPDSVKG 17  
||| |||||  
Db 50 TISSGGTYTYYPDSVKG 66

## RESULT 13

I27887  
Ig heavy chain V region (H37-45) - mouse  
C/Species: Mus musculus (house mouse)

C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C/Accession: I27887

R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.  
EMBO J. 5, 1577-1587, 1986

A/Title: Structural and functional implications of a restricted antibody response to a d  
A/Reference number: A91043; MUID:86300658; PMID:2427335

A/Accession: I27887

A/Molecule type: DNA

A/Residues: 1-121 <CAT>

A/Cross-references: UNIPARC:UPI000017686F

A/Experimental source: strain Balb/c

A/Note: This sequence was determined from the germline gene

C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus h  
C/Species: Mus musculus (house mouse)

C/KeyWords: heterotrimer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 84; DB 2; Length 121;  
Best Local Similarity 88.2%; Pred. No. 1.1e-05;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TISDGSYTYYPDSVKG 17  
||| |||||  
Db 50 TISSGGTYTYYPDSVKG 66

## RESULT 14

S63597

Ig heavy chain, V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000  
C/Accession: S63597

R/Verdaguer, N.; Mateu, M.G.; Bravo, J.; Domingo, E.; Fita, I.  
J. Mol. Biol. 256, 364-376, 1996

A/Title: Induced pocket to accommodate the cell attachment Arg-Gly-Asp motif in a neutre  
A/Reference number: S63596; MUID:96174482; PMID:8594203

A/Accession: S63597

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-123 <VER>

A/Cross-references: UNIPARC:UPI00001154DF; GB:S61215; NID:G1336823; PIDN:AAB36172.1; PIT  
C/Species: Mus musculus (house mouse)

C/KeyWords: heterotrimer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 84; DB 2; Length 123;  
Best Local Similarity 88.2%; Pred. No. 1.1e-05;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TISDGSYTYYPDSVKG 17  
||| |||||  
Db 50 TISSGGTYTYYPDSVKG 66

## RESULT 15

C27888  
Ig heavy chain V region (H37-62) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 16-Aug-1996  
C/Accession: C27888  
C/KeyWords: heterotrimer; immunoglobulin  
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 84; DB 2; Length 124;  
Best Local Similarity 88.2%; Pred. No. 1.1e-05;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TISDGSYTYYPDSVKG 17  
||| |||||  
Db 50 TISSGGTYTYYPDSVKG 66

Search completed: November 21, 2005, 12:22:15  
Job time: 4.14103 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: November 21, 2005, 11:45:55 ; Search time 25.1575 Seconds  
(without alignments)  
476.756 Million cell updates/sec

Title: US-10-632-706-157  
Perfect score: 93  
Sequence: 1 TISDGSSTYTPDSVKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: uniprot\_sprot:\*  
2: uniprot\_tramb1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	93	100.0	98	1	HV57_MOUSE	P18528 mus musculu
2	90	96.8	487	2	Q99KA4_MOUSE	Q99KA4 mus musculu
3	87	93.5	119	2	Q920E7_MOUSE	Q920E7 mus musculu
4	87	93.5	196	2	Q65ZL8_MOUSE	Q65ZL8 mus musculu
5	84	90.3	255	2	Q6RB05_MOUSE	Q6RB05 mus musculu
6	81	87.1	117	1	HV58_MOUSE	P18529 mus musculu
7	73	78.5	117	1	HV59_MOUSE	P18530 mus musculu
8	67	72.0	117	1	HV54_MOUSE	P18525 mus musculu
9	67	72.0	589	2	Q5XHD5_XENILA	Q5XHD5 xenopus lae
10	66	71.0	117	1	HV55_MOUSE	P18526 mus musculu
11	65.5	70.4	97	1	HV56_MOUSE	P18527 mus musculu
12	65	69.9	98	2	Q4TU56_TETNG	Q4TU56 tetraodon n
13	64	68.8	479	2	Q5BK12_RAT	Q5BK12 rattus norv
14	63.5	66.3	464	2	Q4VBH1_RAT	Q4VBH1 rattus norv
15	62	66.7	464	2	Q6MZU6_HUMAN	Q6MZU6 homo sapien
16	60	64.5	99	2	Q4TSM5_TETNG	Q4TSM5 tetraodon n
17	60	64.5	479	2	Q5POK3_RAT	Q5POK3 rattus norv
18	59	63.4	96	2	Q4TSS4_TETNG	Q4TSS4 tetraodon n
19	59	63.4	480	2	Q91XBI_MOUSE	Q91XBI mus musculu
20	59	63.4	584	2	Q6INK3_XENILA	Q6INK3 xenopus lae
21	58.5	62.9	117	1	HV53_MOUSE	P18524 mus musculu
22	58.5	62.9	614	2	Q6DD07_XENILA	Q6DD07 xenopus lae
23	58	62.4	119	1	HV41_HUMAN	P01773 homo sapien
24	58	62.4	119	2	Q5F2I8_MOUSE	Q5F2I8 mus musculu
25	55.5	59.7	367	2	Q5WBX4_XENTR	Q5WBX4 xenopus tro
26	55.5	59.7	486	2	Q91207_MOUSE	Q91207 mus musculu
27	54.5	58.6	121	2	Q9UL71_HUMAN	Q9UL71 homo sapien
28	54.5	58.6	469	2	Q569F4_HUMAN	Q569F4 homo sapien
29	54.5	58.6	593	2	Q6INM5_XENILA	Q6INM5 xenopus lae
30	54	58.1	465	2	Q51UJ0_RAT	Q51UJ0 rattus norv
31	54	58.1	597	2	Q96BB9_HUMAN	Q96BB9 homo sapien

ALIGNMENTS

RESULT 1									
ID	HV57_MOUSE	STANDARD;	PRT;	98 AA.					
AC	P18528;								
DT	01-NOV-1990 (Rel. 16, Created)								
DT	01-NOV-1990 (Rel. 16, Last sequence update)								
DT	10-MAY-2005 (Rel. 47, Last annotation update)								
DE	Ig heavy chain V region 6..96.								
DS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;								
CC	Muroidea; Muridae; Murinae; Mus.								
OX	NCBI_TaxId=10090;								
RM	[1]								
RP	NUCLEOTIDE SEQUENCE.								
RC	STRAIN=BALB/c;								
RX	MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;								
RA	Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;								
RT	"Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response."								
RL	J. Exp. Med. 169:2007-2019(1989).								
CC	-I- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.								
CC	-I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.								
CC	-----								
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.								
CC	-----								
DR	PIR: J0501; HWS96.								
DR	HSSP: P01783; IIGC.								
DR	SMR: P18528; 1-98.								
DR	InterPro: IPR007110; Ig-1-like.								
DR	InterPro: IPR003596; Ig_v.								
DR	SMART: SM00406; IGV, 1.								
DR	PROSITE: PS50835; IG_LIKE, 1.								
FT	IMMUNOGLOBULIN domain; Immunoglobulin V region.								
FT	DOMAIN 1 >98								
FT	NON TER 98								
SO	SEQUENCE 98 AA; 11007 MW; B8644F7F9JFBP95B CRC64;								
-----									
Query Match 100.0%; Score 93; DB 1; Length 98;									
Best Local Similarity 100.0%; Pred. No. 1.4e+06;									
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
-----									
QY	1 TISDGSSTYTPDSVKG 17								
DB	50 TISDGSSTYTPDSVKG 66								
-----									
RESULT 2									
Q99KA4_MOUSE									
ID	Q99KA4_MOUSE PRELIMINARY;	PRT;	487 AA.						

32	54	58.1	1021	2	Q7SAK9_NEUCR	Q7SAK9 neurospora
33	54	58.1	1037	2	Q6MPG6_NEUCR	Q6MPG6 neurospora
34	54	58.1	1090	2	Q4NDB8_PMITC	Q4NDB8 arthrobracte
35	53	57.0	117	1	HV3C_HUMAN	P01768 homo sapien
36	53	57.0	461	2	Q5MTV3_RAT	Q5MTV3 rattus norv
37	53	57.0	465	2	Q6P6C4_HUMAN	Q6P6C4 homo sapien
38	53	57.0	475	2	Q6MZ06_HUMAN	Q6MZ06 homo sapien
39	53	57.0	605	2	Q6GMY2_HUMAN	Q6GMY2 homo sapien
40	52.5	56.5	96	2	Q4SX82_TETNG	Q4SX82 tetraodon n
41	52	55.9	236	2	Q6ZP85_HUMAN	Q6ZP85 homo sapien
42	52	55.9	281	2	Q7SAG0_ASHGO	Q7SAG0 ashbya goss
43	50.5	54.3	116	1	HV05_CARAU	P19181 carassius a
44	50	53.8	121	1	HV3J_HUMAN	P01771 homo sapien
45	50	53.8	494	2	Q96K68_HUMAN	Q96K68 homo sapien

```

AC 099K4;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE 1gh-VJ558 protein.
GN Name=1gh-VJ558;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Datschenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Tomshyukl S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Director MGC Project;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR 1 HMBL; BC004786; AA04786.1; -; mRNA.
DR HSBP; P01810; 2FBY.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR MG1; MG1.96486; 1gh-VJ558.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; 1g-1ike.
DR InterPro; IPR003597; 1g_c1.
DR InterPro; IPR003006; 1g_MHC.
DR InterPro; IPR003596; 1g_v.
DR Pfam; PF07654; C1-bet; 3.
DR SMART; SM00406; 1gV; 1.
DR PROSITE; PS50835; 1g_LIKE; 4.
DR PROSITE; PS00290; 1g_MHC; UNKNOWN_2.
KM Immunoglobulin domain.
SQ SEQUENCE 487 AA; 52555 MW; 7DC8B96DB33077B CRC64;

Query Match 96.8%; Score 90; DB 2; Length 487;
Best Local Similarity 94.1%; Pred. No. 2.3e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TISDGSYTYPPDSVK 17
Db 69 TISDGSYTYPPDNVKG 85

```

```

DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotypic heavy chain variable region
DE (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Aikin J.D., Iape A., Jennings I.G., Horatidis O., Cotton R.G.H.,
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87175592; PubMed=3104915;
RA Lawler A.M., Lin P.S., Gearhart P.J.;
RT "Adult B-cell repertoire is biased toward two heavy-chain variable-
RT region genes that rearrange frequently in fetal pre-B cells."
RL Proc. Natl. Acad. Sci. U.S.A. 84:2454-2458(1987).
DR 1 HMBL; AF307937; AAU09421.1; -; Genomic_DNA.
DR PIR; C25913; C25913.
DR HSBP; P01783; 11GC.
DR SMR; Q920E7; 1-119.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; 1g-1ike.
DR InterPro; IPR003596; 1g_v.
DR SMART; SM00406; 1gV; 1.
DR PROSITE; PS50835; 1g_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13026 MW; F6B90404381CA7C CRC64;

Query Match 93.5%; Score 87; DB 2; Length 119;
Best Local Similarity 94.1%; Pred. No. 1.5e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TISDGSYTYPPDSVK 17
Db 50 TISDGSYTYPPDSVK 66

RESULT 4
ID 065ZL8_MOUSE PRELIMINARY; PRT; 196 AA.
AC 065ZL8;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Vt183-DSP2-JH3-CHI protein (Fragment).
GN Name=Vt183-DSP2-JH3-CHI;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BLB/c;
RC MEDLINE=95362300; PubMed=7635518;
RA Komori T., Sugiyama H.;
RT "An aberrant splicing using a 3' cryptic splice site within the CHI
RT exon induces truncated mu-chain production."
RL Immunology 85:166-170(1995).
DR 1 HMBL; S79401; AAB35023.2; -; mRNA.
DR SMR; Q65ZL8; 20-195.
DR InterPro; IPR003599; 1g.
DR InterPro; IPR007110; 1g-1ike.
DR InterPro; IPR003596; 1g_v.
DR SMART; SM00406; 1gV; 1.
DR PROSITE; PS50835; 1g_LIKE; 1.
FT NON_TER 196
SQ SEQUENCE 196 AA; 21429 MW; 12A381018944B268 CRC64;

```



```

Query Match Similarity      93.5%; Score 87; DB 2; Length 196;
Best Local Similarity      94.1%; Pred. No. 2,66-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TISDGSYTTYYPDSYVK 17
   ||| ||||| ||||| |||
DB 69 TITSGGSYTTYYPDSYVK 85

RESULT 5
Q6KB05_MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE SCFV_B0B5 protein (Fragment).
GN Name=scFv_B0B5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RT Briland J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
RL monoclonal anti-M2 receptor antibody fragments.";
RL J. Biol. Chem. 279:55697-55706(2004).
DR EMBL; AJ746180; CAG34081.1; -; Other_DNA.
DR HSRF; P01837; 1KCR.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
DR NON TER 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 90.3%; Score 84; DB 2; Length 255;
Best Local Similarity 88.2%; Pred. No. 0,0001;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TISDGSYTTYYPDSYVK 17
   ||| ||||| ||||| |||
DB 50 TITSGGSYTTYYPDSYVK 66

RESULT 6
HV58_MOUSE
ID HV58_MOUSE STANDARD; PRT; 117 AA.
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RA MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RL primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
```

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CC -1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR, JTO506, HWM57.
CC PDB, 1I81, X-ray, B=26-115.
CC PDB, 1I8K, X-ray, B=26-115.
CC InterPro, IPR007110, Ig-1like.
CC InterPro, IPR003596, Ig_v.
CC SMART, SM00406, IGV, 1_v.
CC PROSITE, PS50835, IG_LIKE, 1.
CC 3D-structure, Immunoglobulin domain, Immunoglobulin V region, Signal.
CC KW SIGNAL, 1
CC FT CHAIN 1
CC FT REGION 20 117 Ig heavy chain V region 5-76.
CC FT REGION 20 49 Framework-1.
CC FT REGION 50 54 Complementarity-determining-1.
CC FT REGION 55 68 Framework-2.
CC FT REGION 69 85 Complementarity-determining-2.
CC FT REGION 86 117 Framework-3.
CC FT DISULFID 41 115 By similarity.
CC FT NON TER 117 117
CC SQ SEQUENCE 117 AA; 12991 MW; 93A04782B7BB8FA0 CRC64;
CC
CC Query Match 87.1%; Score 81; DB 1; Length 117;
CC Best Local Similarity 88.2%; Pred. No. 0.00013;
CC Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CC
CC Oy 1 TISPGSGYTYPPDSVKG 17
CC |||||
CC Db 69 TISSGGLYTYPPDSVKG 85
CC
CC RESULT 7
CC HV59_MOUSE STANDARD; PRT; 117 AA.
CC ID HV59_MOUSE
CC AC P18530;
CC DT 01-NOV-1990 (Rel. 16, Created)
CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
CC DT 10-MAY-2005 (Rel. 47, Last annotation update)
CC DE Ig heavy chain V region 7-39 precursor.
CC OS Mus musculus (Mouse).
CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
CC OC Muroidea; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
CC (1)
CC RP NUCLEOTIDE SEQUENCE.
CC RC STRAIN=BAB/cj;
CC RX MEDLINE=89279149; PubMed=249654; DOI=10.1084/jem.169.6.2007;
CC RRA Levy N.S.. Malpiero U V., Lebecque S.G., Gearhart P.J.;
CC RT "Early onset of somatic mutation in immunoglobulin VH genes during the
CC primary immune response."
CC J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR, JTO507, HWM39.
CC HSSP, P18529, 118K.
CC SMR, P18530, 20-117.
CC InterPro, IPR007110, Ig-1like.
CC InterPro, IPR003596, IG_v.
CC SMART, SM00406, IGV, 1.
CC PROSITE, PS50835, IG_LIKE, 1.
CC Immunoglobulin domain, Immunoglobulin V region, Signal.
CC

```

```
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 7-39.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; DSCA167D0F1774F CRC64;

Query Match 78.5%; Score 73; DB 1; Length 117;
Best Local Similarity 82.4%; Pred. No. 0.0023;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 TISDGSYYTPYPSVKG 17
Db 69 SISGGSYYTPYPSVKG 85
```

## RESULT 8

```
SV4_MOUSE STANDARD; PRT; 117 AA.
ID HV54_MOUSE
AC P18525;
DT 01-NOV-1990 (Ref. 16, Created)
DT 01-NOV-1990 (Ref. 16, Last sequence update)
DT 10-MAY-2005 (Ref. 47, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/cJ;
RX MEDLINE=69279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Maligiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
primary immune response."
RT J. Exp. Med. 169:2007-2019(1989).
RL J.
CC -1- MISCRLNBOS: This sequence belongs to the VH7183 subfamily.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; JTO505; HVMS84.
DR PIR; JAR1; X-ray; D-.
DR Ensembl; ENSEMBL00000062386; Mus musculus.
DR InterPro; IPR007110; Ig_V.
DR SMART; SM00406; IG_V.1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 5-84.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A46961 CRC64;
```

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Query Match 72.0%; Score 67; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 0.02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```
QY 2 ISDGSYYTPYPSVKG 17
```

```
Db 70 ISNGGSYYTPYPSVKG 85
```

## RESULT 9

```
Q5XHD5_XENLA PRELIMINARY; PRT; 589 AA.
ID Q5XHD5;
AC Q5XHD5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus; Xenopus.
OX NCBI_TaxId=6335;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko U., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohyiuki S., Carninci P., Prange C.,
RA Rha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heltan B., Kettelman M., Madan A., Rodriguez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
RA Schnerch A., Schein U.E., Jones S.J.M., Merra W.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Klein S., Gerhard D.S.,
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC084123; AA884123.1; mRNA.
DR GO; GO:0030106; F-MHC class I receptor activity; IEA.
DR GO; GO:0019883; P-antigen processing, endogenous antigen; IEA.
DR GO; GO:0019885; P-antigen processing, endogenous antigen; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IG1; 4.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PSS0835; IG_LIKE; 5.
DR PROSITE; PSS0230; IG_MHC; UNKNOWN_4.
KW Hypothetical protein.
SQ SEQUENCE 589 AA; 65361 MW; DIA212699D69FCE CRC64;
```

Query Match 72.0%; Score 67; DB 2; Length 589;  
 Best Local Similarity 81.2%; Pred. No. 0.11;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISDGGSTYTPDSYK 17  
 |||||  
 DB 68 ISDGGSTYTPDSYK 83

## RESULT 10

HVS5 MOUSE STANDARD; PRT; 117 AA.

AC P18526;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DS Ig heavy chain V region 345 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

CC NUCLEOTIDE SEQUENCE.

RA STRAIN=BALB/cj;

RC MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

"Early onset of somatic mutation in immunoglobulin VH genes during the

primary immune response."

J. Exp. Med. 169:2007-2019(1989).

-1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.

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CC PIR: J0502; HWS34.

DR HSSP; P01783; IIGC.

DR SMR; P18526; 20-117.

DR Ensemble; ENSMUSG0000062386; Mus musculus.

DR InterPro; IPR007110; IG-1like.

DR SMART; SM00406; IG\_V.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin domain; Immunoglobulin V region; Signal.

FT SIGNAL 1 19 Ig heavy chain V region 345.

FT CHAIN 20 117 Framework-1.

FT REGION 20 49 Complementarity-determining-1.

FT REGION 50 54 Framework-2.

FT REGION 55 68 Complementarity-determining-2.

FT REGION 69 85 Framework-3.

FT REGION 86 117 By similarity.

FT DISULFID 41 115

FT NON TER 117 117

SEQUENCE 117 AA; 12902 MW; 4938084627ACA99A CRC64;

Query Match 71.0%; Score 66; DB 1; Length 117;  
 Best Local Similarity 75.0%; Pred. No. 0.028;  
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISDGGSTYTPDSYK 17  
 |||||  
 DB 70 ISDGGSTYTPDSYK 85

## RESULT 11

HVS6 MOUSE STANDARD; PRT; 97 AA.

AC P18527;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DS Ig heavy chain V region 914.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

CC NUCLEOTIDE SEQUENCE.

RA STRAIN=BALB/cj;

RC MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

"Early onset of somatic mutation in immunoglobulin VH genes during the

primary immune response."

J. Exp. Med. 169:2007-2019(1989).

-1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.

-1- SIMILARITY: Contains 1 Ig-1like (immunoglobulin-1like) domain.

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 the European Bioinformatics Institute. There are no restrictions on its  
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CC PIR: J0504; HWS91.

DR HSSP; P01783; IIGC.

DR SMR; P18527; 1-97.

DR Ensemble; ENSMUSG0000062386; Mus musculus.

DR InterPro; IPR007110; IG-1like.

DR SMART; SM00406; IG\_V.

DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin domain; Immunoglobulin V region.

FT DOMAIN 1 >97 Ig-1like.

FT NON TER 97 97

SEQUENCE 97 AA; 10661 MW; C23CB33F55DA893 CRC64;

Query Match 70.4%; Score 65.5; DB 1; Length 97;  
 Best Local Similarity 82.4%; Pred. No. 0.028;  
 Matches 14; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 TISDGGSTYTPDSYK 17  
 :|||  
 DB 50 SISDGS-TYTPDSYK 65

## RESULT 12

Q4TJ56 TETNG PRELIMINARY; PRT; 98 AA.

AC Q4TJ56;

DT 13-SEP-2005 (TREMBLrel. 31, Created)

DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)

DE Chromosome undetermined SCAF649, whole genome shotgun sequence.

DE (Fragment).

GN ORFNames=GSTENG0004372001;

OS Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Teleostei; Neoteleostei;

OC Acanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

NCBI\_TaxID=99883;

CC NUCLEOTIDE SEQUENCE.

RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,

RA Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Dasilva C., Salanoubat M., Levy M., Boudet N., Casarelli A.,

RA Anthouard V., Uubin C., Casarelli V., Katinka M., Vacherie B.,

RA Biemont C., Skalli Z., Baticelli L., Poulain J., De Berrardinis V.,

RA Crenaud C., Duprat S., Broctier P., Coutanceau J.P., Gonzy J.,

RA Parra G., Lardier G., Chaple C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mestrov J.,

RA Landblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Landel V., Schachter V., Queller F., Saurin W., Scarpelli C.,  
 RA Winkler P., Lander E.S., Weissbach U., Roest Croollus H.,  
 RT "genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NCIBLOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL: CA60100649; CAF87076.1; -; Genomic\_DNA.  
 DR NON TER 1  
 DR SEQUENCE 98 AA; 10862 MW; 0EB7F34DB9C4648D CRC64;  
 QY  
 Query Match 69.9%; Score 65; DB 2; Length 98;  
 Best Local Similarity 70.6%; Pred. No. 0.033;  
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 OY 1 TISDGSYYTYPPDSVKG 17  
 ID Q5BK12.RAT PRELIMINARY; PRT; 479 AA.  
 AC Q5BK12;  
 DT 10-MAY-2005 (TREMBlrel. 30, Created)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
 DE 19aa protein.  
 GN Name=19aa;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NCIBLOTIDE SEQUENCE.  
 RC TISSUE=Splice;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fabley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NCIBLOTIDE SEQUENCE.  
 RC TISSUE=Splice;  
 RG NIH MGC Project;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC091247; AA91247.1; -; mRNA.  
 DR SMR, Q5BK12; 20-241.  
 DR GO: GO:0003823; P: antigen binding; IEA.  
 DR InterPro: IPR003599; IG.

DR InterPro: IPR007110; IG-1like.  
 DR InterPro: IPR003597; IG-cl.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF07654; Cl-sec; 2.  
 DR SMART, SM00409; IG; 3.  
 DR SMART, SM00407; IG; 3.  
 DR SMART, SM00406; IG; 1.  
 DR PROSITE, PSS0835; IG-LIKE; 3.  
 DR PROSITE, PSS0290; IG\_MHC; UNKNOWN\_2.  
 DR PROSITE, PSS0290; IG\_MHC; UNKNOWN\_2.  
 DR SEQUENCE 479 AA; 52329 MW; 8B16164A8437C5 CRC64;  
 QY  
 Query Match 68.8%; Score 64; DB 2; Length 479;  
 Best Local Similarity 70.6%; Pred. No. 0.25;  
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 OY 1 TISDGSYYTYPPDSVKG 17  
 ID Q4VBH1.RAT PRELIMINARY; PRT; 467 AA.  
 AC Q4VBH1;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
 DE LOC29354 protein.  
 GN Name=LOC29354;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NCIBLOTIDE SEQUENCE.  
 RC TISSUE=Thymus;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fabley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NCIBLOTIDE SEQUENCE.  
 RC TISSUE=Thymus;  
 RG NIH MGC Project;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
 CC histocompatibility complex class I molecules (By similarity).  
 DR EMBL: BC095846; AA95846.1; -; mRNA.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-cl.  
 DR InterPro: IPR003597; IG-cl.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF07654; Cl-sec; 3.

DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 2.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 KM Immunoglobulin domain; Repeat.  
 SQ SEQUENCE 467 AA; 51651 MW; 1FF0328F50160ED3 CRC64;

Query Match 66.3%; Score 63.5; DB 2; Length 467;  
 Best Local Similarity 86.7%; Pred. No. 0.3;  
 Matches 13; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

OY 3 SDGGSYTYPPDSVKG 17  
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 Db 72 TDGGS-TYPPDSVKG 85

## RESULT 15

06MZU6\_HUMAN PRELIMINARY; PRT; 464 AA.  
 ID 06MZU6\_HUMAN PRELIMINARY; PRT; 464 AA.  
 AC 06MZU6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686C15213.  
 GN Name=DKFZp686C15213;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 OC Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Rectum tumor;  
 RG The German cDNA Consortium;  
 RA Bloeker H., Boeher M., Brandt P., Mewes H.W., Weil B., Amid C.,  
 RA Osanger A., Rebo G., Han M., Wiemann S.;  
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX640874; CAB45931.1; -; mRNA.  
 DR HSSP; P01861; IADQ.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 KM Hypothetical protein.  
 SQ SEQUENCE 464 AA; 51099 MW; 2PCA72C66E8A0ABC CRC64;

Query Match 66.7%; Score 62; DB 2; Length 464;  
 Best Local Similarity 80.0%; Pred. No. 0.5;  
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 SDGGSYTYPPDSVKG 17  
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 Db 72 SRGGSYTYADSVKG 86

Search completed: November 21, 2005, 12:04:11  
 Job time : 26.1575 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:31 ; Search time 6.41392 Seconds  
(without alignments)  
219.131 Million cell updates/sec

Title: US-10-632-706-157

Sequence: 1 TISDGSSTYTPDSVKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:  
1: /cgn2\_6/ptodata/1/1aa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PTCURS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	120	2	US-08-435-516-1 Sequence 1, Appl
2	93	100.0	120	2	US-08-435-516-2 Sequence 2, Appl
3	93	100.0	120	2	US-08-435-516-3 Sequence 3, Appl
4	93	100.0	123	2	US-09-344-587-13 Sequence 13, Appl
5	93	100.0	300	1	US-08-661-052-4 Sequence 4, Appl
6	93	100.0	300	2	US-09-188-082-4 Sequence 4, Appl
7	93	100.0	300	2	US-09-364-088-4 Sequence 4, Appl
8	93	100.0	300	2	US-09-102-716-4 Sequence 4, Appl
9	93	100.0	301	1	US-08-661-052-14 Sequence 14, Appl
10	93	100.0	301	2	US-09-188-082-14 Sequence 14, Appl
11	93	100.0	301	2	US-09-364-088-14 Sequence 14, Appl
12	93	100.0	301	2	US-09-102-716-14 Sequence 14, Appl
13	93	100.0	352	2	US-09-203-958A-2 Sequence 2, Appl
14	93	100.0	553	1	US-08-661-052-16 Sequence 16, Appl
15	93	100.0	553	2	US-09-188-082-16 Sequence 16, Appl
16	93	100.0	553	2	US-09-364-088-16 Sequence 16, Appl
17	93	100.0	553	2	US-09-102-716-16 Sequence 16, Appl
18	93	100.0	553	2	US-09-840-459-49 Sequence 49, Appl
19	87	93.5	89	2	US-09-497-625A-49 Sequence 49, Appl
20	87	93.5	98	2	US-09-840-459-38 Sequence 38, Appl
21	87	93.5	98	2	US-09-840-459-38 Sequence 38, Appl
22	87	93.5	98	2	US-09-497-625A-38 Sequence 38, Appl
23	87	93.5	98	2	US-09-497-625A-39 Sequence 39, Appl
24	87	93.5	109	1	US-08-793-490-6 Sequence 6, Appl
25	87	93.5	116	1	US-08-888-366-10 Sequence 10, Appl
26	87	93.5	116	1	US-08-888-366-12 Sequence 12, Appl
27	87	93.5	118	2	US-09-269-332-46 Sequence 46, Appl

#### ALIGNMENTS

28	87	93.5	118	2	US-09-269-332-56	Sequence 56, Appl
29	87	93.5	118	2	US-09-269-332-88	Sequence 88, Appl
30	87	93.5	118	2	US-09-269-332-90	Sequence 90, Appl
31	87	93.5	137	2	US-09-269-332-76	Sequence 76, Appl
32	87	93.5	137	2	US-09-269-332-77	Sequence 77, Appl
33	87	93.5	142	2	US-09-069-628-24	Sequence 24, Appl
34	87	93.5	143	2	US-09-069-628-23	Sequence 23, Appl
35	87	93.5	145	2	US-09-069-628-26	Sequence 26, Appl
36	86	92.5	98	2	US-09-840-459-45	Sequence 45, Appl
37	86	92.5	98	2	US-09-497-625A-45	Sequence 45, Appl
38	84	90.3	120	2	US-09-232-290-42	Sequence 42, Appl
39	84	90.3	456	2	US-09-495-880A-11	Sequence 11, Appl
40	83	89.2	123	1	US-08-356-272-3	Sequence 3, Appl
41	83	89.2	124	2	US-09-518-737-2	Sequence 25, Appl
42	82	88.2	141	2	US-09-069-628-25	Sequence 25, Appl
43	82	88.2	141	2	US-08-875-674A-1	Sequence 1, Appl
44	81	87.1	119	2	US-08-875-674A-3	Sequence 3, Appl
45	81	87.1	159	1	US-08-653-402B-2	Sequence 2, Appl

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RESULT 1
US-08-435-516-1
; Sequence 1, Application US/08435516
; Patent No. 6500931
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO Fc RECEPTORS FOR
; TITLE OF INVENTION: IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
; FILING DATE: 04-NOV-1992; -02-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-435-516-1
;
Query Match      100.0%; Score 93; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 7.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TISDGSSTYTPDSVKG 17
Db      50 TISDGSSTYTPDSVKG 66
;
RESULT 2
US-08-435-516-2
; Sequence 2, Application US/08435516
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Patent No. 6500931  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO Fc RECEPTORS FOR  
NUMBER OF INVENTIONS: IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES  
NUMBER OF SEQUENCES: 28  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384  
FILING DATE: 04-NOV-1992; -02-NOV-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: M1-013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-435-516-2

Query Match 100.0%; Score 93; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 7.5e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPPSVKG 17  
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50 TISDGSYYTPPSVKG 66

RESULT 3  
US-08-435-516-3  
Sequence 3, Application US/08435516  
Patent No. 6500931  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO Fc RECEPTORS FOR  
NUMBER OF INVENTIONS: IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES  
NUMBER OF SEQUENCES: 28  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,516  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384  
FILING DATE: 04-NOV-1992; -02-NOV-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: M1-013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-435-516-3

Query Match 100.0%; Score 93; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 7.5e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPPSVKG 17  
|||  
50 TISDGSYYTPPSVKG 66

RESULT 4  
US-09-344-587-13  
Sequence 13, Application US/09344587  
Patent No. 6331402  
GENERAL INFORMATION:  
APPLICANT: Praest, Gerald  
APPLICANT: Nussbaum, Sabine  
APPLICANT: Moesner, Ellen  
APPLICANT: Lenz, Helmut  
TITLE OF INVENTION: REDUCTION OF INTERFERENCE OF IMMUNASSAYS BY SUBSTANCES  
FILE REFERENCE: BMID 9928 4897/00/US-1m  
CURRENT APPLICATION NUMBER: US/09/344,587  
EARLIER FILING DATE: 1999-06-25  
EARLIER APPLICATION NUMBER: DE 19828466.7  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 123  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-344-587-13

Query Match 100.0%; Score 93; DB 2; Length 123;  
Best Local Similarity 100.0%; Pred. No. 7.7e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPPSVKG 17  
|||  
50 TISDGSYYTPPSVKG 66

RESULT 5  
US-08-661-052-4  
Sequence 4, Application US/08661052  
Patent No. 5837243  
GENERAL INFORMATION:  
APPLICANT: Yaehwan M. Deo  
APPLICANT: Robert Graziano  
APPLICANT: Chazian Somaasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
TITLE OF INVENTION: OF ANTI-Fc RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSER: LAHYE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,052  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-661-052-4

Query Match 100.0%; Score 93; DB 1; Length 300;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYYTPDSYVG 17  
Db 50 TISDGSYYTPDSYVG 66

RESULT 6  
US-09-188-082-4  
Sequence 4, Application US/09188082  
Patent No. 6270765  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo  
APPLICANT: Joel Goldstein  
APPLICANT: Robert Graziano  
APPLICANT: Chezian Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD  
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/188,082  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/661,052  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-188-082-4

Query Match 100.0%; Score 93; DB 2; Length 300;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYYTPDSYVG 17  
Db 50 TISDGSYYTPDSYVG 66

RESULT 7  
US-09-364-088-4  
Sequence 4, Application US/09364088  
Patent No. 6365161  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo, et al.  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD  
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street, 24th Floor  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/364,088  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/188,082  
FILING DATE: 07-JUNE-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remillard, Jane E.  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: MXI-043CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-7414  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-364-088-4

Query Match 100.0%; Score 93; DB 2; Length 300;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYYTPDSYVG 17  
Db 50 TISDGSYYTPDSYVG 66

RESULT 8  
US-09-102-716-4  
Sequence 4, Application US/09102716

Patent No. 6395272  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo  
          Joel Goldstein  
          Robert Graziano  
          Cheslan Somaundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
                    OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/102,716  
FILING DATE: 22-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/661,052  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-102-716-4  
Query Match           100.0%; Score 93; DB 2; Length 300;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db           50   TISDGSYTYYPDSVKG 66  
RESULT 9  
US-08-661-052-14  
Sequence 14, Application US/08661052  
Patent No. 5837243  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo  
          Joel Goldstein  
          Robert Graziano  
          Cheslan Somaundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
                    OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,052  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 301 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-661-052-14  
Query Match           100.0%; Score 93; DB 1; Length 301;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy           1   TISDGSYTYYPDSVKG 17  
              |||||  
Db           69   TISDGSYTYYPDSVKG 85  
RESULT 10  
US-09-188-082-14  
Sequence 14, Application US/09188082  
Patent No. 6270765  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo  
          Joel Goldstein  
          Robert Graziano  
          Cheslan Somaundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
                    OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/188,082  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/661,052  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:

LENGTH: 301 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-188-082-14

Query Match 100.0%; Score 93; DB 2; Length 301;  
Best Local Similarity 100.0%; Pred. No. 2,1e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSYVG 17  
DB 69 TISDGSYYTPDSYVG 85

## RESULT 11

US-09-364-088-14  
Sequence 14, Application US/09364088  
Patent No. 6365161  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo, et al.  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRIS-  
ED TITLE OF INVENTION: OF ANTI-PC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSER: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street, 24th floor  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/364,088  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/188,082  
FILING DATE: 07-JUNE-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remillard, Jane E.  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: MXI-043CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-7414  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 301 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-364-088-14

Query Match 100.0%; Score 93; DB 2; Length 301;  
Best Local Similarity 100.0%; Pred. No. 2,1e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSYVG 17  
DB 69 TISDGSYYTPDSYVG 85

## RESULT 12

US-09-102-716-14  
Sequence 14, Application US/09102716  
Patent No. 6395272

GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo  
Joel Goldstein  
Robert Graziano  
Chezian Somasundaram

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRIS-  
ED TITLE OF INVENTION: OF ANTI-PC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:  
ADDRESSER: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/102,716  
FILING DATE: 22-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/661,052  
FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-5941  
TELEFAX: (617)227-7400  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 301 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-102-716-14

Query Match 100.0%; Score 93; DB 2; Length 301;  
Best Local Similarity 100.0%; Pred. No. 2,1e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSYVG 17  
DB 69 TISDGSYYTPDSYVG 85

RESULT 13  
US-09-203-958A-2  
Sequence 2, Application US/09203958A  
Patent No. 6682928

GENERAL INFORMATION:  
APPLICANT: Keler, Tibor

APPLICANT: GOLDSTEIN, Joel  
APPLICANT: GRAZIANO, Robert

APPLICANT: DEO, Yashwant M.  
TITLE OF INVENTION: CELLS EXPRESSING ANTI-PC RECEPTOR

TITLE OF INVENTION: BINDING COMPONENTS  
FILE REFERENCE: MXI-099CPA  
CURRENT APPLICATION NUMBER: US/09/203,958A

CURRENT FILING DATE: 1998-12-02  
PRIOR APPLICATION NUMBER: 60/067232  
PRIOR FILING DATE: 1997-12-02

NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FaetsEQ for Windows Version 4.0  
SEQ ID NO 2

LENGTH: 352  
TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Synthetic construct  
US-09-203-958A-2

Query Match 100.0%; Score 93; DB 2; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSVKG 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 216 TISDGSYYTPDSVKG 232

## RESULT 14

US-08-661-052-16  
Sequence 16, Application US/08661052  
Patent No. 5837243  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo  
APPLICANT: Joel Goldstein  
APPLICANT: Robert Graziano  
APPLICANT: Chetian Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
ZIP: 02109-1875  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,052  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-661-052-16

Query Match 100.0%; Score 93; DB 1; Length 553;  
Best Local Similarity 100.0%; Pred. No. 4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSVKG 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 69 TISDGSYYTPDSVKG 85

## RESULT 15

US-09-188-082-16  
Sequence 16, Application US/09188082  
Patent No. 6270765  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo

APPLICANT: Joel Goldstein  
APPLICANT: Robert Graziano  
APPLICANT: Chetian Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
ZIP: 02109-1875  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/188,082  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/661,052  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-188-082-16

Query Match 100.0%; Score 93; DB 2; Length 553;  
Best Local Similarity 100.0%; Pred. No. 4e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSVKG 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 69 TISDGSYYTPDSVKG 85

Search completed: November 21, 2005, 12:07:39  
Job time : 7.41392 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 11:50:51 ; Search time 21.0476 Seconds  
(without alignments)  
337.478 Million cell updates/sec

Title: US-10-632-706-157

Perfect score: 93  
Sequence: 1 TISDGSSTYTPDSVKG 17

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 segs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA-Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	17	4	US-10-632-706-141
2	93	100.0	17	4	US-10-632-706-145
3	93	100.0	17	4	US-10-632-706-149
4	93	100.0	17	4	US-10-632-706-153
5	93	100.0	17	4	US-10-632-706-157
6	93	100.0	118	3	US-09-144-886-62
7	93	100.0	118	3	US-09-144-886-63
8	93	100.0	118	4	US-10-632-706-59
9	93	100.0	118	4	US-10-632-706-60
10	93	100.0	120	4	US-10-229-335-1
11	93	100.0	120	4	US-10-229-335-2
12	93	100.0	120	4	US-10-229-335-3
13	93	100.0	120	4	US-10-412-406-2
14	93	100.0	120	4	US-10-412-406-10
15	93	100.0	120	4	US-10-412-406-12
16	93	100.0	120	4	US-10-412-406-14
17	93	100.0	120	4	US-10-412-406-16
18	93	100.0	352	3	US-09-203-958A-2
19	93	100.0	352	5	US-10-764-131-2
20	93	100.0	663	4	US-10-412-406-32
21	93	100.0	4852	4	US-10-412-406-33
22	90	96.8	123	3	US-09-144-886-60
23	90	96.8	123	3	US-10-632-706-57
24	87	93.5	17	4	US-10-281-479A-26
25	87	93.5	17	4	US-10-275-180A-26
26	87	93.5	17	4	US-10-286-132A-26
27	87	93.5	17	4	US-10-477-377-9

28	87	93.5	89	3	US-09-840-499-49	Sequence 49, App1
29	87	93.5	89	4	US-10-766-773-49	Sequence 49, App1
30	87	93.5	89	4	US-10-766-610-49	Sequence 49, App1
31	87	93.5	89	4	US-10-733-563-49	Sequence 49, App1
32	87	93.5	98	3	US-09-840-499-38	Sequence 39, App1
33	87	93.5	98	3	US-09-840-499-39	Sequence 39, App1
34	87	93.5	98	4	US-10-766-773-38	Sequence 39, App1
35	87	93.5	98	4	US-10-766-773-39	Sequence 39, App1
36	87	93.5	98	4	US-10-766-610-38	Sequence 39, App1
37	87	93.5	98	4	US-10-766-610-39	Sequence 39, App1
38	87	93.5	98	4	US-10-733-563-38	Sequence 39, App1
39	87	93.5	98	4	US-10-733-563-39	Sequence 39, App1
40	87	93.5	118	3	US-09-423-800-46	Sequence 56, App1
41	87	93.5	118	3	US-09-423-800-56	Sequence 56, App1
42	87	93.5	118	4	US-10-182-018-46	Sequence 46, App1
43	87	93.5	118	4	US-10-182-018-56	Sequence 46, App1
44	87	93.5	118	4	US-10-169-003-46	Sequence 46, App1
45	87	93.5	118	4	US-10-169-003-56	Sequence 56, App1

#### ALIGNMENTS

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RESULT 1
US-10-632-706-141
; Sequence 141, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSOERPER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-141
Query Match 100.0%; Score 93; DB 4; Length 17;
Best local similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 TISDGSSTYTPDSVKG 17
Db 1 TISDGSSTYTPDSVKG 17
RESULT 2
US-10-632-706-145
; Sequence 145, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSOERPER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
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/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 145
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-145

Query Match      100.0%; Score 93; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TISDGSYYTPDSVKG 17
       |||
Db      1 TISDGSYYTPDSVKG 17

RESULT 3
US-10-632-706-149
/ Sequence 149, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT FILING DATE: 2003-08-01
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 149
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-149

Query Match      100.0%; Score 93; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TISDGSYYTPDSVKG 17
       |||
Db      1 TISDGSYYTPDSVKG 17

RESULT 4
US-10-632-706-153
/ Sequence 153, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT FILING DATE: 2003-08-01
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2

/ SEQ ID NO 153
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-153

Query Match      100.0%; Score 93; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TISDGSYYTPDSVKG 17
       |||
Db      1 TISDGSYYTPDSVKG 17

RESULT 5
US-10-632-706-157
/ Sequence 157, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT FILING DATE: 2003-08-01
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 157
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-157

Query Match      100.0%; Score 93; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TISDGSYYTPDSVKG 17
       |||
Db      1 TISDGSYYTPDSVKG 17

RESULT 6
US-09-144-886-62
/ Sequence 62, Application US/09144886
/ Patent No. US20020155114A1
/ GENERAL INFORMATION:
/ APPLICANT: Marks, James D
/ APPLICANT: Amerdortier, Peter
/ TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
/ TITLE OF INVENTION: Botulinum Neurotoxins
/ FILE REFERENCE: 2500.117USO
/ CURRENT FILING DATE: 2002-08-01
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 98
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 62
/ LENGTH: 118
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
/ OTHER INFORMATION: C39 region VH epitope 2
```

US-09-144-886-62

Query Match 100.0%; Score 93; DB 3; Length 118;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYYPDSVKG 17  
|||||  
DB 50 TISDGSYTYYPDSVKG 66

RESULT 7

US-09-144-886-63  
; Sequence 63, Application US/09144886  
; Patent No. US20020155114A1  
; GENERAL INFORMATION:  
; APPLICANT: Marks, James D  
; APPLICANT: Amersdorfer, Peter  
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize  
; TITLE OF INVENTION: Botulinum Neurotoxins  
; FILE REFERENCE: 2500.117USO  
; CURRENT APPLICATION NUMBER: US/09/144,886  
; CURRENT FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 63  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone  
US-09-144-886-63

Query Match 100.0%; Score 93; DB 3; Length 118;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYYPDSVKG 17  
|||||  
DB 50 TISDGSYTYYPDSVKG 66

RESULT 8

US-10-632-706-59  
; Sequence 59, Application US/10632706  
; Publication No. US20040175385A1  
; GENERAL INFORMATION:  
; APPLICANT: MARKS, JAMES D.  
; APPLICANT: AMERSDORFER, PETER  
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
; TITLE OF INVENTION: NEUROTOXINS  
; FILE REFERENCE: 407T-895120US  
; CURRENT APPLICATION NUMBER: US/10/632,706  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US 60/400,721  
; PRIOR FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: US 09/144,806  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 59  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide primer  
US-10-632-706-59

Query Match 100.0%; Score 93; DB 4; Length 118;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYYPDSVKG 17  
|||||  
DB 50 TISDGSYTYYPDSVKG 66

RESULT 9

US-10-632-706-60  
; Sequence 60, Application US/10632706  
; Publication No. US20040175385A1  
; GENERAL INFORMATION:  
; APPLICANT: MARKS, JAMES D.  
; APPLICANT: AMERSDORFER, PETER  
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
; TITLE OF INVENTION: NEUROTOXINS  
; FILE REFERENCE: 407T-895120US  
; CURRENT APPLICATION NUMBER: US/10/632,706  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US 60/400,721  
; PRIOR FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: US 09/144,806  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 60  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: single chain antibody  
US-10-632-706-60

Query Match 100.0%; Score 93; DB 4; Length 118;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYYPDSVKG 17  
|||||  
DB 50 TISDGSYTYYPDSVKG 66

RESULT 10

US-10-229-335-1  
; Sequence 1, Application US/10229335  
; Publication No. US2003014483A1  
; GENERAL INFORMATION:  
; APPLICANT: MEDAREX, INC.  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR  
; IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES  
; NUMBER OF SEQUENCES: 28  
; STREET: P.O. Box 953, 1545 Route 22 East  
; CITY: Annandale  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 09801  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/229,335  
; FILING DATE: 26-Aug-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,516  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MXI-013  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-229-335-1

Query Match 100.0%; Score 93; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17  
|||  
Db 50 TISDGSYTYPPDSVKG 66

RESULT 11  
US-10-229-335-2  
Sequence 2, Application US/10229335  
Publication No. US2003014483A1  
GENERAL INFORMATION:  
APPLICANT: MEDAREX, INC.  
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR  
IMMUNOBLOBLIN G ON HUMAN MONONUCLEAR PHAGOCYTES  
NUMBER OF SEQUENCES: 28  
STREET: P.O. Box 953, 1545 Route 22 East  
CITY: Annandale  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08801  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/229,335  
FILING DATE: 26-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,516  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-229-335-2

Query Match 100.0%; Score 93; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17  
|||  
Db 50 TISDGSYTYPPDSVKG 66

RESULT 12  
US-10-229-335-3

Sequence 3, Application US/10229335  
Publication No. US2003014483A1  
GENERAL INFORMATION:  
APPLICANT: MEDAREX, INC.  
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR  
IMMUNOBLOBLIN G ON HUMAN MONONUCLEAR PHAGOCYTES  
NUMBER OF SEQUENCES: 28  
STREET: P.O. Box 953, 1545 Route 22 East  
CITY: Annandale  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08801  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/229,335  
FILING DATE: 26-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,516  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 120 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-229-335-3

Query Match 100.0%; Score 93; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17  
|||  
Db 50 TISDGSYTYPPDSVKG 66

RESULT 13  
US-10-412-406-2  
Sequence 2, Application US/10412406  
Publication No. US20040058394A1  
GENERAL INFORMATION:  
APPLICANT: BIOGEN, INC.  
APPLICANT: GARBER, Ellen  
APPLICANT: LYNS, Paul  
APPLICANT: SALDHANA, Jose W.  
TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES  
FILE REFERENCE: BIN1100CN  
CURRENT APPLICATION NUMBER: US/10/412,406  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: 60/240,285  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/275,289  
PRIOR FILING DATE: 2001-03-13  
PRIOR APPLICATION NUMBER: 60/299,987  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: PCT/US01/32140  
PRIOR FILING DATE: 2001-10-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 4.0



SEQ ID NO 2  
LENGTH: 120  
TYPE: PRT  
ORGANISM: murine  
US-10-412-406-2

Query Match 100.0%; Score 93; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSVKG 17  
|||||  
DB 50 TISDGSYYTPDSVKG 66

RESULT 14  
US-10-412-406-10

Sequence 10, Application US/10412406  
Publication No. US20040058394A1  
GENERAL INFORMATION:  
APPLICANT: BIOGEN, INC.  
APPLICANT: GARBER, Ellen  
APPLICANT: LYNE, Paul  
APPLICANT: SALDHANA, Jose W.  
TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES  
FILE REFERENCE: BINA100CN  
CURRENT APPLICATION NUMBER: US/10/412,406  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: 60/240,285  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/275,289  
PRIOR FILING DATE: 2001-03-13  
PRIOR APPLICATION NUMBER: 60/299,987  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: PCT/US01/32140  
PRIOR FILING DATE: 2001-10-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-412-406-10

Query Match 100.0%; Score 93; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSVKG 17  
|||||  
DB 50 TISDGSYYTPDSVKG 66

RESULT 15  
US-10-412-406-12

Sequence 12, Application US/10412406  
Publication No. US20040058394A1  
GENERAL INFORMATION:  
APPLICANT: BIOGEN, INC.  
APPLICANT: GARBER, Ellen  
APPLICANT: LYNE, Paul  
APPLICANT: SALDHANA, Jose W.  
TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES  
FILE REFERENCE: BINA100CN  
CURRENT APPLICATION NUMBER: US/10/412,406  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: 60/240,285  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: 60/275,289  
PRIOR FILING DATE: 2001-03-13  
PRIOR APPLICATION NUMBER: 60/299,987  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: PCT/US01/32140

PRIOR FILING DATE: 2001-10-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 120  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-412-406-12

Query Match 100.0%; Score 93; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSVKG 17  
|||||  
DB 50 TISDGSYYTPDSVKG 66

Search completed: November 21, 2005, 12:33:37  
Job time : 22.0476 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 12:04:27 ; Search time 0.31355 Seconds  
(without alignments)  
61.666 Million cell updates/sec

Title: US-10-632-706-157  
Perfect score: 93  
Sequence: 1 TISDGSYYTPDSVKG 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
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8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	81.7	444	7	US-11-172-320-6
2	55	59.1	125	7	US-11-144-248-16
3	54	58.1	98	1	US-10-789-273-10
4	54	58.1	98	7	US-11-144-248-32
5	54	58.1	121	1	US-10-789-273-9
6	54	58.1	138	1	US-10-789-273-4
7	54	58.1	138	1	US-10-789-273-8
8	54	58.1	138	1	US-10-789-273-12
9	54	58.1	470	7	US-11-144-248-46
10	53	57.0	98	7	US-11-144-248-30
11	53	57.0	473	7	US-11-144-248-50
12	51	54.8	122	7	US-11-144-248-24
13	50	53.8	124	7	US-11-144-248-24
14	50	53.8	250	1	US-10-512-184-27
15	50	53.8	470	7	US-11-144-248-45
16	48	51.6	139	1	US-10-721-763-33
17	43	46.2	174	7	US-11-144-248-4
18	43	46.2	470	7	US-11-144-248-49
19	42	45.2	802	1	US-10-510-386-2
20	41	44.1	120	7	US-11-077-978-7
21	40	43.0	102	1	US-10-997-201A-6
22	39	41.9	605	1	US-10-689-742-140
23	39	39.8	1841	7	US-11-057-058-63
24	37	39.8	258	1	US-10-512-184-26
25	37	39.8	327	1	US-10-512-184-62

26	37	39.8	327	1	US-10-512-184-64	Sequence 64, Appl
27	37	39.8	328	1	US-10-512-184-63	Sequence 63, Appl
28	37	39.8	429	1	US-11-074-176-248	Sequence 248, Appl
29	37	39.8	576	1	US-10-512-184-65	Sequence 65, Appl
30	37	39.8	625	1	US-10-512-184-47	Sequence 47, Appl
31	36	38.7	119	7	US-11-010-954-5	Sequence 5, Appl
32	36	38.7	600	1	US-10-131-826A-462	Sequence 462, Appl
33	36	38.7	1142	7	US-11-109-156-22	Sequence 22, Appl
34	35	37.6	203	1	US-10-510-386-122	Sequence 122, Appl
35	35	37.6	218	7	US-11-180-997-2	Sequence 2, Appl
36	35	37.6	394	1	US-10-131-826A-520	Sequence 520, Appl
37	35	37.6	716	1	US-10-131-826A-512	Sequence 512, Appl
38	35	37.6	1316	7	US-11-091-643-4	Sequence 4, Appl
39	35	37.1	133	7	US-11-010-748A-2	Sequence 2, Appl
40	34.5	37.1	133	7	US-11-010-748A-3	Sequence 3, Appl
41	34.5	37.1	133	7	US-11-010-748A-4	Sequence 4, Appl
42	34.5	37.1	626	1	US-11-010-748A-1	Sequence 1, Appl
43	34	36.6	261	1	US-10-512-184-15	Sequence 35, Appl
44	34	36.6	313	1	US-10-512-184-72	Sequence 72, Appl
45	34	36.6	314	1	US-10-982-545-11	Sequence 11, Appl

## ALIGNMENTS

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RESULT 1
US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Karl
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD4 Antibody Immunconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-172-320-6
Query Match 81.7%; Score 76; DB 7; Length 444;
Best Local Similarity 82.4%; Pred. No. 8.5e-06;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 TISDGSYYTPDSVKG 17
DB 50 TISDGSYYTPDSVKG 66
RESULT 2
US-11-144-248-16
; Sequence 16, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.

```

```
/ APPLICANT: Corvalan, Jose R.
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 125
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-16
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Query Match      59.1%; Score 54; DB 7; Length 125;
Best Local Similarity 68.8%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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```
QY      2 ISDGGSTYTPDSYKG 17
         ||| ||| ||| |||
Db       51 ISGGGSTITYADSVKG 66
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RESULT 3
US-10-789-273-10
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/ Sequence 10, Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Basl, Gurliq
/ APPLICANT: Saldanha, Jose
/ APPLICANT: Vednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
/ FILE REFERENCE: BLN-002CP
/ CURRENT APPLICATION NUMBER: US/10/789,273
/ PRIOR FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: US/10/388,389
/ PRIOR FILING DATE: 2003-03-12
/ PRIOR APPLICATION NUMBER: US 10/010,942
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US 60/251,892
/ PRIOR FILING DATE: 2000-12-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-789-273-10
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Query Match      58.1%; Score 54; DB 1; Length 98;
Best Local Similarity 68.8%; Pred. No. 0.0052;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY      2 ISDGGSTYTPDSYKG 17
         ||| ||| ||| |||
Db       51 ISGGGSTITYADSVKG 66
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RESULT 4
US-11-144-248-32
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/ Sequence 32, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
```

```
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 32
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-32
```

```
Query Match      58.1%; Score 54; DB 7; Length 98;
Best Local Similarity 68.8%; Pred. No. 0.0052;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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```
QY      2 ISDGGSTYTPDSYKG 17
         ||| ||| ||| |||
Db       51 ISGGGSTITYADSVKG 66
```

```
RESULT 5
US-10-789-273-9
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```
/ Sequence 9, Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Basl, Gurliq
/ APPLICANT: Saldanha, Jose
/ APPLICANT: Vednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
/ FILE REFERENCE: BLN-002CP
/ CURRENT APPLICATION NUMBER: US/10/789,273
/ PRIOR FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: US/10/388,389
/ PRIOR FILING DATE: 2003-03-12
/ PRIOR APPLICATION NUMBER: US 10/010,942
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US 60/251,892
/ PRIOR FILING DATE: 2000-12-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 121
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-789-273-9
```

```
Query Match      58.1%; Score 54; DB 1; Length 121;
Best Local Similarity 68.8%; Pred. No. 0.0065;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 ISDGGSTYTPDSYKG 17
         ||| ||| ||| |||
Db       51 ISGGGSTITYADSVKG 66
```

```
RESULT 6
US-10-789-273-4
```

```
/ Sequence 4, Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Basl, Gurliq
/ APPLICANT: Saldanha, Jose
/ APPLICANT: Vednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
/ FILE REFERENCE: BLN-002CP
```

```

CURRENT APPLICATION NUMBER: US/10/789,273
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US/10/388,389
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/010,942
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ IDS: 63
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 138
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-10-789-273-4

```

Query Match	58.1%;	Score 54;	DB 1;	Length 138;
Similarity	58.8%;	Pred. No. 0.0075;		
Best Local				
Matches	10;	Conservative	2;	Mismatches 5;
				Indels 0;
				Gaps 0;

```

QY      1 TISDGGSYTYYPDSVKG 17
        :| || ||| |: |||
Db      69 SIRSGGRTYYSDNVKG 85

```

```

RESULT 7
US-10-789-273-8
; Sequence 8, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldama, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELM-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3d6 heavy chain variable region
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-789-273-8

```

Query Match	58.1%	Score 54;	DB 1;	Length 138;
Best Local Similarity	58.8%	Pred. NO. 0.0075;		
Matches 10;	Conservative	2;	Mismatches 5;	Indels 0;
			Gaps	0

```

QY      1 TISDGGSYTYYPDSVKG 17
          :| | | | | :| | |
Db      69 SIRSGGRTYSDNVKG 85

```

RESULT 8  
US-10-789-273-12  
; Sequence 12, Application US/10789273  
; Publication No. US20050249725A1

```

GENERAL INFORMATION:
APPLICANT: Basl, Gurlyq
APPLICANT: Saldanha, Jose
APPLICANT: Yednock, Ted
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
FILE REFERENCE: ELN-002CP
CURRENT APPLICATION NUMBER: US/10/789, 273
CURRENT FILING DATE: 2004-02-27
PRIORITY APPLICATION NUMBER: US/10/388, 389
PRIORITY FILING DATE: 2003-03-12
PRIORITY APPLICATION NUMBER: US 10/010, 942
PRIORITY FILING DATE: 2001-12-06
PRIORITY APPLICATION NUMBER: US 60/251, 892
PRIORITY FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 138
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Humanized 3d6 light chain variable region
FEATURES:
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-10-789-273-12

```

Query Match	58.1%	Score 54	DB 1	Length 138
Best Local Similarity	58.8%	Pred. Nc	0.0075	
Matches 10	Conservative	2	Mismatches 5	Indels 0
			Gaps	0

```
QY      1 TISDGSYTTYPPDSVKG 17
        :| || ||| |: |||
Db      69 SIRSGGRTYYSDNVKG 85
```

```

1      RESULT 9
2      US-11-144-248--46
3      ; Sequence 46, Application US/11144248
4      ; Publication No. US20050244408A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Cohen, Bruce D.
7      ; APPLICANT: Beebe, Jean
8      ; APPLICANT: Miller, Penelope E.
9      ; APPLICANT: Moyer, James D.
10     ; APPLICANT: Corvajan, Jose R.
11     ; APPLICANT: Gallo, Michael
12     ; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
13     ; FILE REFERENCE: ABX-PF2
14     ; CURRENT APPLICATION NUMBER: US/11/144,248
15     ; CURRENT FILING DATE: 2005-06-02
16     ; PRIOR APPLICATION NUMBER: US/10/038,591
17     ; PRIOR FILING DATE: 2002-01-04
18     ; PRIOR APPLICATION NUMBER: 60/259,927
19     ; PRIOR FILING DATE: 2001-01-05
20     ; NUMBER OF SEQ ID NOS: 60
21     ; SOFTWARE: PatentIn Ver. 2.1
22     ; SEQ ID NO 46
23     ; LENGTH: 470
24     ; TYPE: PRT
25     ; ORGANISM: Homo sapiens
26     ; US-11-144-248--46

```

Query Match	58.1%	Score 54	DB 7	Length 470
Best Local Similarity	68.8%	Pred. No.	0.038	
Matches 11, Conservative	0	Mismatches	5	Indels 0
				Gaps 0

```

QY      2 ISDGGSYTYYPDSVKG 17
          ||| |
Db      70 ISGSGGSTYYADSVKG 85

```

## RESULT 10

```
US-11-144-248-30
/ Sequence 30, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 30
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-30
```

```
Query Match      57.0%; Score 53; DB 7; Length 98;
Best Local Similarity 68.8%; Pred. No. 0.0075;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      2 ISDGSGYTYYPDSVKG 17
Db      51 ISSGSGTYTYADSVKG 66
```

## RESULT 11

```
US-11-144-248-50
/ Sequence 50, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 50
/ LENGTH: 473
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-50
```

```
Query Match      57.0%; Score 53; DB 7; Length 473;
Best Local Similarity 68.8%; Pred. No. 0.04;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      2 ISDGSGYTYYPDSVKG 17
Db      70 ISSGSGTYTYADSVKG 85
```

## RESULT 12

## US-11-144-248-24

```
/ Sequence 24, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-24
```

```
Query Match      54.8%; Score 51; DB 7; Length 122;
Best Local Similarity 62.5%; Pred. No. 0.02;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      2 ISDGSGYTYYPDSVKG 17
Db      51 ITGSGGTYTYADSVKG 66
```

## RESULT 13

```
US-11-144-248-8
/ Sequence 8, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-8
```

```
Query Match      53.8%; Score 50; DB 7; Length 124;
Best Local Similarity 62.5%; Pred. No. 0.029;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      2 ISDGSGYTYYPDSVKG 17
Db      50 ISGSGGTYTYADSVKG 65
```

## RESULT 14

```
US-10-512-184-27
```

```
; Sequence 27, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: gcfv SGB3 with
; OTHER INFORMATION: specificity against Fusarium spp.; originates from
; OTHER INFORMATION: Gallus gallus.
US-10-512-184-27
```

```
Query Match          53.8%; Score 50; DB 1; Length 250;
Best Local Similarity 62.5%; Pred. No. 0.061;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      2  ISDGSYTYYPDSYVG 17
          |||||:||||
Db      53  ISDGSFTGYGAVK 68
```

```
RESULT 15
US-11-144-248-45
; Sequence 45, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PP2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-45
```

```
Query Match          53.8%; Score 50; DB 7; Length 470;
Best Local Similarity 62.5%; Pred. No. 0.12;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
OY      2  ISDGSYTYYPDSYVG 17
          |||||:||||
Db      70  ISGSGTTFYADSVK 85
```

Search completed: November 21, 2005, 12:33:52  
Job time : 1.41136 secs

**This Page Blank (uspio)**



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:32 ; Search time 40.1648 Seconds  
(without alignments)  
328.182 Million cell updates/sec

Title: US-10-632-706-158

Perfect score: 154  
Sequence: 1 QVQLVQSGGVMHPRSLKLSKSGSGPTFS 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_21:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003s:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	30	ADR38764	Adx38764 Mouse hea
2	154	100.0	30	ADR38756	Adx38756 Mouse hea
3	154	100.0	30	ADR38768	Adx38768 Mouse hea
4	154	100.0	30	ADR38760	Adx38760 Mouse hea
5	138	89.6	97	ADY3868	Ady3868 Anti-SARS
6	138	89.6	97	ADY3868	Ady3868 Anti-SARS
7	138	89.6	114	ABE11024	ABE11024 Human ant
8	138	89.6	115	ABE11024	ABE11024 Human ant
9	138	89.6	115	ABE11028	ABE11028 Human ant
10	138	89.6	115	ABE11023	ABE11023 Human ant
11	138	89.6	115	ABE11027	ABE11027 Human ant
12	138	89.6	115	ABE11025	ABE11025 Human ant
13	138	89.6	115	ABE11031	ABE11031 Human ant
14	138	89.6	115	ABE11022	ABE11022 Human ant
15	138	89.6	115	ABE11020	ABE11020 Human ant
16	138	89.6	115	ABE11029	ABE11029 Human ant
17	138	89.6	115	ABE11030	ABE11030 Human ant
18	138	89.6	115	ABE11019	ABE11019 Human ant
19	138	89.6	115	ABE11026	ABE11026 Human ant
20	138	89.6	115	ABE11021	ABE11021 Human ant
21	138	89.6	115	ABE11021	ABE11021 Human ant
22	138	89.6	115	ABE11021	ABE11021 Human ant
23	138	89.6	115	ABE11021	ABE11021 Human ant
24	138	89.6	115	ABE11021	ABE11021 Human ant

25	138	89.6	115	9	AEA08905	AEA08905 Heavy cha
26	138	89.6	115	9	AEA08988	AEA08988 Heavy cha
27	138	89.6	115	9	AEA08911	AEA08911 Heavy cha
28	138	89.6	115	9	AEA08913	AEA08913 Heavy cha
29	138	89.6	115	9	AEA08983	AEA08983 Heavy cha
30	138	89.6	115	9	AEA08994	AEA08994 Heavy cha
31	138	89.6	115	9	AEA08989	AEA08989 Heavy cha
32	138	89.6	115	9	AEA08903	AEA08903 Heavy cha
33	138	89.6	115	9	AEA08995	AEA08995 Heavy cha
34	138	89.6	115	9	AEA08985	AEA08985 Heavy cha
35	138	89.6	115	9	AEA08987	AEA08987 Heavy cha
36	138	89.6	115	9	AEA08915	AEA08915 Heavy cha
37	138	89.6	115	9	AEA08990	AEA08990 Heavy cha
38	138	89.6	115	9	AEA08981	AEA08981 Heavy cha
39	138	89.6	115	9	AEA08985	AEA08985 Heavy cha
40	138	89.6	115	9	AEA08989	AEA08989 Heavy cha
41	138	89.6	115	9	AEA08901	AEA08901 Heavy cha
42	138	89.6	115	9	AEA08982	AEA08982 Heavy cha
43	138	89.6	115	9	AEA08984	AEA08984 Heavy cha
44	138	89.6	115	9	AEA08986	AEA08986 Heavy cha

#### ALIGNMENTS

RESULT 1  
ID ADR38764 standard; peptide, 30 AA.  
XX ADR38764;  
XX  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX  
XX Mouse heavy chain anti-BONT-antibody framework 1 seqid 166.  
XX  
XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
XX framework 1.  
XX  
XX OS Mus sp.  
XX  
XX US2004175385-A1.  
XX  
XX  
XX 09-SEP-2004.  
XX  
XX 01-AUG-2003; 2003US-00632706.  
XX  
XX 31-AUG-1998; 98US-00144886.  
XX 01-AUG-2002; 2002US-0400721P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX Marks JD, Amerdoffer P;  
XX  
XX WPI; 2004-652009/63.  
XX  
XX  
XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
XX useful for diagnosing botulism or for treating pathologies associated  
XX with botulinum neurotoxin poisoning.  
XX  
XX Example 4; SEQ ID NO 166; 110pp; English.  
XX  
XX The invention describes an isolated antibody (I) that specifically binds  
XX to an epitope specifically bound by an antibody expressed by a specific  
XX clone where (I) binds to and neutralises botulinum neurotoxin type A  
XX (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
XX specifically bound by an antibody expressed by a clone chosen from clone  
XX S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WRI(V), WRI(T), 3-1,  
XX 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
XX neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
XX comprising BONT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I) ; and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I) ; and a kit comprising (I). (I) is useful for neutralising  
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain anti-BONT-antibody framework region 1.  
 CC  
 XX  
 SQ Sequence 30 AA;  
 Query Match 100.0%; Score 154; DB 8; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-13;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QVQLVDSGGGVHPGRSLKLSKCSAGSGFTFS 30  
 1 QVQLVDSGGGVHPGRSLKLSKCSAGSGFTFS 30  
 DB 1 QVQLVDSGGGVHPGRSLKLSKCSAGSGFTFS 30  
 RESULT 2  
 ADR38756  
 ID ADR38756 standard; peptide; 30 AA.  
 XX  
 AC ADR38756;  
 DT 02-DEC-2004 (first entry)  
 XX  
 XX Mouse heavy chain anti-BONT-antibody framework 1 segid 158.  
 XX  
 KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
 KW framework 1.  
 XX  
 OS Mus sp.  
 XX  
 PN US2004175385-A1.  
 XX  
 PD 09-SEP-2004.  
 XX  
 PF 01-AUG-2003; 2003US-00632706.  
 XX  
 PR 31-AUG-1998; 98US-00144886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 PI  
 PI Marks JD, Amerdorfer P;  
 DR WPI; 2004-652009/63.  
 DR  
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 XX  
 XX Example 4; SEQ ID NO 158; 110pp; English.  
 XX  
 CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S23, C25, C33, 1C6, 3D12, B4, 1F3, huC25, A1, A2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralises botulinum

CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
 CC comprising BONT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I) ; and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I) ; and a kit comprising (I). (I) is useful for neutralising  
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
 CC enables rapid detection or diagnosis of botulism. This is the amino acid  
 CC sequence of mouse heavy chain anti-BONT-antibody framework region 1.  
 CC  
 XX  
 SQ Sequence 30 AA;  
 Query Match 100.0%; Score 154; DB 8; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-13;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QVQLVDSGGGVHPGRSLKLSKCSAGSGFTFS 30  
 1 QVQLVDSGGGVHPGRSLKLSKCSAGSGFTFS 30  
 DB 1 QVQLVDSGGGVHPGRSLKLSKCSAGSGFTFS 30  
 RESULT 3  
 ADR38768  
 ID ADR38768 standard; peptide; 30 AA.  
 XX  
 AC ADR38768;  
 DT 02-DEC-2004 (first entry)  
 XX  
 XX Mouse heavy chain anti-BONT-antibody framework 1 segid 170.  
 XX  
 KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
 KW framework 1.  
 XX  
 OS Mus sp.  
 XX  
 PN US2004175385-A1.  
 XX  
 PD 09-SEP-2004.  
 XX  
 PF 01-AUG-2003; 2003US-00632706.  
 XX  
 PR 31-AUG-1998; 98US-00144886.  
 PR 01-AUG-2002; 2002US-0400721P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 PI  
 PI Marks JD, Amerdorfer P;  
 DR WPI; 2004-652009/63.  
 DR  
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulism or for treating pathologies associated  
 PT with botulinum neurotoxin poisoning.  
 XX  
 XX Example 4; SEQ ID NO 170; 110pp; English.  
 XX  
 CC The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone

50 Sequence 30 AA;

Query Match	100.0%	Score 154;	DB 8;	Length 30;
Best Local Similarity	100.0%	Pred. No. 2.5e-13;		
Matches	30;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0
QY	1	QVQLVDSGGGVNHPGRSLKLSGASGSPFS	30	
Db	1	QVQLVDSGGGVNHPGRSLKLSGASGSPFS	30	

RESULT 4  
ADR38760  
ID ADR38760 standard; peptide; 30 AA.

DB Mouse heavy chain anti-BONT-antibody framework 1 segid 162.

antibacterial; antibody; botulinum neurotoxin type A; BONT/A; BONT/A neutralising epitope; anti-botulinum neurotoxin antibody; toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain; framework 1.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.  
PR  
vvv

PA (REGC ) UNIV CALIFORNIA.

PI Marks JD, Amersdorfer P;

DR WPI; 2004-652009/63.

PT New Isolated antibody that neutralizes botulinum neurotoxin type A,

PT with botulinum neurotoxin poisoning.

PS Example 4; SEQ ID NO 162; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds

CC clone where (I) binds to and neutralises botulinum neurotoxin type A .

CC clone where (I) binds to and neutralises botulinum neurotoxin type A .

CC clone where (I) binds to and neutralises botulinum neurotoxin type A .

(BoNT/A) An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S23, G39, 1C6, 3D12, B4, 1F3, hMc25, A4.1, A4.2, WR1 (V), WR1 (T), 3-1, 3-8, 3-10 and INGL, where (I) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). Also described are: a polypeptide (II) comprising BoNT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I); producing (I); and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralising BoNT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulinum or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I) enables rapid detection or diagnosis of botulinism. This is the amino acid sequence of mouse heavy chain anti-BoNT-antibody framework region 1.

```

SQ Sequence 30 AA;
Query Match 100.0%; Score 154; DB 8; Length 30;
Best Local Similarity 100.0%; Pval. No. 2.5e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

RESULT 5  
AAB40091  
ID AAB40091 standard; protein; 97 AA.

Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 617.

KM Human: neutralising antibody: interleukin-12; IL-12; antiinflammatory;  
 KM complementarily determining region: CDR; antiinflammatory; antihistitic;  
 KM antisclerotic; neuroprotective; antipoststatic; antiaschematic; cardiac;  
 KM antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KM multiple sclerosis; rheumatoid arthritis.

**OS Homo sapiens.**

PN W0200056772-A1.

PD 28-SEP-2000

PF 24-MAR-2000; 2000WO-US007946.

PR 25-MAR-1999; 99US-0126603P.

PA (BADI ) BASF AG.  
PA (GEMY ) GENETICS INST INC.

PA (GEMY ) GENETICS INST INC.

PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DB, White M;

PI Veidman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;

XX

DR WPI; 2000-638250/61.

PT New human antibody 5

PT. disease and multiple sclerosis.

PT. disease and multiple sclerosis.

PT. disease and multiple sclerosis.

XX PS Claim 75; Page 121; 377pp; English.

XX CC This invention relates to a new human antibody specific for human

CC interleukin-12 (IL-12). The invention also includes antigen binding

CC portions that bind to IL-12. Sequences AA839485-839516 represent human

CC anti-IL-12 antibody heavy and light chain complementarity determining

CC region (CDR) amino acid sequences, and also includes variable region

CC amino acid sequences. Other variable region amino acid sequences are

CC given in AA839517-839560 and AA840068-840149. Sequences AA839561-839771

CC represent anti-IL-12 CDR3 related amino acid sequences, AA839772-840063

CC represent other CDR sequences. Light chain CDR3 consensus sequences are

CC given in AA840064-840067. Primers used in the identification and

CC construction of the antibodies of the invention are given in AAC61062-

CC C61071. The antibody of the invention is a neutralizing antibody and has

CC antineoplastic; antitachytic; antisclerotic; antiinflammatory;

CC neuroprotective; antiparasitic; antischismatic; cardiant; antiparasitic;

CC antibacterial and immunosuppressive activity. The antibodies or antigen-

CC binding fragments are useful in the treatment of disorders associated

CC with detrimental release of human IL-12, especially Crohn's disease,

CC multiple sclerosis and rheumatoid arthritis. They can also be used in the

CC manufacture of a pharmaceutical composition to treat human IL-12

CC disorders

XX SQ Sequence 97 AA;

XX Query Match 89.6%; Score 138; DB 3; Length 97;

XX Best Local Similarity 86.7%; Pred. No. 1.1e-10;

XX Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVDSGGGVVHPGRSLKLSGSGSPTFS 30

DB 1 EVQLVDSGGGVVHPGRSLKLSGSGSPTFS 30

RESULT 6

ADY93868

ID ADY93868 standard; protein; 97 AA.

XX AC ADY93868;

XX DT 16-JUN-2005 (first entry)

XX DB Anti-SARS DP44 germ-line antibody VH region EQ ID NO:18.

XX KW glycoprotein; respiratory-gen.; virucide; sars coronavirus infection;

XX KM antibody; heavy chain variable region.

XX OS SARS coronavirus.

XX PN US2005069869-A1.

XX PD 31-MAR-2005.

XX PF 04-AUG-2004; 2004US-00911838.

XX PR 04-AUG-2003; 2003US-0492529P.

XX PR 09-OCT-2003; 2003US-0510251P.

XX PR 18-FEB-2004; 2004US-0585670P.

XX PR 26-APR-2004; 2004US-0565595P.

XX PA (AMBR/) AMBROSINO D.

XX PA (HERR/) HERNANDEZ H.

XX PA (GREE/) GREENOUGH T.

XX PA (LUZU/) LUZURIAGA K.

XX PA (SOMA/) SOMASUNDARAN M.

XX PA (BABC/) BABCOCK G J.

XX PA (THOM/) THOMAS W D.

XX PA (SULL/) SULLIVAN J.

XX PI Ambrosino D, Hernandez H, Greenough T, Luzuriaga K,

XX PI Somasundaran M, Babcock GJ, Thomas WD, Sullivan J;

DR WPI; 2005-252952/26.

XX PT New isolated nucleic acid encoding a SARS-CoV spike glycoprotein

XX PT polypeptide, and optimized for expression in a human host, useful for

XX PT diagnosing, preventing and/or treating SARS-CoV infection.

XX PS Example 17; SEQ ID NO 18; 138pp; English.

XX CC The invention relates to an isolated nucleic acid comprising a sequence

CC encoding a SARS coronavirus (SARS-CoV) spike glycoprotein (S protein), or

CC its fragment, where the sequence has been optimized for expression in a

CC human host. Also described: (1) a nucleic acid expression vector

CC comprising the above nucleic acid; (2) an isolated cell comprising the

CC expression vector of (1); (3) a polypeptide encoded by the above nucleic

CC acid; (4) an isolated polypeptide comprising an extracellular portion of

CC the SARS-CoV S polypeptide located between amino acids 15-119 of

CC ADY93852, or its fragment; (5) an isolated antibody, or its antigen

CC binding fragment, that specifically binds to the polypeptide of (3); (6)

CC an isolated antibody, or its antigen binding fragment, that specifically

CC binds to an antigen binding fragment of an anti-S protein antibody; (7) a

CC composition comprising a polypeptide of (4) or an antibody, or its

CC antigen binding fragment, and a pharmaceutical carrier; (8) making an S

CC protein, or its fragment, of SARS-CoV; (9) making an antibody, or its

CC antigen binding fragment, that specifically binds to an S protein of SARS

CC -CoV; (10) evaluating a biological sample for the presence of SARS-CoV;

CC (11) evaluating an antibody, or its antigen binding fragment, for

CC inhibition of infection by SARS-CoV; (12) treating a subject at risk for,

CC or exposed to SARS-CoV; (13) an immunocombustible comprising the antibody

CC of (5) linked to a therapeutic agent; (14) an isolated nucleic acid

CC molecule encoding the antibody, its antigen-binding portion, variable

CC heavy chain or variable light chain of (5); (15) an expression vector

CC comprising the nucleic acid molecule of (14); (16) a host cell comprising

CC the expression vector of (15); (17) a transgenic mammal comprising human

CC immunoglobulin heavy and light chain transgenes, where the mouse

CC expresses the antibody of (5); (18) a hybridoma prepared from the mammal

CC of (17), where the hybridoma produces the antibody; and (19) preparing an

CC anti-S protein antibody. The methods and compositions of the present

CC invention are useful for the diagnosis, prevention and/or treatment of

CC SARS-CoV infection. The present sequence represents an anti-SARS antibody

XX heavy chain variable region from the present invention.

XX SQ Sequence 97 AA;

XX Query Match 89.6%; Score 138; DB 9; Length 97;

XX Best Local Similarity 86.7%; Pred. No. 1.1e-10;

XX Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVDSGGGVVHPGRSLKLSGSGSPTFS 30

DB 1 EVQLVDSGGGVVHPGRSLKLSGSGSPTFS 30

RESULT 7

AEAL1024

ID AEAL1024 standard; protein; 114 AA.

XX AC AEAL1024;

XX DT 26-JUL-2005 (first entry)

XX DE Human anti-IL-4R heavy chain variable region, SEQ ID NO:66.

XX KW HIV infection; anti-hiv; infection; inflammation; antiinflammatory;

XX KM cancer; cytostatic; antibody; chimeric antibody;

XX KM heavy chain variable region; antibody engineering; anti-IL-4R.

XX OS Homo sapiens.

XX PN WO2005047325-A2.

XX PD 26-MAY-2005.

XX PF 04-NOV-2004; 2004WO-US037241.

```

PR 07-NOV-2003; 2003US-0517970P.
XX (AMGE-) AMGEN INC.
PA
XX Aldrich T, Shen W, Jacobsen FW, Morris AE, Allen MJ,
PI N-PSDB; AEA11010.
XX MPI; 2005-372347/38.
XX DR
XX N-PSDB; AEA11010.
XX
XX polypeptide having cynomolgus monkey antibody heavy chain variable region
XX or light chain variable region, useful in diagnosing antigen in
XX biological samples, and for treating disease e.g., inflammation and
XX cancer.
XX
XX Example 3; SEQ ID NO 66; 138bp; English.
XX
XX
XX The invention relates to an isolated polypeptide (I) comprising (a) one
XX of 4 sequences: AEA10964, AEA10966, AEA10968 and AEA10970 or
XX AEA10972, and antibody heavy chain variable region, or (b) AEA10968, and
XX antibody light chain variable region. In (I), the antibody heavy chain or
XX light chain variable region is a cynomolgus monkey antibody heavy chain or
XX light chain variable region or cynomolgus monkey antibody light chain variable
XX variable region or cynomolgus monkey antibody light chain variable
XX region. The antibody heavy chain variable region or light chain variable
XX region is a human or mouse antibody heavy chain variable region or light
XX chain variable region. Also included are: an isolated polynucleotide (II)
XX comprising a sequence encoding (I); an isolated antibody (AI) comprising
XX a first polypeptide having SEQ ID No. 6, 8, 10, 12, 14 or 20, and a
XX second polypeptide having SEQ ID No. 30; a method of evaluating (M1) the
XX effects of an antibody, comprising introducing into a cynomolgus monkey
XX chimeric antibody comprising light chain and heavy chain variable regions
XX from an antibody and light chain and heavy chain constant regions from a
XX cynomolgus monkey; and evaluating the effects of the chimeric antibody in
XX the cynomolgus monkey; an expression vector (VI) comprising (II); a cell
XX (III) comprising VI; and a method of producing (I). (AI) further
XX comprises a human antibody heavy chain variable region and a human
XX antibody light chain variable region or a mouse antibody heavy chain
XX variable region and a mouse antibody light chain variable region. (III)
XX is useful for producing a chimeric antibody, which involves incubating
XX (III) under conditions suitable for expression of the chimeric antibody,
XX and isolating the chimeric antibody. (I) or (AI) is useful for diagnosing
XX antigen in biological samples, and for treating diseases such as HIV,
XX inflammation and cancer. The present sequence represents an anti-IL-4R
XX heavy chain variable region used to make the chimeric antibodies of the
XX invention.
XX
XX Sequence 114 AA:
XX
XX Query Match 89.6%; Score 138; DB 9; Length 114;
XX Best Local Similarity 86.7%; Pred. No. 1.3e-10;
XX Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0
XX
XX 1 OVQLVSGGVVHPRSLKSCAGSGPTFS 30
XX :|||||||:|||||||
XX 1 EVQLVSGGGLVHPGSLRLSCAGSGPTFS 30
XX
XX
XX RESULT 8
XX ABB07232
XX ID ABB07232 standard; protein; 115 AA.
XX AC ABB07232;
XX XX
XX DT 26-MAR-2002 (first entry)
XX
XX Anti-IL-4 receptor MAb 12B5 heavy chain variable region.
XX
XX Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;
XX antitickling; dermatological; anticancer; antiinflammatory; cytostatic;
XX antitumoric; immunosuppressive; tuberculostatic; ophthalmological;
XX antineuric; antithyroid.
XX
XX Homo sapiens.
XX OS

```

XX	Key	Location/Qualifiers
FH	Region	31..35
FT	Region	/note= "complementarity determining region (CDR) 1"
FT	Region	50..65
FT	Region	/note= "complementarity determining region (CDR) 2"
FT	Region	98..104
FT	Region	/note= "complementarity determining region (CDR) 3"
XX		
PN	WO200192340-A2.	
PD		
XX	06-DEC-2001.	
PF		
XX	25-MAY-2001; 2001WO-US017094.	
PR		
PR	26-MAY-2000; 2000US-00579808.	
PR	19-SEP-2000; 2000US-00665343.	
PR	15-FEB-2001; 2001US-00785934.	
PR	01-MAY-2001; 2001US-00847816.	
PA	(IMMUNEX CORP.	
PX		
PI	Plumneke JD;	
XX		
DR	WPI; 2002-114332/15.	
DR	N-PSTDB; ABA94332.	
XX		
PT	Novel human antibody which binds human interleukin (IL)-4 receptor and is capable of inhibiting IL-4 induced biological activity, functions as IL-4 antagonist and is useful for treating septic arthritis, scleroderma.	
PS	Claim 4; Page 75-76; 85pp; English.	
XX		
CC	The invention relates to a human antibody (an interleukin (IL)-4 antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of inhibiting an IL-4-induced biological activity. (I) is also useful for inhibiting both IL-4-induced biological activity and IL-13-induced biological activity in vivo in a human, and for treating septic arthritis in a human afflicted with septic arthritis. (I) is also used for treating conditions such as septic/reactive arthritis, dermatitis herpetiformis, urticaria (especially chronic idiopathic urticaria), ulcers, gastric inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease, inflammatory bowel disease, other disorders of the digestive system in which IL-4 plays a role (e.g., IL-4-induced inflammation of part of the gastrointestinal tract), conditions in which IL-4-induced barrier disruption plays a role (e.g. conditions characterized by decreased epithelial barrier function in the lung or gastrointestinal tract), scleroderma, hypertrophic scarring, Whipple's disease, benign prostate hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to medication, Kawasaki disease, sickle cell disease or crisis, Churg-Strauss syndrome, Grave's disease, pre-eclampsia, Sjogren's syndrome, autoimmune lymphoproliferative syndrome, autoimmune haemolytic anemia, Barrett's esophagus, autoimmune uveitis, tuberculosis, nephrosis, pemphigus vulgaris or bullous pemphigoid (autoimmune blistering diseases), and myasthenia gravis (an autoimmune muscular disease). IL-4 antagonists also find use as adjuvants to allergy immunotherapy and as vaccine adjuvants, especially when directed the immune response toward a T <sub>H</sub> 1 response would be beneficial in treating or preventing the disease. The present sequence represents an anti-IL-4 receptor monoclonal antibody (MAb) 12B5 heavy chain variable region	
XX		
SQ	Sequence 115 AA;	
Query Match	89.6%; Score 138; DB 5; Length 115;	
Best Local Similarity	86.7%; Pred. No. 1.4e-10;	
Matches	26; Conservative 3; Mismatches 1; Indels 0; Gaps 0	
Gy	1 QVQLVQSGGGLVHPGRSLKLSGAGSGFFTS 30 :     ::   :	
Dh	1 RVQLVDSGGGLVHPGGSRLRLSCAGSGFFTS 30 :     ::   :	

RESULT 9

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ID AEA11028
AC AEA11028 standard; protein, 115 AA.
AD AEA11028;
XX AEA11028;
DT 28-JUN-2005 (first entry)
DE Human anti-IL-4R heavy chain variable region, SEQ ID NO:70.
XX
XX HIV infection; anti-hiv, infection; inflammation; antiinflammatory;
XX cancer; cytostatic; antibody; chimeric antibody;
XX heavy chain variable region; antibody engineering; anti-IL-4R.
XX
XX Homo sapiens.
XX
XX WO2005047325-A2.
XX
XX 26-MAY-2005.
XX
XX 04-NOV-2004; 2004WO-US037241.
XX
XX 07-NOV-2003; 2003US-0517970P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Aldrich T, Shen W, Jacobsen FW, Morris AE, Allen MJ;
XX
XX WPI; 2005-372347/38.
XX
XX N-PSDB; AEA11014.
XX
XX
XX polypeptide having cynomolgus monkey antibody heavy chain variable region
XX or light chain variable region, useful in diagnosing antigen in
XX biological samples, and for treating disease e.g., inflammation and
XX cancer.
XX
XX
XX Example 3; SEQ ID NO 70; 138pp; English.
XX
XX
XX The invention relates to an isolated polypeptide (I) comprising (a) one
XX of 4 sequences: AEA10964, AEA10966, AEA10968 and AEA10970 or
XX AEA10972, and antibody heavy chain variable region, or (b) AEA10988, and
XX antibody light chain variable region. In (I), the antibody heavy chain or
XX light chain variable region is a cynomolgus monkey antibody heavy chain
XX variable region or cynomolgus monkey antibody light chain variable
XX region. The antibody heavy chain variable region or light chain variable
XX region is a human or mouse antibody heavy chain variable region or light
XX chain variable region. Also included are: an isolated polynucleotide (II)
XX comprising a sequence encoding (I); an isolated antibody (A1) comprising
XX a first polypeptide having SEQ ID No. 6, 8, 10, 12, 14 or 20, and a
XX second polypeptide having SEQ ID No. 30; a method of evaluating (M1) the
XX effects of an antibody, comprising introducing into a cynomolgus monkey a
XX chimeric antibody comprising light chain and heavy chain variable regions
XX from an antibody and light chain and heavy chain constant regions from a
XX cynomolgus monkey; and evaluating the effects of the chimeric antibody in
XX the cynomolgus monkey; an expression vector (VI) comprising (II); a cell
XX (III) comprising VI; and a method of producing (I). (A1) further
XX comprises a human antibody heavy chain variable region and a human
XX antibody light chain variable region or a mouse antibody heavy chain
XX variable region and a mouse antibody light chain variable region. (III)
XX is useful for producing a chimeric antibody, which involves incubating
XX (III) under conditions suitable for expression of the chimeric antibody,
XX and isolating the chimeric antibody. (I) or (A1) is useful for diagnosing
XX antigen in biological samples, and for treating diseases such as HIV,
XX inflammation and cancer. The present sequence represents an anti-IL-4R
XX heavy chain variable region used to make the chimeric antibodies of the
XX invention.
XX
XX Sequence 115 AA;
XX
XX Query Match 89.6%; Score 138; DB 9; Length 115;
XX Best Local Similarity 86.7%; Pred. No. 1.4e-10;
XX Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0

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Db 1 EVOLVSGGGLVHPGGSIRLSCAGSGFTFS 30

RESULT 10  
ID AEA11023  
AEA11023 standard; protein; 115 AA.  
XX AEA11023;  
DT 28-JUL-2005 (first entry)  
DE Human anti-IL-4R heavy chain variable region, SEQ ID NO:65.  
XX HIV infection; anti-hiv; infection; inflammatory; anti-inflammatory;  
XX cancer; cytostatic; antibody; chimeric antibody;  
XX heavy chain variable region; antibody engineering; anti-IL-4R.  
XX Homo sapiens.  
XX MO2005047325-A2.  
XX PN 26-MAY-2005.  
XX PD 04-NOV-2004; 2004WO-US037241.  
XX PF 07-NOV-2003; 2003US-0517970P.  
XX PR (AMGE-) AMGEN INC.  
XX PA Aldrich T, Shen W, Jacobsen FW, Morris AE, Allen MJ;  
PI WPI; 2005-372347/38.  
XX DR N-PSDB; AEA11009.  
PT Polypeptide having cynomolgus monkey antibody heavy chain variable region  
PT or light chain variable region, useful in diagnosing antigen in  
PT biological samples, and for treating disease e.g., inflammation and  
XX cancer.  
XX PT  
PS Example 3; SEQ ID NO 65; 138pp; English.  
XX CC The invention relates to an isolated polypeptide (I) comprising (a) one  
XX of 4 sequences: AEA10964, AEA10966, AEA10968 and AEA10970 or  
XX AEA10972; and antibody heavy chain variable region, or (b) AEA10988, and  
XX antibody light chain variable region. In (I), the antibody heavy chain or  
XX light chain variable region is a cynomolgus monkey antibody heavy chain  
XX variable region or cynomolgus monkey antibody light chain variable  
XX region. The antibody heavy chain variable region or light chain variable  
XX region is a human or mouse antibody heavy chain variable region or light  
XX chain variable region. Also included are: an isolated polynucleotide (II)  
XX comprising a sequence encoding (I); an isolated antibody (A1) comprising  
XX a first polypeptide having SEQ ID No. 6, 8, 10, 12, 14 or 20, and a  
XX second polypeptide having SEQ ID No. 30; a method of evaluating (M1) the  
XX effects of an antibody, comprising introducing into a cynomolgus monkey a  
XX chimeric antibody comprising light chain and heavy chain variable regions  
XX from an antibody and antibody light chain and heavy chain constant regions from a  
XX cynomolgus monkey, and evaluating the effects of the chimeric antibody in  
XX the cynomolgus monkey; an expression vector (VI) comprising (II); a cell  
XX (III) comprising VI; and a method of producing (I). (A1) further  
XX comprises a human antibody heavy chain variable region and a human  
XX antibody light chain variable region or a mouse antibody heavy chain  
XX variable region and a mouse antibody light chain variable region. (III)  
XX is useful for producing a chimeric antibody, which involves incubating  
XX (III) under conditions suitable for expression of the chimeric antibody,  
XX and isolating the chimeric antibody. (I) or (A1) is useful for diagnosing  
XX antigen in biological samples, and for treating diseases such as HIV,  
XX inflammation and cancer. The present sequence represents an anti-IL-4R  
XX heavy chain variable region used to make the chimeric antibodies of the  
XX invention.  
XX Sequence 115 AA;  
XX





is useful for producing a chimeric antibody, which involves incubating (iii) under conditions suitable for expression of the chimeric antibody, and isolating the chimeric antibody (i) or (ai) is useful for diagnosing antigen in biological samples, and for treating diseases such as HIV, inflammation and cancer. The present sequence represents an anti-IL-4R heavy chain variable region used to make the chimeric antibodies of the invention.

XX Sequence 115 AA;

Query Match 89.6%; Score 138; DB 9; Length 115;

Best Local Similarity 86.7%; Pred. No. 1,4e-10; Mismatches 26; Conservative 3; Indels 0; Gaps 0;

1 QVQLVQSGGIVHPGRLKISCSAGSGFTFS 30  
1 EVQLVQSGGIVHPGSLRLSCAGSGFTFS 30

#### RESULT 13

AEAI1031 standard; protein; 115 AA.

XX AEA11031;

XX 28-JUL-2005 (first entry)

XX Human anti-IL-4R heavy chain variable region, SEQ ID NO:73.

XX HIV infection; anti-hiv; infection; inflammation; antiinflammatory;

XX cancer; cytostatic; antibody; chimeric antibody;

XX heavy chain variable region; antibody engineering; anti-IL-4R.

XX Homo sapiens.

XX WO2005047325-A2.

XX 26-MAY-2005.

XX 04-NOV-2004; 2004WO-US037241.

XX 07-NOV-2003; 2003US-0517970P.

XX (AMGE-) AMGEN INC.

XX Aldrich T, Shen W, Jacobsen FW, Morris AE, Allen MJ;

XX WPI; 2005-372347/38.

XX N-PSDB; AEA11017.

XX Polypeptide having cynomolgus monkey antibody heavy chain variable region or light chain variable region, useful in diagnosing antigen in biological samples, and for treating disease e.g., inflammation and cancer.

XX Example 3; SEQ ID NO 73; 138pp; English.

XX The invention relates to an isolated polypeptide (i) comprising (a) one of 4 sequences: AEA10964, AEA10966, AEA10968 and AEA10970 or AEA10972, and antibody heavy chain variable region, or (b) AEA10988, and antibody light chain variable region. In (i), the antibody heavy chain or light chain variable region is a cynomolgus monkey antibody heavy chain variable region or cynomolgus monkey antibody light chain variable region. The antibody heavy chain variable region or light chain variable region is a human or mouse antibody heavy chain variable region or light chain variable region. In (i), the antibody heavy chain or light chain variable region is a cynomolgus monkey antibody heavy chain variable region or cynomolgus monkey antibody light chain variable region. The antibody heavy chain variable region or light chain variable region is a human or mouse antibody heavy chain variable region or light chain variable region. Also included are: an isolated polynucleotide (ii) comprising a sequence encoding (i); an isolated antibody (ai) comprising a first polypeptide having SEQ ID No. 6, 8, 10, 12, 14 or 20, and a second polypeptide having SEQ ID No. 30; a method of evaluating (iii) the effects of an antibody, comprising introducing into a cynomolgus monkey a chimeric antibody comprising light chain and heavy chain variable regions from an antibody and light chain and heavy chain constant regions from a cynomolgus monkey, and evaluating the effects of the chimeric antibody in

the cynomolgus monkey; an expression vector (vi) comprising (ii); a cell (iii) comprising vi; and a method of producing (i). (ai) further comprises a human antibody heavy chain variable region and a human antibody light chain variable region or a mouse antibody heavy chain variable region and a mouse antibody light chain variable region. (iii) is useful for producing a chimeric antibody, which involves incubating (iii) under conditions suitable for expression of the chimeric antibody, and isolating the chimeric antibody. (i) or (ai) is useful for diagnosing antigen in biological samples, and for treating diseases such as HIV, inflammation and cancer. The present sequence represents an anti-IL-4R heavy chain variable region used to make the chimeric antibodies of the invention.

XX Sequence 115 AA;

Query Match 89.6%; Score 138; DB 9; Length 115;

Best Local Similarity 86.7%; Pred. No. 1,4e-10; Mismatches 26; Conservative 3; Indels 0; Gaps 0;

1 QVQLVQSGGIVHPGRLKISCSAGSGFTFS 30  
1 EVQLVQSGGIVHPGSLRLSCAGSGFTFS 30

#### RESULT 14

AEAI1022 standard; protein; 115 AA.

XX AEA11022;

XX 28-JUL-2005 (first entry)

XX Human anti-IL-4R heavy chain variable region, SEQ ID NO:64.

XX HIV infection; anti-hiv; infection; inflammation; antiinflammatory;

XX cancer; cytostatic; antibody; chimeric antibody;

XX heavy chain variable region; antibody engineering; anti-IL-4R.

XX Homo sapiens.

XX WO2005047325-A2.

XX 26-MAY-2005.

XX 04-NOV-2004; 2004WO-US037241.

XX 07-NOV-2003; 2003US-0517970P.

XX (AMGE-) AMGEN INC.

XX Aldrich T, Shen W, Jacobsen FW, Morris AE, Allen MJ;

XX WPI; 2005-372347/38.

XX N-PSDB; AEA11008.

XX Polypeptide having cynomolgus monkey antibody heavy chain variable region or light chain variable region, useful in diagnosing antigen in biological samples, and for treating disease e.g., inflammation and cancer.

XX Example 3; SEQ ID NO 64; 138pp; English.

XX The invention relates to an isolated polypeptide (i) comprising (a) one of 4 sequences: AEA10964, AEA10966, AEA10968 and AEA10970 or AEA10972, and antibody heavy chain variable region, or (b) AEA10988, and antibody light chain variable region. In (i), the antibody heavy chain or light chain variable region is a cynomolgus monkey antibody heavy chain variable region or cynomolgus monkey antibody light chain variable region. The antibody heavy chain variable region or light chain variable region is a human or mouse antibody heavy chain variable region or light chain variable region. Also included are: an isolated polynucleotide (ii) comprising a sequence encoding (i); an isolated antibody (ai) comprising a first polypeptide having SEQ ID No. 6, 8, 10, 12, 14 or 20, and a



CC second polypeptide having SEQ ID No. 30; a method of evaluating (M1) the  
 CC effects of an antibody, comprising introducing into a cynomolgus monkey a  
 CC chimeric antibody comprising light chain and heavy chain variable regions  
 CC from an antibody and light chain and heavy chain constant regions from a  
 CC cynomolgus monkey, and evaluating the effects of the chimeric antibody in  
 CC the cynomolgus monkey; an expression vector (VI) comprising (II); a cell  
 CC comprising a human antibody heavy chain variable region and a human  
 CC antibody light chain variable region or a mouse antibody heavy chain  
 CC variable region and a mouse antibody light chain variable region. (III)  
 CC is useful for producing a chimeric antibody, which involves incubating  
 CC (III) under conditions suitable for expression of the chimeric antibody,  
 CC and isolating the chimeric antibody. (I) or (A1) is useful for diagnosing  
 CC antigen in biological samples, and for treating diseases such as HIV,  
 CC inflammation and cancer. The present sequence represents an anti-IL-4R  
 CC heavy chain variable region used to make the chimeric antibodies of the  
 CC invention.

XX Sequence 115 AA;

Query Match 89.6%; Score 138; DB 9; Length 115;

Best Local Similarity 86.7%; Pred. No. 1.4e-10;

Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVQSGGIVHPRGSLKSCAGSGFTFS 30

DB 1 EVQLVQSGGIVHPRGSLKSCAGSGFTFS 30

RESULT 15

AEAI1020  
 ID AEA11020 standard; protein; 115 AA.

XX AEA11020;

DT 28-JUL-2005 (first entry)

XX Human anti-IL-4R heavy chain variable region, SEQ ID NO:62.

DE HIV infection; anti-HIV; infection; inflammation; anti-inflammatory;

XX cancer; cytosol; antibody; chimeric antibody;

KW heavy chain variable region; antibody engineering; anti-IL-4R.

XX Homo sapiens.

OS WO2005047325-A2.

XX 26-MAY-2005.

XX 04-NOV-2004; 2004WO-US037241.

XX 07-NOV-2003; 2003US-0517970P.

XX (AMGE-) AMGEN INC.

PI Aldrich T, Shen W, Jacobsen FW, Morris AE, Allen MJ;

XX MPI: 2005-372347/38.

DR N-PSDB; AEA11006.

XX Polypeptide having cynomolgus monkey antibody heavy chain variable region  
 PT or light chain variable region, useful in diagnosing antigen in  
 PT biological samples, and for treating disease e.g., inflammation and  
 PT cancer.

XX Example 3, SEQ ID NO 62, 138pp, English.

PS The invention relates to an isolated polypeptide (I) comprising (a) one  
 CC of 4 sequences: AEA10964, AEA10966, AEA10968 and AEA10970 or  
 CC AEA10972, and antibody heavy chain variable region, or (b) AEA10988, and  
 CC antibody light chain variable region. In (I), the antibody heavy chain or  
 CC light chain variable region is a cynomolgus monkey antibody heavy chain  
 CC variable region or cynomolgus monkey antibody light chain variable

CC region. The antibody heavy chain variable region or light chain variable  
 CC region is a human or mouse antibody heavy chain variable region or light  
 CC chain variable region. Also included are: an isolated polynucleotide (II)  
 CC comprising a sequence encoding (I); an isolated antibody (A1) comprising  
 CC a first polypeptide having SEQ ID No. 6, 8, 10, 12, 14 or 20, and a  
 CC second polypeptide having SEQ ID No. 30; a method of evaluating (M1) the  
 CC effects of an antibody, comprising introducing into a cynomolgus monkey a  
 CC chimeric antibody comprising light chain and heavy chain variable regions  
 CC from an antibody and light chain and heavy chain constant regions from a  
 CC cynomolgus monkey, and evaluating the effects of the chimeric antibody in  
 CC the cynomolgus monkey; an expression vector (VI) comprising (II); a cell  
 CC comprising a human antibody heavy chain variable region and a human  
 CC antibody light chain variable region or a mouse antibody heavy chain  
 CC variable region and a mouse antibody light chain variable region. (III)  
 CC is useful for producing a chimeric antibody, which involves incubating  
 CC (III) under conditions suitable for expression of the chimeric antibody,  
 CC and isolating the chimeric antibody. (I) or (A1) is useful for diagnosing  
 CC antigen in biological samples, and for treating diseases such as HIV,  
 CC inflammation and cancer. The present sequence represents an anti-IL-4R  
 CC heavy chain variable region used to make the chimeric antibodies of the  
 CC invention.

XX Sequence 115 AA;

Query Match 89.6%; Score 138; DB 9; Length 115;

Best Local Similarity 86.7%; Pred. No. 1.4e-10;

Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVQSGGIVHPRGSLKSCAGSGFTFS 30

DB 1 EVQLVQSGGIVHPRGSLKSCAGSGFTFS 30

Search completed: November 21, 2005, 12:20:03  
 Job time : 41.1648 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 ; Search time 7.30769 Seconds  
(without alignments)  
394.395 Million cell updates/sec

Title: US-10-632-706-158

Sequence: 1 QVQLVQSGGSGVHPGRSLRLSCAGSGFTFS 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	89.6	116	2 S12557	Ig heavy chain - h
2	137	89.0	119	1 GIHUNI	Ig heavy chain V-I
3	137	89.0	121	2 S19666	Ig heavy chain V r
4	134	87.0	94	2 PLO120	Ig heavy chain V-I
5	134	87.0	98	2 PLO116	Ig heavy chain V-I
6	134	87.0	98	2 S29546	Ig heavy chain V-I
7	134	87.0	113	2 S57410	Ig heavy chain V-J
8	134	87.0	113	2 S38490	Ig heavy chain V-J
9	134	87.0	118	2 S31116	Ig heavy chain - h
10	134	87.0	119	2 S31111	Ig heavy chain - h
11	134	87.0	119	2 F36005	Ig heavy chain V r
12	134	87.0	120	2 S31112	Ig heavy chain - h
13	134	87.0	121	2 S36005	Ig heavy chain V r
14	134	87.0	122	2 S31117	Ig heavy chain - h
15	134	87.0	122	2 E36005	Ig heavy chain V r
16	134	87.0	122	2 S31119	Ig heavy chain - h
17	134	87.0	128	2 S48797	Ig heavy chain V r
18	134	87.0	130	2 S31601	Ig heavy chain V r
19	134	87.0	130	2 PLO098	Ig heavy chain pre
20	134	87.0	132	2 S31603	Ig heavy chain V r
21	134	87.0	133	2 S31590	Ig heavy chain V-I
22	134	87.0	133	2 A39028	Ig heavy chain V-I
23	134	87.0	134	2 S31679	Ig heavy chain V r
24	134	87.0	137	2 S31701	Ig heavy chain V r
25	134	87.0	139	2 S31674	Ig heavy chain V r
26	131	85.1	97	2 S44115	Ig heavy chain V r
27	131	85.1	114	2 S46390	Ig heavy chain V-I
28	131	85.1	122	1 M3HUMA	Ig heavy chain V-I
29	130	84.4	97	2 S26886	Ig heavy chain V r

30	130	84.4	120	2 S36273	Ig heavy chain V r
31	130	84.4	127	2 S38489	Ig heavy chain - h
32	129	83.8	96	2 PH0873	Ig heavy chain V r
33	128	83.1	115	2 S57445	Ig heavy chain V-J
34	128	83.1	151	2 A60943	Ig heavy chain pre
35	127	82.5	98	2 S29543	Ig heavy chain V r
36	127	82.5	134	2 S31688	Ig heavy chain V r
37	127	82.5	135	2 S31598	Ig heavy chain V r
38	127	82.5	140	2 S70442	Ig heavy chain pre
39	126	81.8	123	2 S38493	Ig heavy chain - h
40	126	81.8	134	2 S31699	Ig heavy chain V r
41	125	81.2	97	2 S26885	Ig heavy chain V-I
42	125	81.2	121	1 GIHUNI	Ig heavy chain V-I
43	125	81.2	122	1 M3HUMA	Ig heavy chain V-I
44	125	81.2	126	1 GIHUNI	Ig heavy chain V-I
45	125	81.2	127	2 S19878	Ig heavy chain V r

## ALIGNMENTS

## RESULT 1

S12557  
Ig heavy chain - human (fragment)

C/Date: 21-Nov-1993 #sequence\_revision 13-Mar-1997 #text\_change 21-Jan-2000

C/Accession: S12557

R/Macnude, F.; Shin, E.K.; Hirabayashi, Y.; Nagaoka, H.; Yoshida, M.C.; Zong, S.Q.; Honji

EMBO J. 9, 2501-2506, 1990

A/Title: Organization of variable region segments of the human immunoglobulin heavy chain

nt8.

A/Reference number: S12557; MUID:90316107; PMID:2114977

A/Accession: S12557

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-116 <MAT>

A/Cross-references: UNIPARC:UPI000013D80E

A/Superfamily: Immunoglobulin V region; Immunoglobulin homology

F/34-116/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 89.6%; Score 138; DB 2; Length 116;

Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db

1 QVQLVQSGGSGVHPGRSLRLSCAGSGFTFS 30

20 RVQLVQSGGSGVHPGRSLRLSCAGSGFTFS 49

RESULT 2

GIHUNI

Ig heavy chain V-III region (Nie) - human

C/Species: Homo sapiens (man)

C/Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004

C/Accession: A91668; A02053

R/Ponstingl, H.; Hilschmann, N.

Hoppe-Sejler's Z. Physiol. Chem. 357, 1571-1604, 1976

A/Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

igen Primärstruktur.

A/Reference number: A91668; MUID:77070269; PMID:826475

A/Accession: A91668

A/Molecule type: protein

A/Residues: 1-119 <PON>

A/Cross-references: UNIPROT:P01770; UNIPARC:UPI000012CEFA

A/Note: the sequence of the gamma-1 C region of this chain is also given

R/Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hoppe-Sejler's Z. Physiol. Chem. 357, 1515-1940, 1976

A/Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob

embroider cleavage products, and the disulfide bridges.

A/Reference number: A91667; MUID:77070267; PMID:1002129

A/Accession: A91667

C/Comment: This chain was isolated from an IgG1 myeloma protein.

A:Gene: GDB:IGHV  
A:Cross-references: GDB:128528; OMIM:147070  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyroglutamic acid (Gln) #status experimental  
F:23-96/Disulfide bonds: #status experimental

Query Match 89.0%; Score 137; DB 1; Length 119;  
Best Local Similarity 90.0%; Pred. No. 2.6e-11;  
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSGAGSFTFS 30  
DB 1 QVQLVSGGCVVHPGRSLKLSGAGSFTFS 30

## RESULT 3

S19666  
Ig heavy chain V region (VH3JH4) - human  
C:Species: Homo sapiens (man)  
C>Date: 22-Jan-1993 #sequence\_rev1sion 22-Jan-1993 #text\_change 20-Jun-2000  
C:Accession: S19666  
R:Markes, J.D.; Hoozenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 227, 581-597, 1991  
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage  
A:Reference number: S19663; MUID:92085276; PMID:11748994  
A:Accession: S19666  
A:Molecule type: mRNA  
A:Residues: 1-121 <MM>  
A:Cross-references: UNIPARC:UPI0000115F55; EMBL:X61646; NID:937688; PIDN:CAA43827.1; PIDF:15-98/Domain: immunoglobulin homology <IMM>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 89.0%; Score 137; DB 2; Length 121;  
Best Local Similarity 90.0%; Pred. No. 2.7e-11;  
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSGAGSFTFS 30  
DB 1 QVQLVSGGCVVHPGRSLKLSGAGSFTFS 30

## RESULT 4

PL0120  
Ig heavy chain V-III region (TD-Vo) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 07-Jun-1990 #sequence\_rev1sion 07-Jun-1990 #text\_change 31-Dec-2004  
C:Accession: PL0120  
R:Bird, J.; Gallil, N.; Link, M.; Stites, D.; Sklar, J.  
J. Exp. Med. 168, 229-245, 1988  
A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A:Reference number: PL0116; MUID:88286083; PMID:2840480  
A:Accession: PL0120  
A:Molecule type: mRNA  
A:Residues: 1-94 <BR>  
A:Cross-references: UNIPROT:Q8WTK1; UNIPROT:Q9UJ93; UNIPARC:UPI0000176A2C  
A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL  
A:Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement  
C:Superfamily: immunoglobulin homology  
C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin  
F:31-35/Region: complementarity-determining 1  
F:43-65/Region: complementarity-determining 2

Query Match 87.0%; Score 134; DB 2; Length 94;  
Best Local Similarity 86.7%; Pred. No. 5.3e-11;  
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSGAGSFTFS 30  
DB 1 QVQLVSGGCVVHPGRSLKLSGAGSFTFS 30

## RESULT 5

PL0116  
Ig heavy chain V-III region (AW-Vx) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 07-Jun-1990 #sequence\_rev1sion 07-Jun-1990 #text\_change 23-Jul-1999  
C:Accession: PL0116; S26892  
R:Bird, J.; Gallil, N.; Link, M.; Stites, D.; Sklar, J.  
J. Exp. Med. 168, 229-245, 1988

Query Match 87.0%; Score 134; DB 2; Length 98;  
Best Local Similarity 86.7%; Pred. No. 5.5e-11;  
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSGAGSFTFS 30  
DB 1 QVQLVSGGCVVHPGRSLKLSGAGSFTFS 30

S29546  
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 07-Jan-1994 #sequence\_rev1sion 17-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S29546; S26888  
R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S29543  
A:Accession: S29546  
A:Molecule type: DNA  
A:Residues: 1-98 <TO>  
A:Cross-references: UNIPARC:UPI00002DD16; EMBL:Z17394; NID:932843; PIDN:CAA78997.1; PIDF:15-98/Domain: immunoglobulin homology <IMM>  
C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin  
F:31-35/Region: complementarity-determining 1  
F:49-65/Region: complementarity-determining 2

Query Match 87.0%; Score 134; DB 2; Length 98;  
Best Local Similarity 86.7%; Pred. No. 5.5e-11;  
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSGAGSFTFS 30  
DB 1 QVQLVSGGCVVHPGRSLKLSGAGSFTFS 30

## RESULT 6

S29546  
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 07-Jan-1994 #sequence\_rev1sion 17-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S29546; S26888  
R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S29543  
A:Accession: S29546  
A:Molecule type: DNA  
A:Residues: 1-98 <TO>  
A:Cross-references: UNIPARC:UPI00002DD16; EMBL:Z17394; NID:932843; PIDN:CAA78997.1; PIDF:15-98/Domain: immunoglobulin homology <IMM>  
C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin  
F:31-35/Region: complementarity-determining 1  
F:49-65/Region: complementarity-determining 2

Query Match 87.0%; Score 134; DB 2; Length 98;  
Best Local Similarity 86.7%; Pred. No. 5.5e-11;  
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGVSHPGASVKLTSGKSCAGSGFTFS 30  
|||:|||||:|||||:|||||:|||||  
Db 1 QVQLVESGGGVQPGPGRSRLRSITCAASGFTFS 30

RESULT 7  
S57410  
Ig heavy chain V-J region - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 10-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S57410  
R:Paterson, G.; Kennedy, P.G.E.; Willison, H.J.  
Submitted to the EMBL Data Library, June 1995  
A:Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neuropathic patients.  
A:Reference number: S57408  
A:Accession: S57410  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-113 <PAT>  
A:Cross-references: UNIPARC:UPI00001137A9; EMBL:X87893; NID:9871363; PIDN:CAA61144.1; PI  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 113;  
Best Local Similarity 86.7%; Pred. No. 6.4e-11;  
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGVSHPGASVKLTSGKSCAGSGFTFS 30  
|||:|||||:|||||:|||||:|||||  
Db 1 QVQLVESGGGVQPGPGRSRLRSITCAASGFTFS 30

RESULT 8  
S38490  
Ig heavy chain - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S38490  
R:Mark, J.D.; Overhand, W.H.; Bye, J.M.; Finnern, R.; Gortick, B.D.; Voak, D.; Thorpe, S.  
Submitted to the EMBL Data Library, June 1993  
A:Description: Human antibody fragments specific for human blood group antigens from a B cell hybridoma.  
A:Reference number: S38488  
A:Accession: S38490  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-113 <MAR>  
A:Cross-references: UNIPARC:UPI0000116549; EMBL:Z23030; NID:9414027; PIDN:CAA80565.1; PI  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 113;  
Best Local Similarity 86.7%; Pred. No. 6.4e-11;  
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGVSHPGASVKLTSGKSCAGSGFTFS 30  
|||:|||||:|||||:|||||:|||||  
Db 1 QVQLVESGGGVQPGPGRSRLRSITCAASGFTFS 30

RESULT 9

S31116  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 31-Dec-2004  
C:Accession: S31116  
R:Raaphorst, F.M.; Timmer, B.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
Burr, J. Immunol. 22, 247-251, 1992  
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement  
A:Reference number: S31104; MUID:92111633; PMID:1730252

A:Accession: S31116  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-118 <RAA>  
A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176E37; EMBL:X62966  
C:Superfamily: immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 118;  
Best Local Similarity 86.7%; Pred. No. 6.6e-11;  
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGVSHPGASVKLTSGKSCAGSGFTFS 30  
|||:|||||:|||||:|||||:|||||  
Db 1 QVQLVESGGGVQPGPGRSRLRSITCAASGFTFS 30

RESULT 10

S31111  
Ig heavy chain - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C:Accession: S31111  
R:Raaphorst, F.M.; Timmer, B.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,  
Burr, J. Immunol. 22, 247-251, 1992  
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement  
A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31111  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-119 <RAA>  
A:Cross-references: UNIPARC:UPI0000176DC2; EMBL:X62959  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 119;  
Best Local Similarity 86.7%; Pred. No. 6.7e-11;  
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGVSHPGASVKLTSGKSCAGSGFTFS 30  
|||:|||||:|||||:|||||:|||||  
Db 1 QVQLVESGGGVQPGPGRSRLRSITCAASGFTFS 30

RESULT 11

F36005  
Ig heavy chain V region (M49) - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 31-Dec-2004  
C:Accession: F36005  
R:Schroeder, U.; H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A:Reference number: A36005; MUID:90349571; PMID:2117273  
A:Accession: F36005  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-119 <SCH>  
A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C32; GB:M34026  
C:Genetics:  
A:Gene: IGH@; IGHV1  
A:Cross-references: GDB:118731; OMIM:146910  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 119;  
Best Local Similarity 86.7%; Pred. No. 6.7e-11;

Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSGAGSGFTFS 30  
 |||||:|||||:|||||:|||||:|||||  
 Db 1 QVQLVSGGCVVQPGRSRLRLSCAASGFTFS 30

## RESULT 12

S31112

Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999

C/Accession: S31112

R/Rapporteur, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, B.; J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement

A/Reference number: S31104; MUID:9211633; PMID:1730252

A/Accession: S31112

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-120 <RAA>

A/Cross-references: UNIPARC:UPI0000176C8C; EMBL:X62961

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 120;

Best Local Similarity 86.7%; Pred. No. 6.7e-11;

Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSGAGSGFTFS 30  
 |||||:|||||:|||||:|||||:|||||  
 Db 1 QVQLVSGGCVVQPGRSRLRLSCAASGFTFS 30

## RESULT 13

G36005

Ig heavy chain V region (M74) - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 31-Dec-2004

C/Accession: G36005

R/Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

A/Reference number: A36005; MUID:90349571; PMID:2117273

A/Accession: G36005

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-121 <SCH>

A/Cross-references: UNIPROT:Q8WUK1, UNIPARC:UPI0000176C2C; GB:M34031

C/Genetics: GDB:IGH0; IGHDI1

A/Cross-references: GDB:118731; OMIM:146910

A/Map position: 14q32.33-14q32.33

C/Superfamily: immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 121;

Best Local Similarity 86.7%; Pred. No. 6.8e-11;

Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSGAGSGFTFS 30  
 |||||:|||||:|||||:|||||:|||||  
 Db 1 QVQLVSGGCVVQPGRSRLRLSCAASGFTFS 30

## RESULT 14

S31117

Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999

C/Accession: S31117

R/Rapporteur, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, B.; J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement

A/Reference number: S31104; MUID:9211633; PMID:1730252

A/Accession: S31117

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-122 <RAA>

A/Cross-references: UNIPARC:UPI0000176C8D; EMBL:X62967

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 122;

Best Local Similarity 86.7%; Pred. No. 6.8e-11;

Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSGAGSGFTFS 30  
 |||||:|||||:|||||:|||||:|||||  
 Db 1 QVQLVSGGCVVQPGRSRLRLSCAASGFTFS 30

## RESULT 15

E36005

Ig heavy chain V region (M72) - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998

C/Accession: E36005

R/Schroeder Jr., H.W.; Wang, J.Y.

Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene ;

A/Reference number: A36005; MUID:90349571; PMID:2117273

A/Accession: E36005

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-122 <SCH>

A/Cross-references: UNIPARC:UPI0000176C30; GB:M34030

C/Genetics: GDB:IGH0; IGHDI1

A/Cross-references: GDB:118731; OMIM:146910

A/Map position: 14q32.33-14q32.33

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 122;

Best Local Similarity 86.7%; Pred. No. 6.8e-11;

Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSGAGSGFTFS 30  
 |||||:|||||:|||||:|||||:|||||  
 Db 1 QVQLVSGGCVVQPGRSRLRLSCAASGFTFS 30

Search completed: November 21, 2005, 12:22:15

Job time : 7.30769 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55 ; Search time 44.3956 Seconds  
(without alignments)  
476.756 Million cell updates/sec

Title: US-10-632-706-158  
Perfect score: 154  
Sequence: 1 QVQLVDSGSGGVHPGRSLKLSGASGPTFS 30

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	137	89.0	119	1	HVJ1_HUMAN
2	134	87.0	613	2	Q8WUK1_HUMAN
3	131	85.1	122	1	HVJ3_HUMAN
4	131	85.1	461	2	Q5W7V3_RAT
5	129	83.8	116	2	Q9UL93_HUMAN
6	129	83.8	465	2	Q510J0_RAT
7	127	82.5	240	2	Q652C9_HUMAN
8	127	82.5	479	2	Q5BK12_RAT
9	126	81.8	475	2	Q5RFE5_HUMAN
10	125	81.2	121	1	HVJ1_HUMAN
11	125	81.2	122	1	HVJ3_HUMAN
12	125	81.2	126	1	HVJ3_HUMAN
13	125	81.2	483	2	Q566J7_MOUSE
14	124	80.5	113	2	Q9UL90_HUMAN
15	124	80.5	467	2	Q4VBH1_RAT
16	124	80.5	472	2	Q6N089_HUMAN
17	124	80.5	573	2	Q8WU38_HUMAN
18	123	79.9	98	1	HVJ7_MOUSE
19	123	79.9	122	2	Q9UL84_HUMAN
20	123	79.9	487	2	Q99KA4_MOUSE
21	123	79.9	606	2	Q6GMV2_HUMAN
22	122	79.2	470	2	Q6GCN4_HUMAN
23	121	78.6	118	2	Q9UL91_HUMAN
24	121	78.6	119	1	HVJ3_HUMAN
25	121	78.6	120	1	HVJ3_HUMAN
26	121	78.6	147	2	Q9Y509_HUMAN
27	121	78.6	478	2	Q6P181_HUMAN
28	120	77.9	117	1	HVJ4_MOUSE
29	120	77.9	131	2	Q9UL88_HUMAN
30	120	77.9	464	2	Q6WZU6_HUMAN
31	120	77.9	473	2	Q6WZV7_HUMAN

32	120	77.9	479	2	Q5P0K9_RAT	Q5P0K9_rattus norv
33	119	77.3	97	1	HVJ5_MOUSE	P18527_mus musc
34	119	77.3	114	1	HVJ3_HUMAN	P01763_homo sapien
35	119	77.3	519	2	Q6N092_HUMAN	Q6N092_homo sapien
36	118	76.6	112	2	Q9HCC1_HUMAN	Q9HCC1_homo sapien
37	118	76.6	115	2	HVJ3_HUMAN	P01780_homo sapien
38	118	76.6	115	1	HVJ3_HUMAN	P01779_homo sapien
39	118	76.6	116	1	HVJ3_HUMAN	P01764_homo sapien
40	118	76.6	117	1	HVJ3_HUMAN	P18526_mus musc
41	118	76.6	119	1	HVJ5_MOUSE	P01774_homo sapien
42	118	76.6	119	1	HVJ3_HUMAN	Q652L8_mus musc
43	118	76.6	499	2	Q6N5K4_MOUSE	Q6N5K4_homo sapien
44	118	76.6	544	2	Q6P395_HUMAN	Q6P395_homo sapien
45	118	76.6				

## ALIGNMENTS

RESULT 1  
HVJ1\_HUMAN STANDARD; PRT; 119 AA.  
ID HVJ1\_HUMAN  
AC P01770;  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig heavy chain V-II region N1B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OC NCBI\_TaxID=9606;  
OK [1]  
RN MEDLINE=77070269; PubMed=826475;  
RP PROTEIN SEQUENCE.  
RX Drexler L., Schwarz J., Reichel W., Hilschmann N.;  
RA Ponserting H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein N1B). III. The chymotryptic  
RT peptides of the H-chain, alignment of the tryptic peptides and  
RT discussion of the complete structure.";  
RT Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RL [2]  
RN DISULFIDE BOND.  
RX MEDLINE=77070267; PubMed=1002129;  
RA Drexler L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein N1B). I: purification and  
RT characterization of the protein, the L- and H-chains, the cyanogen  
RT bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
CC -I- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma  
CC protein.  
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC PIR; A51668; G1HUNI.  
CC HSP; P01772; 2F84.  
CC SMR; P01770; 1-119.  
CC GO; GO:0005576; C:extracellular region; NAS.  
CC GO; GO:0003823; F:antigen binding; NAS.  
CC GO; GO:0006955; P:immune response; NAS.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003596; Ig\_V.  
CC SMART; SM00406; IGV; 1.  
CC PROSITE; PS50835; IG\_LIKE; 1.  
CC Direct protein sequencing; Immunoglobulin domain;  
CC Immunoglobulin V region; Pyrolysine carboxylic acid.  
CC DOMAIN 1 112 Ig-like.

FT MOD RES 1 1 Pyrrolidone carboxylic acid.  
FT DISUPID 22 96  
FT NON TER 119  
SQ SEQUENCE 119 AA, 13243 MW, C96935A6E55E165B CRC64;  
Query Match 89.0%; Score 137; DB 1; Length 119;  
Best Local Similarity 90.0%; Pred. No. 9e-11;  
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
CY 1 QVQLVSGGCVGHPGRSLKSLGCSGPTFS 30  
DB 1 QVQLVSGGCVGHPGRSLKSLGCSGPTFS 30  
RESULT 2  
Q8WUK1\_HUMAN  
ID Q8WUK1\_HUMAN PRELIMINARY; PRT; 613 AA.  
AC Q8WUK1;  
DT 01-MAR-2002 (TRENBLUREL. 20; Created)  
DT 01-MAR-2002 (TRENBLUREL. 20; Last sequence update)  
DT 01-MAR-2004 (TRENBLUREL. 26; Last annotation update)  
DE IGHM protein.  
GN Name=IGHM;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NOCLOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuller G.D.,  
RA Klausner R.D., Colling F.S., Wagner L., Sherman C.M., Schuller G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stappleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshlyak S., Carninci P., Prange C.,  
RA Raba S.S., Loguailano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Pahay J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,  
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NOCLOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;  
RL Submitted (BCC-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NOCLOTIDE SEQUENCE.  
RX PubMed=2117273;  
RA Schroeder H.W., Jr., Wang J.Y.;  
RT "Preferential utilization of conserved immunoglobulin heavy chain  
RT variable gene segments during human fetal life";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).  
RN [4]  
RP NOCLOTIDE SEQUENCE.  
RX PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;  
RA Chislier A.M., Fumoux F., Fumoux P., Tomalle C.;  
RT "IGM kappa/lambda BBV human B cell clone: an early step of  
RT differentiation of fetal B cells or a distinct B lineage?";  
RL Mol. Immunol. 29:1363-1373(1992).  
RN [5]  
RP NOCLOTIDE SEQUENCE.

RX PubMed=1730252;  
RA Raaphorst F.M., Timmers B., Kenter M.J., Van Tol M.J., Vossen J.M.,  
RA Schuurman R.K.;  
RT "Restricted utilization of germ-line VH3 genes and short diverse third  
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte  
RL Eur. J. Immunol. 22:247-251(1992).  
RN [6]  
RP NOCLOTIDE SEQUENCE.  
RX PubMed=1904154;  
RA Neale G.A., Kitchingman G.R.;  
RT "mRNA transcripts initiating within the human immunoglobulin mu heavy  
RT chain enhancer region contain a non-translatable exon and are  
RT extremely heterogeneous at the 5' end";  
RL Nucleic Acids Res. 19:2427-2433(1991).  
RN [7]  
RP NOCLOTIDE SEQUENCE.  
RX PubMed=2840480; DOI=10.1084/jem.168.1.229;  
RA Bird J., Gailly N., Link M., Stiles D., Sklar J.;  
RT "Continuing rearrangement but absence of somatic hypermutation in  
RT immunoglobulin genes of human B cell precursor leukemia";  
RL J. Exp. Med. 168:229-245(1988).  
RN [8]  
RP NOCLOTIDE SEQUENCE.  
RX PubMed=2538551; DOI=10.1084/jem.169.4.1391;  
RA Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;  
RT "Early human IGH gene assembly in Epstein-Barr virus-transformed fetal  
RT B cell lines. Preferential utilization of the most 5H-proximal D  
RT segment (DQ52) and two unusual VH-related rearrangements";  
RL J. Exp. Med. 169:1391-1403(1989).  
RN [9]  
RP NOCLOTIDE SEQUENCE.  
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;  
RA Hillson U.L., Kerr N.S., Opplinger I.R., Mannik M., Sasse E.H.;  
RT "The structural basis of germline-encoded VH3 immunoglobulin binding  
RT to staphylococcal protein A";  
RL J. Exp. Med. 178:331-336(1993).  
RN [10]  
RP NOCLOTIDE SEQUENCE.  
RX EMBL/BC020240; A020240.1; mRNA.  
DR PIR; F36005; F36005.  
DR PIR; G36005; G36005.  
DR PIR; PH1642; PH1642.  
DR PIR; PH1643; PH1643.  
DR PIR; PH1645; PH1645.  
DR PIR; PH1646; PH1646.  
DR PIR; PL0098; PL0098.  
DR PIR; PL0120; PL0120.  
DR PIR; S15590; S15590.  
DR PIR; S31116; S31116.  
DR PIR; S31119; S31119.  
DR PIR; S70442; S70442.  
DR HSSP; P01861; 1ADO.  
DR SMR; Q8WUK1.20-242.  
DR Ensembl; ENSG00000130076; Homo sapiens.  
DR InterPro; IPR007110; Ig-1like.  
DR InterPro; IPR003597; Ig C1.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig V.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 5.  
DR PROSITE; PSS0290; IG\_MHC; UNKNOWN\_3.  
KW Immunoglobulin domain.  
SQ SEQUENCE 613 AA; 67296 MW; 60CF5950871E315 CRC64;  
Query Match 87.0%; Score 134; DB 2; Length 613;  
Best Local Similarity 86.7%; Pred. No. 1.1e-09;  
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
CY 1 QVQLVSGGCVGHPGRSLKSLGCSGPTFS 30  
DB 20 QVQLVSGGCVGHPGRSLKSLGCSGPTFS 49



```

RESULT 3
HV3G HUMAN STANDARD; PRT; 122 AA.
ID HV3G_HUMAN
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DS Ig heavy chain V-II region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
XN
XP PROTEIN SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment."
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: This mu chain was isolated from the plasma of a
CC patient with macroglobulinemia. (immunoglobulin-like) domain.
CC -1- SIMILARITY: Contains 1 Ig-like.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A02051; M3H0AM.
DR HSSP; P01772; 2PB4.
DR SMR; P01768; 2PB4.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG-V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrolydine carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrolydine carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0R17D252F1C2 CRC64;

Query Match 85.1%; Score 131; DB 1; Length 122;
Best Local Similarity 83.3%; Pred. No. 6.1e-10;
Matches 25; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVQSGGIVHPGRSLKSCASGFTFS 30
DB 1 QVQLVSGGIVHPGRSLKSCASGFTFS 30
ID HV3G_HUMAN PRELIMINARY; PRT; 461 AA.
AC Q5M7V3;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE LOC67586 protein.
GN Name=LOC67586;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
XN
XP NUCLEOTIDE SEQUENCE.
RX MEDLINE=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Urdin T.B., Toshiyuki G., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC
CC EMBL; BC088423; AAH8423.1; -; mRNA.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF07654; CI-sect; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 461 AA; 50949 MW; 25EA48CE6E0F5A9 CRC64;

Query Match 85.1%; Score 131; DB 2; Length 461;
Best Local Similarity 83.3%; Pred. No. 2.2e-09;
Matches 25; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVQSGGIVHPGRSLKSCASGFTFS 30
DB 20 EVQLVSGGIVHPGRSLKSCASGFTFS 49
ID Q5M7V3_HUMAN PRELIMINARY; PRT; 116 AA.
AC Q9UJ93;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
XN
XP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RA Wu X., Liu B., Van der Werwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).

```

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RESULT 5
Q5M7V3_HUMAN PRELIMINARY; PRT; 116 AA.
ID Q5M7V3;
AC Q9UJ93;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
XN
XP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
RA Wu X., Liu B., Van der Werwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).

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RN [2]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA Hilleen J.L., Kair N.S., Oppliger I.R., Mannik M., Sasse E.H.,
RT "The structural basis of germine-encoded VH3 immunoglobulin binding
RT to staphylococcal protein A."
RN J. Exp. Med. 178:331-336(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA PubMed=2840480;
RA Bird U., Gallil N., Link M., Stiles D., Sklar J.,
RT "Continuing rearrangement but absence of somatic hypermutation in
RT immunoglobulin genes of human B cell precursor leukemia."
RN J. Exp. Med. 168:229-245(1988).
RL EMBL, AF035021; AAD56257.1; -, mRNA.
DR PIR, PH1644; PH1644.
DR PIR, P10120; P10120.
DR HSHP, P01772; 2PB4.
DR SMR, Q9U93; 1-116.
DR Interpro: IPR007110; Ig-like.
DR Interpro: IPR003596; Ig_v.
DR SMART, SM00406; IGV, 1-LIKE, 1.
DR PROSITE, PS50835; IG_LIKE, 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD0601 CRC64;

Query Match 83.8%; Score 129; DB 2; Length 116;
Best Local Similarity 86.2%; Pred. No. 1.1e-09;
Matches 25; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 2 VOLVOSGGGVHVRGRLSKLSCAGSGFTFS 30
ID 051030_RAT PRELIMINARY; PRT; 465 AA.
AC 051030
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical LOC299354.
GN Name=LOC299354;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marziani K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heltón E., Kettelman M., Madan A., Rodríguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RA NIH MGC Project;
RA Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL, BC088271; AAH88271.1; -, mRNA.
DR Interpro: IPR003599; Ig.
DR Interpro: IPR007110; Ig-like.
DR Interpro: IPR003597; Ig_c1.
DR Interpro: IPR003596; Ig_v.
DR Pfam, PR07654; C1-set; 3.
DR SMART, SM00409; IGV, 2.
DR SMART, SM00407; IGV, 2.
DR SMART, SM00406; IGV, 1.
DR PROSITE, PS50835; IG_LIKE, 4.
KM Hypothetical protein; Immunoglobulin domain; Repeat.
SQ SEQUENCE 465 AA; 51699 MW; 97CA533A213A424F CRC64;

Query Match 83.8%; Score 129; DB 2; Length 465;
Best Local Similarity 80.0%; Pred. No. 4.2e-09;
Matches 24; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Cy 1 QVOLVOSGGGVHVRGRLSKLSCAGSGFTFS 30
Db 20 EVOLVSGGGLVPGSRSLKSCAGSGFTFS 49

RESULT 7
ID 055ZC9_HUMAN PRELIMINARY; PRT; 240 AA.
AC 055ZC9
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C1q/7;
RA MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.B., Wing M.G., Winter G.,
RT "Complement recruitment using bispecific diabodies."
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL, Y13056; CAJ73499.1; -, mRNA.
DR Interpro: IPR003599; Ig.
DR Interpro: IPR007110; Ig-like.
DR Interpro: IPR003596; Ig_v.
DR SMART, SM00409; IGV, 2.
DR SMART, SM00406; IGV, 2.
DR PROSITE, PS50835; IG_LIKE, 2.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F4B373 CRC64;

Query Match 82.5%; Score 127; DB 2; Length 240;
Best Local Similarity 83.3%; Pred. No. 4.2e-09;
Matches 25; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 QVOLVOSGGGVHVRGRLSKLSCAGSGFTFS 30
Db 1 QVOLVOSGGGVHVRGRLSKLSCAGSGFTFS 30

RESULT 8

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Q5BK12.RAT  
ID Q5BK12.RAT PRELIMINARY; PRT; 479 AA.  
AC Q5BK12  
DT 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
DE Igna protein.  
DS  
OS Name=Igna;  
GN Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Rattus.  
NC NCB1\_TaxID=10116;  
NX [1]  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Spleen.  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
RA Datchenko L., Matusin B., Farmer A.A., Rubin G.M., Hong L.,  
RA Stepieton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalski U., Smallus D.B.,  
RA Schnerch A., Schin J.E., Jones S.J.M., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RG NIH MGC Project;  
RL EMBL; BC091247; AA91247.1; mRNA.  
DR SMR; Q5BK12; 20-241.  
DR GO: GO:0003823; P:antigen binding; ISA.  
DR InterPro; IPR003599; IG\_1like.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003597; IG\_1like.  
DR InterPro; IPR003596; IG\_1like.  
DR InterPro; IPR003596; IG\_1like.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 3.  
DR SMART; SM00407; IG; 3.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
SQ SEQUENCE 479 AA; 52329 MW; 8B146164AE8437C5 CRC64;

Query Match 82.8%; Score 127; DB 2; Length 479;  
Best Local Similarity 80.0%; Pred. No. 8.2e-09;  
Matches 24; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
DE Anti-Rhd monoclonal T125 gamma1 heavy chain precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
NC NCB1\_TaxID=9606;  
NX [1]  
RN NUCLEOTIDE SEQUENCE.  
RP Gaucher C., Klein P., Bellard R.;  
RT "Sequence determination of the recombinant human anti-Rhd monoclonal  
RT antibody T125."  
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY894992; AA862028.1; mRNA.  
DR InterPro; IPR003599; IG\_1like.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003597; IG\_1like.  
DR InterPro; IPR003596; IG\_1like.  
DR InterPro; IPR003596; IG\_1like.  
DR Pfam; PF07654; Cl-set; 3.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG; 3.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Signal.  
FT SIGNAL.  
FT CHAIN.  
FT CHAIN.  
SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;

Query Match 81.8%; Score 126; DB 2; Length 475;  
Best Local Similarity 82.8%; Pred. No. 1.1e-08;  
Matches 24; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 QVQLVSGGAVHPGRSLKSCAGSGFTF 29  
DB 20 QVQLVSGGAVHPGRSLKSLCTASGFTF 48

RESULT 10  
HV3J HUMAN STANDARD; PRT; 121 AA.  
ID HV3J HUMAN  
AC P01771.  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DS Ig heavy chain V-III region H1L.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
NC NCB1\_TaxID=9606;  
NX [1]  
RN PROTEIN SEQUENCE.  
RP MEDLINE=79124695; PubMed=420800;  
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;  
RT "Amino acid sequence of the VH region of human myeloma  
RT cryoimmunoglobulin IgG H1L."  
RL Biochemistry 18:553-560(1979).  
CC -1- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma  
CC protein.  
CC -1- SIMILARITY: Contains 1 Ig-1like (immunoglobulin-like) domain.  
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC PIR: A02054; G1HHL.  
DR HSPF; P01772; 2F84.

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DR SMR; P01771; 2-121.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrolydione carboxylic acid.
FT DOMAIN 1 112
FT MOD RES 1 1 Pyrolydione carboxylic acid.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 81.2%; Score 125; DB 1; Length 121;
Best Local Similarity 80.0%; Pred. No. 4e-09; 3; Indels 0; Gaps 0;
Matches 24; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 QVQVVGSGGVHPRSLKSLSCAGSGFTFS 30
Db 1 QVQLVQAGGAVPGRSLRLSCAASGFTFS 30

RESULT 11
HV3H_HUMAN STANDARD; PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G.; Lehman D.; Putnam F.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL Biochemistry 13;2482-2498(1974).
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC -----
CC PIR; A02052; M3HUGA.
DR HSSP; P01772; 2FB4.
DR SMR; P01769; 5-122.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrolydione carboxylic acid.
FT DOMAIN 1 112
FT MOD RES 1 1 Pyrolydione carboxylic acid.
FT NON TER 122 122
SQ SEQUENCE 122 AA; 13167 MW; 74ESB6959E84100A CRC64;

Query Match 81.2%; Score 125; DB 1; Length 122;
Best Local Similarity 76.7%; Pred. No. 4.1e-09; 3; Indels 0; Gaps 0;
Matches 23; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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OY 1 QVQVVGSGGVHPRSLKSLSCAGSGFTFS 30
Db 1 QVQLVQAGGAVPGRSLRLSCAASGFTFS 30

RESULT 12
HV3H_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E.; Jung H.-D.; Palm W.; Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marguier M.; Delsenhofer U.; Huber R.; Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC -----
CC PIR; A02055; G1HUKL.
DR PDB; 2FB4; X-ray; H=2-126.
DR PDB; 2IG3; X-ray; H=2-126.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrolydione carboxylic acid.
FT DOMAIN 1 112
FT MOD RES 1 1 Pyrolydione carboxylic acid.
FT DISULFID 22 96
FT DISULFID 105 110
FT NON TER 126 126
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 16 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT HELIX 62 64
FT STRAND 65 65
FT TURN 66 67
FT STRAND 68 73
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FT TURN 74 77  
 FT STRAND 78 83  
 FT HELIX 88 90  
 FT STRAND 92 99  
 FT STRAND 106 106  
 FT TURN 107 108  
 FT STRAND 109 109  
 FT STRAND 113 116  
 FT STRAND 120 124  
 SQ SEQUENCE 126 AA; 13718 MW; BAD71B52B16F8776 CRC64;

Query Match 81.2%; Score 125; DB 1; Length 126;  
 Best Local Similarity 80.0%; Pred. No. 4.2e-09;  
 Matches 24; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 OVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30  
 Db 1 OVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30

RESULT 13  
 OS667\_MOUSE PRELIMINARY; PRT; 483 AA.  
 AC OS667\_MOUSE PRELIMINARY; PRT; 483 AA.  
 DT 10-MAY-2005 (TREMBlrel. 30, Created)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
 DE LOC544903 protein.  
 GN Name=LOC544903;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Dichtchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=FVB/N; TISSUE=Colon;  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RG NIH MGC Project;  
 RU Subtilized (Apr-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC093501; AAH93501.1; -; mRNA.  
 DR SRR; QS667; 20-240.  
 DR GO; GO:0003823; F:antigen binding; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_W.  
 DR Pfam; PF07654; C1-sec; 2.  
 DR SMART; SM00409; IG; 3.

DR SMART; SM00407; IG\_C1; 3.  
 DR SMART; SM00406; IG\_V; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 SQ SEQUENCE 483 AA; 52371 MW; 20357D7F51A2886 CRC64;

Query Match 81.2%; Score 125; DB 2; Length 483;  
 Best Local Similarity 82.8%; Pred. No. 1.5e-08;  
 Matches 24; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 VOLVQSGGVVHPGRSLKLSGAGSGFTFS 30  
 Db 21 VOLVQSGGVVHPGRSLKLSGAGSGFTFS 49

RESULT 14  
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 ID OS90\_HUMAN PRELIMINARY; PRT; 113 AA.  
 AC OS90\_HUMAN PRELIMINARY; PRT; 113 AA.  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RX MEDLINE=96277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
 RA Wu X., Liu B., Van der Werf P.L., Kall N.N., Benney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 RN NUCLEOTIDE SEQUENCE.  
 RP PubMed=1730252;  
 RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,  
 RA Schuurman R.K.;  
 RT "Restricted utilization of germ-line VH3 genes and short diverse third  
 complementarily-determining regions (CD3) in human fetal B lymphocyte  
 immunoglobulin heavy chain rearrangements.";  
 RL Eur. J. Immunol. 22:247-251(1992).  
 DR EMBL; AF035024; AAD56260.1; -; mRNA.  
 DR PIR; S78486; S78486.  
 DR HSSP; F01772; 2FB4.  
 DR SRR; Q9UL90; 1-113.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003596; IG\_V.  
 DR SMART; SM00406; IG\_V; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 80.5%; Score 124; DB 2; Length 113;  
 Best Local Similarity 80.0%; Pred. No. 5.2e-09;  
 Matches 24; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 OVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30  
 Db 1 OVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30

RESULT 15  
 OS90\_HUMAN PRELIMINARY; PRT; 467 AA.  
 ID OS90\_HUMAN PRELIMINARY; PRT; 467 AA.  
 AC OS90\_HUMAN PRELIMINARY; PRT; 467 AA.  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, last annotation update)  
 DE LOC299354 protein.  
 GN Name=LOC299354;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxId=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Tymus;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
 RA Datchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,  
 RA Schnerch A., Schein J.B., Jones S.U.M., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Tymus;  
 RG NIH MGC Project;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
 CC histocompatibility complex class I molecules (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC EMBL, BC095846; AA095846.1; -; mRNA.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; C1-beet; 3.  
 DR SMART: SM00409; IG; 2.  
 DR SMART: SM00407; IGC1; 2.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG LIKE; 4.  
 KW Immunoglobulin domain; Repeat.  
 KW SEQUENCE 467 AA; 51651 MW; 1FF0328F5016ED3 CRC64;

Query Match 80.5%; Score 124; DB 2; Length 467;  
 Best Local Similarity 76.7%; Pred. No. 2,1e-08;  
 Matches 23; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQVQSGGCVVHPRGRSLKSLSCAGSGFTFS 30  
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 DB 20 EVQLVETGGGLVQPGRSIKSLSCVAGSFTFS 49

Search completed: November 21, 2005, 12:04:12  
 Job time : 45.3956 secs

GenCore version 5.1.6  
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OM protein - protein search, using BW model

Run on: November 21, 2005, 11:49:31 / Search time 11.3187 Seconds  
(without alignments)  
219.131 Million cell updates/sec

Title: US-10-632-706-158  
Perfect score: 154  
Sequence: 1 QVQLVQSGGGLVHPGSRLLKLSGAGSGFTFS 30

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
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2: /cgn2\_6/ptodata/1/1aa/6-COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/H-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PCVTUS-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RS-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	89.6	97	2	US-09-534-717-617 Sequence 617, App
2	137	89.0	98	2	US-09-534-717-667 Sequence 667, App
3	137	89.0	115	2	US-09-726-219A-167 Sequence 167, App
4	137	89.0	115	2	US-09-534-717-23 Sequence 23, App
5	137	89.0	115	2	US-09-534-717-33 Sequence 33, App
6	137	89.0	115	2	US-09-534-717-37 Sequence 37, App
7	137	89.0	115	2	US-09-534-717-39 Sequence 39, App
8	137	89.0	115	2	US-09-534-717-41 Sequence 41, App
9	137	89.0	115	2	US-09-534-717-43 Sequence 43, App
10	137	89.0	115	2	US-09-534-717-45 Sequence 45, App
11	137	89.0	115	2	US-09-534-717-47 Sequence 47, App
12	137	89.0	115	2	US-09-534-717-51 Sequence 51, App
13	137	89.0	115	2	US-09-534-717-55 Sequence 55, App
14	137	89.0	115	2	US-09-534-717-57 Sequence 57, App
15	137	89.0	115	2	US-09-534-717-59 Sequence 59, App
16	137	89.0	115	2	US-09-534-717-61 Sequence 61, App
17	137	89.0	115	2	US-09-534-717-63 Sequence 63, App
18	137	89.0	115	2	US-09-534-717-65 Sequence 65, App
19	137	89.0	115	2	US-09-534-717-71 Sequence 71, App
20	137	89.0	115	2	US-09-534-717-73 Sequence 73, App
21	137	89.0	115	2	US-09-534-717-75 Sequence 75, App
22	137	89.0	115	2	US-09-534-717-77 Sequence 77, App
23	137	89.0	115	2	US-09-534-717-79 Sequence 79, App
24	137	89.0	115	2	US-09-534-717-81 Sequence 81, App
25	137	89.0	115	2	US-09-534-717-83 Sequence 83, App
26	137	89.0	115	2	US-09-534-717-85 Sequence 85, App
27	137	89.0	115	2	US-09-534-717-87 Sequence 87, App

28	137	89.0	225	2	US-09-456-090A-68 Sequence 68, App
29	137	89.0	225	2	US-09-456-090A-94 Sequence 94, App
30	137	89.0	225	2	US-09-456-090A-100 Sequence 100, App
31	137	89.0	225	2	US-09-456-090A-106 Sequence 106, App
32	137	89.0	225	2	US-09-453-234-62 Sequence 62, App
33	137	89.0	225	2	US-09-453-234-68 Sequence 68, App
34	137	89.0	225	2	US-09-453-234-94 Sequence 94, App
35	137	89.0	225	2	US-09-453-234-100 Sequence 100, App
36	137	89.0	225	2	US-09-453-234-106 Sequence 106, App
37	137	89.0	225	2	US-09-453-234-112 Sequence 112, App
38	137	89.0	225	2	US-09-453-234-118 Sequence 118, App
39	137	89.0	225	2	US-09-453-234-124 Sequence 124, App
40	137	89.0	225	2	US-09-453-234-130 Sequence 130, App
41	137	89.0	225	2	US-09-453-234-136 Sequence 136, App
42	137	89.0	225	2	US-09-453-234-142 Sequence 142, App
43	137	89.0	225	2	US-09-453-234-148 Sequence 148, App
44	137	89.0	225	2	US-09-453-234-154 Sequence 154, App
45	137	89.0	225	2	US-09-453-234-160 Sequence 160, App

ALIGNMENTS

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RESULT 1
US-09-534-717-617
Sequence 617, Application US/09534717
Patent No. 6914128
GENERAL INFORMATION:
APPLICANT: Jochen, Salfield et al.
TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
FILE REFERENCE: BBI-093CP
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/126,603
EARLIER FILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 617
LENGTH: 97
TYPE: PRT
ORGANISM: Homo sapiens
US-09-534-717-617

Query Match      89.6% Score 138, DB 2; Length 97;
Best Local Similarity 86.7% Pred. No. 1.8e-11;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QVQLVQSGGGLVHPGSRLLKLSGAGSGFTFS 30
DB      1 EVQLVQSGGGLVHPGSRLLKLSGAGSGFTFS 30

RESULT 2
US-09-534-717-667
Sequence 667, Application US/09534717
Patent No. 6914128
GENERAL INFORMATION:
APPLICANT: Jochen, Salfield et al.
TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
FILE REFERENCE: BBI-093CP
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/126,603
EARLIER FILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 667
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-09-534-717-667

Query Match      89.0% Score 137, DB 2; Length 98;
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Best Local Similarity 90.0%; Pred.No.2.5e-11;  
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGGVHPGRSLKLSGASGFTFS 30  
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Db 1 QVQLVSGGGVHPGRSLRLSCASGFTFS 30

RESULT 3  
US-09-726-219A-167  
! Sequence 167, Application US/09726219A  
! Patent No. 6806079  
! GENERAL INFORMATION:  
! ADDITIONAL Comment: Method:down

Query Match 89.0%; Score 137; DB 2; Length 115;  
Best Local Similarity 90.0%; Pred No. 2.9e-11;  
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0

**Oy**      1 QVQLVQSGGGVNHPRGRSLKLSACAGSEFTPS 30  
**Db**      1 QVQLVQSGGGSVPGRSLRLSCAASGFTPS 30

RESULT 4  
US-09-534-717-23  
; Sequence 23, Application US/09534717  
; Patent No. 6914128  
; GENERAL INFORMATION:  
; APPLICANT: Jochen, Salfeld et al.

1. TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing

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CURRENT APPLICATION NUMBER: US/09/534,717
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/126,603
EARLIER FILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: PatentIn Ver. 2.0

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Query Match	89.04%	Score 137	DB 2	length 115
Best Local Similarity	90.04%	Pred. No. 2.9e-11		
Matches 27, Conservative	1	Mismatches 2	Indels 0	Gaps 0

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|||:  
|||  
**Dd**    1 QVQLVDSGGGVNQPGRSLRLSCAASGFTFS 30  
|||  
|||:

REBULT 5  
 US-09-534-717-33  
 ; Sequence 33, Application US/09534717  
 ; Patent No. 6914128  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jochen, Salfeld et al.  
 ; INVENTOR: Jochen, Salfeld et al.

Query Match	89.04	Score 137	DB 2	Length 115
Best Local Similarity	90.04	Pred. No. 2.9e-11		
Matches 27	Conservative 1	Mismatches 2	Indels 0	Gaps 0

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QY      1 QVQLVQSGGSGVHPGRSLKLSGAGSGFTFS 30
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DB      1 QVQLVQSGGSGVHPGRSLRLSCAAGSGFTFS 30

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RESULT 6
US-09-534-717-37
: Sequence 37, Application US/09534717
: Patent No. 6914128
: GENERAL INFORMATION:
: APPLICANT: Jochen, Salfeld et al.
: TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
: FILE REFERENCE: BBI-093CP
: CURRENT APPLICATION NUMBER: US/09/534,717
: CURRENT FILING DATE: 2000-03-24
: EARLIER APPLICATION NUMBER: 60/126,603
: EARLIER FILING DATE: March 25, 1999
: NUMBER OF SEQ ID NOS: 675
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 37
: LENGTH: 115
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-534-717-37

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Query Match 89.0%; Score 137; DB 2; Length 115;



Best Local Similarity 90.0%; Pred. No. 2.9e-11;  
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 1 0VOLVOSGGGVOPGRSLRLSLSCASGSGFTFS 30

## RESULT 7

US-09-534-717-39

Sequence 39, Application US/09534717

Patent No. 6914128

GENERAL INFORMATION:

APPLICANT: Jochen, Salfeld et al.

TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing

FILE REFERENCE: BBI-093CP

CURRENT FILING DATE: 2000-03-24

EARLIER APPLICATION NUMBER: 60/126,603

EARLIER FILING DATE: March 25, 1999

NUMBER OF SEQ ID NOS: 675

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 39

LENGTH: 115

TYPE: PRT

ORGANISM: Homo sapiens

US-09-534-717-39

Query Match 89.0%; Score 137; DB 2; Length 115;  
Best Local Similarity 90.0%; Pred. No. 2.9e-11;

Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 0VOLVOSGGVHPGRSLKSLSCASGSGFTFS 30  
Db 1 0VOLVOSGGGVOPGRSLRLSLSCASGSGFTFS 30

## RESULT 8

US-09-534-717-41

Sequence 41, Application US/09534717

Patent No. 6914128

GENERAL INFORMATION:

APPLICANT: Jochen, Salfeld et al.

TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing

FILE REFERENCE: BBI-093CP

CURRENT FILING DATE: 2000-03-24

EARLIER APPLICATION NUMBER: 60/126,603

EARLIER FILING DATE: March 25, 1999

NUMBER OF SEQ ID NOS: 675

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 41

LENGTH: 115

TYPE: PRT

ORGANISM: Homo sapiens

US-09-534-717-41

Query Match 89.0%; Score 137; DB 2; Length 115;  
Best Local Similarity 90.0%; Pred. No. 2.9e-11;

Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 0VOLVOSGGVHPGRSLKSLSCASGSGFTFS 30  
Db 1 0VOLVOSGGGVOPGRSLRLSLSCASGSGFTFS 30

## RESULT 9

US-09-534-717-43

Sequence 43, Application US/09534717

Patent No. 6914128

GENERAL INFORMATION:

APPLICANT: Jochen, Salfeld et al.

TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing

FILE REFERENCE: BBI-093CP

CURRENT APPLICATION NUMBER: US/09/534,717

CURRENT FILING DATE: 2000-03-24

EARLIER APPLICATION NUMBER: 60/126,603

EARLIER FILING DATE: March 25, 1999

NUMBER OF SEQ ID NOS: 675

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 43

LENGTH: 115

TYPE: PRT

ORGANISM: Homo sapiens

US-09-534-717-43

Query Match 89.0%; Score 137; DB 2; Length 115;  
Best Local Similarity 90.0%; Pred. No. 2.9e-11;

Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 0VOLVOSGGVHPGRSLKSLSCASGSGFTFS 30  
Db 1 0VOLVOSGGGVOPGRSLRLSLSCASGSGFTFS 30

## RESULT 10

US-09-534-717-45

Sequence 45, Application US/09534717

Patent No. 6914128

GENERAL INFORMATION:

APPLICANT: Jochen, Salfeld et al.

TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing

FILE REFERENCE: BBI-093CP

CURRENT FILING DATE: 2000-03-24

EARLIER APPLICATION NUMBER: 60/126,603

EARLIER FILING DATE: March 25, 1999

NUMBER OF SEQ ID NOS: 675

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 45

LENGTH: 115

TYPE: PRT

ORGANISM: Homo sapiens

US-09-534-717-45

Query Match 89.0%; Score 137; DB 2; Length 115;  
Best Local Similarity 90.0%; Pred. No. 2.9e-11;

Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 0VOLVOSGGVHPGRSLKSLSCASGSGFTFS 30  
Db 1 0VOLVOSGGGVOPGRSLRLSLSCASGSGFTFS 30

## RESULT 11

US-09-534-717-47

Sequence 47, Application US/09534717

Patent No. 6914128

GENERAL INFORMATION:

APPLICANT: Jochen, Salfeld et al.

TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing

FILE REFERENCE: BBI-093CP

CURRENT FILING DATE: 2000-03-24

EARLIER APPLICATION NUMBER: 60/126,603

EARLIER FILING DATE: March 25, 1999

NUMBER OF SEQ ID NOS: 675

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 47

LENGTH: 115

TYPE: PRT

ORGANISM: Homo sapiens

US-09-534-717-47

Query Match 89.0%; Score 137; DB 2; Length 115;  
Best Local Similarity 90.0%; Pred. No. 2.9e-11;

	Matches	27;	Conservative	1;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1	QVQLVQSGGCGVHPGRSLKLS	CAGSGFTFS	30						
		:								
Dd	1	QVQLVQSGGCGVYPGRSLRLS	CAASGFTFS	30						

RESULT 12  
US-09-534-717-51  
; Sequence 51, Application US/09534717  
; Patent No. 6914138

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1  APPLICANT: Jochen, Salteid et al.
2  TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
3  FILE REFERENCE: BSI-093CP
4  CURRENT APPLICATION NUMBER: US/09/534,717
5  CURRENT FILING DATE: 2000-03-24
6  EARLIER APPLICATION NUMBER: 60/126,603
7  EARLIER FILING DATE: March 25, 1999
8  NUMBER OF SEQ ID NOS: 675
9  SOFTWARE: PatentIn Ver. 2.0
10 SEQ ID NO 51
11 LENGTH: 115
12 TYPE: PRT
13 ORGANISM: Homo sapiens
14 US-09-534-717-51

```

Query	Match	Similarity	89.0%	Score 137	DB 2	Length 115
Best	Local	Similarity	90.0%	Pred. No. 2.9e-11		
Matches	27	Conservative	1	Mismatches	2	Indels
						Gaps 0

  

Qy	1	QV	V	Q	G	G	G	V	H	P	R	S	L	K	T	S	C	A	G	S	G	T	F	S	30
Db	1	Q	V	L	V	O	S	G	G	V	O	P	R	S	L	R	L	C	A	S	G	T	F	S	30

```

RESULT 13
US-09-534-717-53
; Sequence 53, Application US/09534717
; Patent No. 691418
; GENERAL INFORMATION:

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: TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
:
: FILE REFERENCE: B01-0933CP
:
: CURRENT APPLICATION NUMBER: US/09/534,717
:
: CURRENT FILING DATE: 2000-03-24
:
: EARLIER APPLICATION NUMBER: 60/126,603
:
: EARLIER FILING DATE: March 25, 1999
:
: NUMBER OF SEQ ID NOS: 675
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 53
:
: LENGTH: 115
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: US-09-534-717-53

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Qy	1	QVQLVDSGGGVVHPSRLKLSGAGSGFTFS	30
Qb	1	QVQLVDSGGGVVHPSRLKLSGAGSGFTFS	30

```

RESULT 14
US-09-534-717-55
; Sequence 55, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Saifeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP

```

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/
/ CURRENT APPLICATION NUMBER: US/09/534,717
/ CURRENT FILING DATE: 2000-03-24
/ EARLIER APPLICATION NUMBER: 60/126,603
/ EARLIER FILING DATE: March 25, 1999
/ NUMBER OF SEQ ID NOS: 675
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 55
/
/ LENGTH: 115
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/
US-09-534-717-55

```

Query Match	89.0%	Score 137,	DB 2;	Length 115;
Best Local Similarity	90.0%;	Pred. No. 2,98-11/;		
Matches 27;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 QVQLVQSGGAVHHPGRSLKLSCAAGSGFTFS 30  
| | | | | : | | | | |  
DB 1 QVQLVQSGGAVQPGRLSLRLSCAAGSFTFS 30

RESULT 15  
US-09-534-717-57  
; Sequence 57, Application US/09534717  
; Patent No. 6014128

```

:
: APPLICANT: Jochen, Satefield et al.
: TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
: FILE REFERENCE: BBI-093CP
: CURRENT APPLICATION NUMBER: US/09/534, 717
: CURRENT FILING DATE: 2000-03-24
: EARLIER APPLICATION NUMBER: 60/126, 603
: EARLIER FILING DATE: March 25, 1999
: NUMBER OF SEQ ID NOS: 675
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 57
: LENGTH: 115
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-534-717-57

```

Query Match	89.0%	Score 137	DB 2	Length 115
Best Local Similarity	90.0%	Pred. No. 2,9e-11		
Matches 27	Conservative 1	Mismatches 2	Indels 0	Gaps 0
QY	1	QVQLVDSGGGVHPGRSLKLTSCAGSGTFFS	30	
Db	1	QVQLVDSGGGVHPGRSLRSLSCAGSGTFFS	30	

Search completed: November 21, 2005, 12:07:39  
Job time : 11.3187 secs

Search completed: November 21, 2005, 12:07:39  
Job time : 11.3187 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:50:51 Search time 37.1429 Seconds  
(without alignments)  
337,478 Million cell updates/sec

Title: US-10-632-706-158

Perfect score: 154  
Sequence: 1 QVQLVSGGCVHPGRSLKLSGAGSGFTFS 30

Scoring table:  
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA Main.\*

1: /cgn2\_6/ptodata/1/pubdpar/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubdpar/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubdpar/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubdpar/US10\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubdpar/US10A\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubdpar/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154	100.0	30	4	US-10-632-706-158 Sequence 158, App
2	154	100.0	30	4	US-10-632-706-158 Sequence 162, App
3	154	100.0	30	4	US-10-632-706-158 Sequence 166, App
4	154	100.0	30	4	US-10-632-706-158 Sequence 170, App
5	138	89.6	97	5	US-10-884-830-617 Sequence 617, App
6	138	89.6	97	5	US-10-911-838-18 Sequence 18, App
7	138	89.6	115	5	US-10-982-359-16 Sequence 16, App
8	138	89.6	115	5	US-10-982-359-18 Sequence 18, App
9	138	89.6	115	5	US-10-982-359-20 Sequence 20, App
10	138	89.6	115	5	US-10-982-359-22 Sequence 22, App
11	138	89.6	115	5	US-10-982-359-24 Sequence 24, App
12	138	89.6	115	5	US-10-982-359-26 Sequence 26, App
13	138	89.6	115	5	US-10-982-359-28 Sequence 28, App
14	138	89.6	115	5	US-10-982-359-30 Sequence 30, App
15	138	89.6	115	5	US-10-982-359-32 Sequence 32, App
16	138	89.6	115	5	US-10-982-359-34 Sequence 34, App
17	138	89.6	115	5	US-10-982-359-36 Sequence 36, App
18	138	89.6	115	5	US-10-982-359-38 Sequence 38, App
19	138	89.6	115	5	US-10-982-359-40 Sequence 40, App
20	138	89.6	116	4	US-10-408-901-14 Sequence 14, App
21	138	89.6	116	4	US-10-408-901-22 Sequence 22, App
22	138	89.6	116	4	US-10-687-799-54 Sequence 54, App
23	138	89.6	116	4	US-10-911-838-13 Sequence 13, App
24	138	89.6	119	5	US-10-815-449-5 Sequence 5, App
25	138	89.6	446	4	US-10-408-901-38 Sequence 38, App
26	138	89.6	446	4	US-10-408-901-46 Sequence 46, App
27	138	89.6	850	5	US-10-450-763-34993 Sequence 34993, A

28	137	89.0	98	5	US-10-884-830-667 Sequence 667, App
29	137	89.0	115	4	US-10-803-622-167 Sequence 167, App
30	137	89.0	115	4	US-10-803-623-167 Sequence 167, App
31	137	89.0	115	5	US-10-884-830-23 Sequence 23, App
32	137	89.0	115	5	US-10-884-830-33 Sequence 33, App
33	137	89.0	115	5	US-10-884-830-37 Sequence 37, App
34	137	89.0	115	5	US-10-884-830-39 Sequence 39, App
35	137	89.0	115	5	US-10-884-830-41 Sequence 41, App
36	137	89.0	115	5	US-10-884-830-43 Sequence 43, App
37	137	89.0	115	5	US-10-884-830-45 Sequence 45, App
38	137	89.0	115	5	US-10-884-830-47 Sequence 47, App
39	137	89.0	115	5	US-10-884-830-51 Sequence 51, App
40	137	89.0	115	5	US-10-884-830-53 Sequence 53, App
41	137	89.0	115	5	US-10-884-830-55 Sequence 55, App
42	137	89.0	115	5	US-10-884-830-57 Sequence 57, App
43	137	89.0	115	5	US-10-884-830-59 Sequence 59, App
44	137	89.0	115	5	US-10-884-830-61 Sequence 61, App
45	137	89.0	115	5	US-10-884-830-63 Sequence 63, App

#### ALIGNMENTS

```
RESULT 1
US-10-632-706-158
Sequence 158, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
TITLE OR INVENTION: NEUROTOXINS
FILE REFERENCE: 407T-895120US
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 10/632,706
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 158
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-158
Query Match 100.0%; Score 154; DB 4; Length 30;
Best local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 QVQLVSGGCVHPGRSLKLSGAGSGFTFS 30
Db 1 QVQLVSGGCVHPGRSLKLSGAGSGFTFS 30
RESULT 2
US-10-632-706-162
Sequence 162, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
TITLE OR INVENTION: NEUROTOXINS
FILE REFERENCE: 407T-895120US
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 10/632,706
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 2002-08-01
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; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-162

Query Match      100.0%; Score 154; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QVQLVSGGSGVHPRGRLSKLSCAGSGFTFS 30
DB      1 QVQLVSGGSGVHPRGRLSKLSCAGSGFTFS 30

RESULT 3
US-10-632-706-166
; Sequence 166, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 166
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-166

Query Match      100.0%; Score 154; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QVQLVSGGSGVHPRGRLSKLSCAGSGFTFS 30
DB      1 QVQLVSGGSGVHPRGRLSKLSCAGSGFTFS 30

RESULT 4
US-10-632-706-170
; Sequence 170, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 170
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-170

Query Match      100.0%; Score 154; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QVQLVSGGSGVHPRGRLSKLSCAGSGFTFS 30
DB      1 QVQLVSGGSGVHPRGRLSKLSCAGSGFTFS 30

RESULT 5
US-10-884-830-617
; Sequence 617, Application US/10884830
; Publication No. US20050004354A1
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfield et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/10/884,830
; PRIOR FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/534,717
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 617
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-830-617

Query Match      89.6%; Score 138; DB 5; Length 97;
Best Local Similarity 86.7%; Pred. No. 1.3e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QVQLVSGGSGVHPRGRLSKLSCAGSGFTFS 30
DB      1 EVQLVSGGSLVHPGSLRLSKLSCAGSGFTFS 20

RESULT 6
US-10-911-838-18
; Sequence 18, Application US/10911838
; Publication No. US20050069869A1
; GENERAL INFORMATION:
; APPLICANT: AMEROSINO, Donna
; APPLICANT: HERNANDEZ, Hector
; APPLICANT: GREENOUGH, Thomas
; APPLICANT: IZURIAGA, Katherine
; APPLICANT: SOMASUNDARAN, Mohan
; APPLICANT: BABCOCK, Gregory J.
; APPLICANT: THOMAS, JR., William D.
; APPLICANT: SULLIVAN, John
; TITLE OF INVENTION: SARS NUCLEIC ACIDS, PROTEINS, ANTIBODIES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: MJI-002
; CURRENT APPLICATION NUMBER: US/10/911,838
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 60/565595
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US 60/545670
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/510251
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/492529
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PRIOR FILING DATE: 2003-08-04  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: PasteSeq for Windows Version 4.0  
SEQ ID NO 18  
LENGTH: 97  
TYPE: PR1  
ORGANISM: SARS-Associated Coronavirus  
US-10-911-838-18

Query Match 89.6%; Score 138; DB 5; Length 97;  
Best Local Similarity 86.7%; Pred. No. 1.5e-10;  
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30  
Db 1 EVOLVQSGGLVHPGSLRLSCAGSGFTFS 30

RESULT 7  
US-10-982-359-16  
Sequence 16, Application US/10982359  
Publication No. US20050112694A1  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR  
FILE REFERENCE: 3492-A  
CURRENT FILING DATE: 2004-11-04  
PRIOR FILING DATE: 2003-11-07  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 16  
LENGTH: 115  
TYPE: PR1  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-10-982-359-16

Query Match 89.6%; Score 138; DB 5; Length 115;  
Best Local Similarity 86.7%; Pred. No. 1.5e-10;  
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30  
Db 1 EVOLVQSGGLVHPGSLRLSCAGSGFTFS 30

RESULT 8  
US-10-982-359-18  
Sequence 18, Application US/10982359  
Publication No. US20050112694A1  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR  
FILE REFERENCE: 3492-A  
CURRENT FILING DATE: 2004-11-04  
PRIOR FILING DATE: 2003-11-07  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 18  
LENGTH: 115  
TYPE: PR1  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-10-982-359-18

Query Match 89.6%; Score 138; DB 5; Length 115;  
Best Local Similarity 86.7%; Pred. No. 1.5e-10;  
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30  
Db 1 EVOLVQSGGLVHPGSLRLSCAGSGFTFS 30

RESULT 9  
US-10-982-359-20  
Sequence 20, Application US/10982359  
Publication No. US20050112694A1  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR  
FILE REFERENCE: 3492-A  
CURRENT FILING DATE: 2004-11-04  
PRIOR FILING DATE: 2003-11-07  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 20  
LENGTH: 115  
TYPE: PR1  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-10-982-359-20

Query Match 89.6%; Score 138; DB 5; Length 115;  
Best Local Similarity 86.7%; Pred. No. 1.5e-10;  
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30  
Db 1 EVOLVQSGGLVHPGSLRLSCAGSGFTFS 30

RESULT 10  
US-10-982-359-22  
Sequence 22, Application US/10982359  
Publication No. US20050112694A1  
GENERAL INFORMATION:  
APPLICANT: Carter, Paul J.  
TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR  
FILE REFERENCE: 3492-A  
CURRENT FILING DATE: 2004-11-04  
PRIOR FILING DATE: 2003-11-07  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 22  
LENGTH: 115  
TYPE: PR1  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-10-982-359-22

Query Match 89.6%; Score 138; DB 5; Length 115;  
Best Local Similarity 86.7%; Pred. No. 1.5e-10;  
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30  
Db 1 EVOLVQSGGLVHPGSLRLSCAGSGFTFS 30

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RESULT 11
US-10-982-359-24
; Sequence 24, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Zhou, Hongxing
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
; CURRENT APPLICATION NUMBER: US/10/982,359
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-982-359-24

Query Match      89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QVQLVSGGSGVHVRGRIKLSGCSGSGFTFS 30
:|||||:|||||:|||||:|||||:|||||
DB      1 EVQLVSGGSGLVHFGSLRLSCAGSGFTFS 30

RESULT 12
US-10-982-359-26
; Sequence 26, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Zhou, Hongxing
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
; CURRENT APPLICATION NUMBER: US/10/982,359
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-982-359-26

Query Match      89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QVQLVSGGSGVHVRGRIKLSGCSGSGFTFS 30
:|||||:|||||:|||||:|||||:|||||
DB      1 EVQLVSGGSGLVHFGSLRLSCAGSGFTFS 30

RESULT 13
US-10-982-359-28
; Sequence 28, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Zhou, Hongxing
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
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; CURRENT APPLICATION NUMBER: US/10/982,359
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-982-359-28

Query Match      89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QVQLVSGGSGVHVRGRIKLSGCSGSGFTFS 30
:|||||:|||||:|||||:|||||:|||||
DB      1 EVQLVSGGSGLVHFGSLRLSCAGSGFTFS 30

RESULT 14
US-10-982-359-30
; Sequence 30, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Zhou, Hongxing
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
; CURRENT APPLICATION NUMBER: US/10/982,359
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-982-359-30

Query Match      89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QVQLVSGGSGVHVRGRIKLSGCSGSGFTFS 30
:|||||:|||||:|||||:|||||:|||||
DB      1 EVQLVSGGSGLVHFGSLRLSCAGSGFTFS 30

RESULT 15
US-10-982-359-32
; Sequence 32, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Zhou, Hongxing
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
; CURRENT APPLICATION NUMBER: US/10/982,359
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 115
; TYPE: PRT
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ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-10-982-359-32

Query Match 89.6%; Score 138; DB 5; Length 115;  
Best Local Similarity 86.7%; Pred. No. 1.5e-10;  
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 QVQLVQSGGSGVHPGRSLKLSGAGSGFTFS 30  
:|||||:|||||:|||||  
Db 1 EVQLVQSGGSGLVHPGRSLKLSGAGSGFTFS 30

Search completed: November 21, 2005, 12:33:37  
Job time : 37.1429 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 12:04:27 ; Search time 0.549451 Seconds  
(without alignments)  
61.686 Million cell updates/sec

Title: US-10-632-706-158  
Perfect score: 134  
Sequence: 1 OVQLVOSGGGVHPGRSLKLSGAGSGFTFS 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
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3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
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8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	81.2	139	1	US-10-721-763-33 Sequence 33, Appl
2	123	79.9	98	7	US-11-144-248-30 Sequence 30, Appl
3	123	79.9	473	7	US-11-144-248-50 Sequence 50, Appl
4	120	77.9	138	1	US-10-789-273-4 Sequence 4, Appl
5	120	77.9	263	1	US-10-512-184-29 Sequence 29, Appl
6	120	77.9	444	7	US-11-172-320-6 Sequence 6, Appl
7	119	77.3	470	7	US-11-144-248-49 Sequence 49, Appl
8	118	76.6	98	1	US-10-789-273-10 Sequence 10, Appl
9	118	76.6	98	7	US-11-144-248-32 Sequence 32, Appl
10	118	76.6	121	1	US-10-789-273-9 Sequence 9, Appl
11	118	76.6	122	7	US-11-144-248-24 Sequence 24, Appl
12	118	76.6	125	7	US-11-144-248-16 Sequence 16, Appl
13	118	76.6	138	1	US-10-789-273-8 Sequence 8, Appl
14	118	76.6	138	1	US-10-789-273-12 Sequence 12, Appl
15	118	76.6	470	7	US-11-144-248-46 Sequence 46, Appl
16	115	74.7	118	1	US-10-648-816-9 Sequence 9, Appl
17	115	74.7	118	1	US-10-648-816-11 Sequence 11, Appl
18	115	74.7	118	1	US-10-648-816-14 Sequence 14, Appl
19	115	74.7	121	1	US-10-648-816-15 Sequence 15, Appl
20	114	74.0	470	7	US-11-144-248-45 Sequence 45, Appl
21	112	72.7	124	7	US-11-144-248-8 Sequence 8, Appl
22	109	70.8	118	1	US-10-648-816-10 Sequence 10, Appl
23	109	70.8	118	1	US-10-648-816-12 Sequence 12, Appl
24	109	70.8	118	1	US-10-648-816-13 Sequence 13, Appl
25	109	70.8	121	1	US-10-648-816-16 Sequence 16, Appl

26	106.5	69.2	102	1	US-10-997-201A-6 Sequence 6, Appl
27	106	68.8	120	7	US-11-077-978-7 Sequence 7, Appl
28	106	68.8	121	7	US-11-077-978-2 Sequence 2, Appl
29	106	68.8	121	7	US-11-077-978-3 Sequence 3, Appl
30	105	68.2	123	1	US-10-932-334-88 Sequence 88, Appl
31	105	68.2	123	1	US-10-932-334-92 Sequence 92, Appl
32	105	68.2	124	1	US-10-932-334-13 Sequence 13, Appl
33	102	66.2	119	7	US-11-010-954-5 Sequence 5, Appl
34	98	63.6	116	7	US-11-174-186-17 Sequence 17, Appl
35	96	62.3	120	1	US-10-932-334-71 Sequence 71, Appl
36	96	62.3	123	1	US-10-932-334-87 Sequence 87, Appl
37	96	62.3	124	1	US-10-932-334-70 Sequence 70, Appl
38	96	62.3	143	1	US-10-932-334-52 Sequence 52, Appl
39	96	62.3	143	1	US-10-932-334-52 Sequence 52, Appl
40	94	61.0	116	7	US-11-174-186-18 Sequence 18, Appl
41	94	61.0	579	7	US-11-174-186-11 Sequence 41, Appl
42	93	60.4	76	1	US-10-839-799-113 Sequence 113, App
43	93	60.4	121	1	US-10-502-145-17 Sequence 17, Appl
44	92	59.7	117	1	US-10-932-334-76 Sequence 76, Appl
45	92	59.7	118	1	US-10-932-334-75 Sequence 75, Appl

## ALIGNMENTS

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RESULT 1
US-10-721-763-33
; Sequence 33, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KAHUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTI BODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721,763
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-33

Query Match      81.2%  Score 125, DB 1, Length 139;
Best Local Similarity 76.7%  Pred. No. 9e-09;
Matches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

CY      1 OVQLVOSGGGVHPGRSLKLSGAGSGFTFS 30
DB      20 EVQLVSGGGVLPGRSLKLSGAGSGFTFS 49

RESULT 2
US-11-144-248-30
; Sequence 30, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvathan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
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; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 98
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-144-248-30

Query Match          79.9%; Score 123; DB 7; Length 98;
Best Local Similarity 80.0%; Pred. No. 1,1e-08;
Matches 24; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLVSGGQVHPGRSLKLSGAGSGFTFS 30
Db 1 QVQLVSGGGLVYKPGSLRLSCAASGFTFS 30

RESULT 3
US-11-144-248-50
; Sequence 50, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: AER-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 473
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-144-248-50

Query Match          79.9%; Score 123; DB 7; Length 473;
Best Local Similarity 80.0%; Pred. No. 4,2e-08;
Matches 24; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLVSGGQVHPGRSLKLSGAGSGFTFS 30
Db 20 QVQLVSGGGLVYKPGSLRLSCAASGFTFS 49

RESULT 4
US-10-789-273-4
; Sequence 4, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurid
; APPLICANT: Saidanna, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLROID PEPTIDE
; FILE REFERENCE: ELM-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
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; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PR
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-789-273-4

Query Match          77.9%; Score 120; DB 1; Length 138;
Best Local Similarity 76.7%; Pred. No. 3,2e-08;
Matches 23; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLVSGGQVHPGRSLKLSGAGSGFTFS 30
Db 20 EVQLVSGGGLVYKPGASLKLSGAGSGFTFS 49

RESULT 5
US-10-512-184-29
; Sequence 29, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 263
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv SPRII7
; OTHER INFORMATION: with specificity against Fusarium spp.; originates
; OTHER INFORMATION: from Mus musculus.
US-10-512-184-29

Query Match          77.9%; Score 120; DB 1; Length 263;
Best Local Similarity 76.7%; Pred. No. 5,5e-08;
Matches 23; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVSGGQVHPGRSLKLSGAGSGFTFS 30
Db 3 EVQLVSGGGLVYKPGNSLKLSGAGSGFTFS 32

RESULT 6
US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Anke
; APPLICANT: Adolf, Guenther
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
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PRIOR FILING DATE: August 21, 2002  
PRIOR APPLICATION NUMBER: US 60/405,956  
PRIOR FILING DATE: August 26, 2002  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 444  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Humanised Murine Antibody B1W4 4 Heavy Chain  
US-11-172-320-6

Query Match 77.9%; Score 120; DB 7; Length 444;  
Best Local Similarity 76.7%; Pred. No. 8.5e-08;  
Matches 23; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 QVQLVQSGGGLVHPGSRSLKSCASGFTFS 30  
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS 30

RESULT 7  
US-11-144-248-49  
Sequence 49, Application US/11144248  
Publication No. US20050244408A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce D.  
APPLICANT: Beebe, Jean  
APPLICANT: Miller, Penelope E.  
APPLICANT: Moyer, James D.  
APPLICANT: Corvajan, Jose R.  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
FILE REFERENCE: ABX-PP2  
CURRENT APPLICATION NUMBER: US/11/144,248  
CURRENT FILING DATE: 2005-06-02  
PRIOR APPLICATION NUMBER: US/10/038,591  
PRIOR FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: 60/259,927  
PRIOR FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 49  
LENGTH: 470  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-144-248-49

Query Match 77.3%; Score 119; DB 7; Length 470;  
Best Local Similarity 76.7%; Pred. No. 1.1e-07;  
Matches 23; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 QVQLVQSGGGLVHPGSRSLKSCASGFTFS 30  
Db 20 QAQLVESGGGLVQPGGSLRLSCAASGFTFS 49

RESULT 8  
US-10-789-273-10  
Sequence 10, Application US/10789273  
Publication No. US20050249725A1  
GENERAL INFORMATION:  
APPLICANT: Basil, Gurig  
APPLICANT: Saldanha, Jose  
APPLICANT: Yednock, Ted  
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
FILE REFERENCE: ELN-002CP  
CURRENT APPLICATION NUMBER: US/10/789,273  
CURRENT FILING DATE: 2004-02-27  
PRIOR APPLICATION NUMBER: US/10/388,389  
PRIOR FILING DATE: 2003-03-12

PRIOR APPLICATION NUMBER: US 10/010,942  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: US 60/251,892  
PRIOR FILING DATE: 2000-12-06  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-789-273-10

Query Match 76.6%; Score 118; DB 1; Length 98;  
Best Local Similarity 73.3%; Pred. No. 4e-08;  
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 QVQLVQSGGGLVHPGSRSLKSCASGFTFS 30  
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS 30

RESULT 9  
US-11-144-248-32  
Sequence 32, Application US/11144248  
Publication No. US20050244408A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce D.  
APPLICANT: Beebe, Jean  
APPLICANT: Miller, Penelope E.  
APPLICANT: Moyer, James D.  
APPLICANT: Corvajan, Jose R.  
APPLICANT: Gallo, Michael  
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
FILE REFERENCE: ABX-PP2  
CURRENT APPLICATION NUMBER: US/11/144,248  
CURRENT FILING DATE: 2005-06-02  
PRIOR APPLICATION NUMBER: US/10/038,591  
PRIOR FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: 60/259,927  
PRIOR FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 32  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-144-248-32

Query Match 76.6%; Score 118; DB 7; Length 98;  
Best Local Similarity 73.3%; Pred. No. 4e-08;  
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 QVQLVQSGGGLVHPGSRSLKSCASGFTFS 30  
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS 30

RESULT 10  
US-10-789-273-9  
Sequence 9, Application US/10789273  
Publication No. US20050249725A1  
GENERAL INFORMATION:  
APPLICANT: Basil, Gurig  
APPLICANT: Saldanha, Jose  
APPLICANT: Yednock, Ted  
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
FILE REFERENCE: ELN-002CP  
CURRENT APPLICATION NUMBER: US/10/789,273  
CURRENT FILING DATE: 2004-02-27  
PRIOR APPLICATION NUMBER: US/10/388,389  
PRIOR FILING DATE: 2003-03-12  
PRIOR APPLICATION NUMBER: US 10/010,942

```
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US 60/251,892
/ PRIOR FILING DATE: 2000-12-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 121
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-789-273-9
```

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Query Match          76.6%; Score 118; DB 1; Length 121;
Best Local Similarity 73.3%; Pred. No. 4.8e-08;
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 QVQLVSGGCVHPGRSLKLSGASGFTFS 30
       :|::|::|::|::|::|::|::|::|::|
DB      1 EVQLLESGGGLVPGGSLRLSCAASGFTFS 30
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```
RESULT 11
US-11-144-248-24
/ Sequence 24; Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
```

```
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PP2
/ CURRENT APPLICATION NUMBER: US/11/144,248
```

```
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-24
```

```
Query Match          76.6%; Score 118; DB 7; Length 122;
Best Local Similarity 73.3%; Pred. No. 4.8e-08;
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 QVQLVSGGCVHPGRSLKLSGASGFTFS 30
       :|::|::|::|::|::|::|::|::|::|
DB      1 EVQLLESGGGLVPGGSLRLSCAASGFTFS 30
```

```
RESULT 12
US-11-144-248-16
/ Sequence 16; Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
```

```
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PP2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
```

```
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 125
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-16
```

```
Query Match          76.6%; Score 118; DB 7; Length 125;
Best Local Similarity 73.3%; Pred. No. 4.9e-08;
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 QVQLVSGGCVHPGRSLKLSGASGFTFS 30
       :|::|::|::|::|::|::|::|::|::|
DB      1 EVQLLESGGGLVPGGSLRLSCAASGFTFS 30
```

```
RESULT 13
US-10-789-273-8
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```
/ Sequence 8; Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Basl, Gurliq
/ APPLICANT: Saldanha, Jose
```

```
/ APPLICANT: Vednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
```

```
/ TITLE OF INVENTION: BETA-AMYLOID PEPTIDES
/ FILE REFERENCE: ELN-002CP
/ CURRENT APPLICATION NUMBER: US/10/789,273
```

```
/ PRIOR FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: US/10/388,389
/ PRIOR FILING DATE: 2003-03-12
/ PRIOR APPLICATION NUMBER: US 10/010,942
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US 60/251,892
/ PRIOR FILING DATE: 2000-12-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 138
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanized 3d6 heavy chain variable region
/ NAME/KEY: SIGNAL
/ LOCATION: (1)...(19)
US-10-789-273-8
```

```
Query Match          76.6%; Score 118; DB 1; Length 138;
Best Local Similarity 73.3%; Pred. No. 5.3e-08;
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 QVQLVSGGCVHPGRSLKLSGASGFTFS 20
       :|::|::|::|::|::|::|::|::|::|
DB      20 EVQLLESGGGLVPGGSLRLSCAASGFTFS 49
```

```
RESULT 14
US-10-789-273-12
/ Sequence 12; Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Basl, Gurliq
/ APPLICANT: Saldanha, Jose
```

```
/ APPLICANT: Vednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
/ TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
/ FILE REFERENCE: ELN-002CP
/ CURRENT APPLICATION NUMBER: US/10/789,273
/ CURRENT FILING DATE: 2004-02-27
```

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; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3D6 light chain variable region
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-789-273-12

```

Query March 76.6%; Score 118; DB 1; Length 138;  
 Best Local Similarity 73.3%; Pred. No. 5,3e-08;  
 Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVHPGSRSLKLSGAGSGFTFS 30  
 DB 20 EVQLLESGGGLVQPGGSLRLSCAASGFTFS 49

```

RESULT 15
US-11-144-248-46
; Sequence 46, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvatan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-46

```

Query March 76.6%; Score 118; DB 7; Length 470;  
 Best Local Similarity 73.3%; Pred. No. 1,5e-07;  
 Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVHPGSRSLKLSGAGSGFTFS 30  
 DB 20 EVQLLESGGGLVQPGGSLRLSCAASGFTFS 49

Search completed: November 21, 2005, 12:33:52  
 Job time : 0.649451 secb

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:32 ; Search time 6.69414 Seconds  
(without alignments)  
328.182 Million cell updates/sec

Title: US-10-632-706-159

Perfect score: 32

Sequence: 1 DYDMH 5

Scoring table: BLASTN62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseq21:\*  
2: geneseq1980s:\*  
3: geneseq1990s:\*  
4: geneseq2000s:\*  
5: geneseq2001s:\*  
6: geneseq2002s:\*  
7: geneseq2003s:\*  
8: geneseq2004s:\*  
9: geneseq2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	32 100.0	5	ADR38765	Adi38765 Mouse hea
2	32 100.0	5	ADR38761	Adi38761 Mouse hea
3	32 100.0	5	ADR38757	Adi38757 Mouse hea
4	32 100.0	5	ADR38769	Adi38769 Mouse hea
5	32 100.0	142	3 AAG00943	Aag00943 Human bec
6	32 100.0	144	3 ABG20497	Abg20497 Novel hum
7	32 100.0	180	6 ABU70539	Abu70539 Human adi
8	32 100.0	253	6 ADS09256	Ads09256 Human c-M
9	32 100.0	319	8 ADS44811	Ads44811 Bacterial
10	32 100.0	341	6 ABM68679	Abm68679 Phototrib
11	32 100.0	457	8 ADN18693	Adn18693 Bacterial
12	32 100.0	465	8 ABN18693	Abn18693 Bacterial
13	32 100.0	473	5 ABB92826	Abb92826 Herbicida
14	32 100.0	493	4 AAM93283	Aam93283 Human pol
15	32 100.0	493	8 ADI30731	Adi30731 Human pro
16	32 100.0	523	5 ABB97214	Abb97214 Novel hum
17	32 100.0	564	3 AAY68736	Aay68736 Short cha
18	32 100.0	564	3 AAB43224	Aab43224 Human ORF
19	32 100.0	564	3 AAY69295	Aay69295 A human h
20	32 100.0	564	8 ADF08477	Adf08477 Human HSP
21	32 100.0	564	8 ABM82354	Abm82354 Tumour-as
22	32 100.0	579	7 ADE09984	Ade09984 Novel pro
23	32 100.0	581	3 AAB58463	Aab58463 Lung can
24	32 100.0	585	4 ABG11793	Abg11793 Novel hum

25	32	100.0	596	4	ABG04416
26	32	100.0	607	6	ADA54819
27	32	100.0	640	4	ABG20499
28	32	100.0	858	4	ABB66508
29	32	100.0	973	4	AAY97696
30	32	100.0	973	8	ADR21541
31	29	90.6	20	4	AAB57691
32	29	90.6	20	4	AAB58101
33	29	90.6	20	4	AAB55829
34	29	90.6	20	5	ABJ05221
35	29	90.6	20	5	ABP63246
36	29	90.6	50	6	AAY40779
37	29	90.6	50	6	ABM37298
38	29	90.6	85	5	ABB04486
39	29	90.6	139	4	ABB63457
40	29	90.6	139	4	AAB63286
41	29	90.6	282	5	ABP25940
42	29	90.6	293	3	AAG52812
43	29	90.6	303	3	AAG52811
44	29	90.6	392	3	AAG52810
45	29	90.6	397	8	ADY04516

#### ALIGNMENTS

RESULT 1  
ADR38765 standard; peptide; 5 AA.

ADR38765;

02-DEC-2004 (first entry)

Mouse heavy chain anti-BoNT-antibody CDR1 seqid 167.

antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;

BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;

toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;

CDR1, complementarity determining region 1.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PT 01-AUG-2002; 2002US-0400721P.

PA (REGC ) UNIV CALIFORNIA.

PI Marks JD, Ameredorfer P;

XX WPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A, useful for diagnosing botulism or for creating pathologies associated with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 167; 110pp; English.

The invention describes an isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone 325, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1, 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). Also described are: a polypeptide (II) comprising BoNT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I); and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain anti-BONT-antibody CRD1.  
XX  
SQ Sequence 5 AA;  
XX  
Query Match 100.0%; Score 32; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYDMH 5  
1 DYDMH 5  
DB 1 DYDMH 5  
XX  
RESULT 2  
ADR38761  
ID ADR38761 standard; peptide; 5 AA.  
XX  
AC ADR38761;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Mouse heavy chain anti-BONT-antibody CRD1 seqid 163.  
XX  
XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
KM CRD1; complementarity determining region 1.  
XX  
OS Mus sp.  
XX  
PN US2004175385-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 01-AUG-2003; 2003US-00632706.  
XX  
PR 31-AUG-1998; 98US-00144886.  
XX  
PR 01-AUG-2002; 2002US-0400721P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Marks JD, Amerdorfer P;  
XX  
DR WPI; 2004-652009/63.  
XX  
PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
XX  
XX Example 4; SEQ ID NO 163; 110pp; English.  
XX  
XX The invention describes an isolated antibody (I) that specifically binds  
XX to an epitope specifically bound by an antibody expressed by a specific  
XX clone where (I) binds to and neutralises botulinum neurotoxin type A  
XX (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
XX specifically bound by an antibody expressed by a clone chosen from clone  
XX S25, C25, C33, 1C6, 3D12, B4, 1F3, huC25, A1, A2, WRI(V), WRI(T), 3-1,  
XX 3-8, 3-10 and ING1, where (I) binds to and neutralises botulinum

CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
CC comprising BONT/A neutralising epitope having an epitope that is  
CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I); and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising  
CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain anti-BONT-antibody CRD1.  
XX  
SQ Sequence 5 AA;  
XX  
Query Match 100.0%; Score 32; DB 8; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYDMH 5  
1 DYDMH 5  
DB 1 DYDMH 5  
XX  
RESULT 3  
ADR38757  
ID ADR38757 standard; peptide; 5 AA.  
XX  
AC ADR38757;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Mouse heavy chain anti-BONT-antibody CRD1 seqid 159.  
XX  
XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
KM CRD1; complementarity determining region 1.  
XX  
OS Mus sp.  
XX  
PN US2004175385-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 01-AUG-2003; 2003US-00632706.  
XX  
PR 31-AUG-1998; 98US-00144886.  
XX  
PR 01-AUG-2002; 2002US-0400721P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Marks JD, Amerdorfer P;  
XX  
DR WPI; 2004-652009/63.  
XX  
PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
XX  
XX Example 4; SEQ ID NO 159; 110pp; English.  
XX  
XX The invention describes an isolated antibody (I) that specifically binds  
XX to an epitope specifically bound by an antibody expressed by a specific  
XX clone where (I) binds to and neutralises botulinum neurotoxin type A  
XX (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
XX specifically bound by an antibody expressed by a clone chosen from clone



CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising a botulinum neurotoxin which  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which (I) is  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulinism. This is the amino acid  
 CC sequence of mouse heavy chain anti-BoNT-antibody CRD1.

XX Sequence 5 AA;

Query Match 100.0%; Score 32; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYDMH 5  
 Db 1 DYDMH 5

RESULT 4

ID ADR38769 standard; peptide; 5 AA.

XX ADR38769;

XX 02-DEC-2004 (first entry)

DE Mouse heavy chain anti-BoNT-antibody CDRI seqid 171.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A.

KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;

KW CDRI; complementarity determining region 1.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC ) UNIV CALIFORNIA.

XX Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,  
 PT useful for diagnosing botulinism or for creating pathologies associated  
 PT with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 171; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds  
 CC to an epitope specifically bound by an antibody expressed by a specific  
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A

CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
 CC specifically bound by an antibody expressed by a clone chosen from clone  
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum  
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
 CC comprising BoNT/A neutralising epitope having an epitope that is  
 CC specifically bound by an antibody expressed by clones as mentioned in (I)  
 CC ; producing (I); and a composition (III) comprising several anti-  
 CC botulinum neurotoxin antibodies, where each antibody is specific for a  
 CC different epitope of a botulinum neurotoxin and the combination of  
 CC antibodies shows greater toxin neutralisation than the single antibodies  
 CC in surplus. The following are disclosed: a pharmaceutical composition  
 CC comprising (I); and a kit comprising a botulinum neurotoxin which  
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
 CC specific for a different epitope of the botulinum neurotoxin and the  
 CC combination of antibodies shows greater toxin neutralisation than the  
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinism  
 CC or for treating pathologies associated with botulinum neurotoxin  
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
 CC enables rapid detection or diagnosis of botulinism. This is the amino acid  
 CC sequence of mouse heavy chain anti-BoNT-antibody CRD1.

XX Sequence 5 AA;

Query Match 100.0%; Score 32; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYDMH 5  
 Db 1 DYDMH 5

RESULT 5

ID AAG00943 standard; protein; 142 AA.

XX AAG00943;

XX 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 5024.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KW gene therapy; chromosome mapping.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST ) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX N-PSDB; AAC00949.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 13; SEQ ID NO 5024; 71pp + Sequence listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of  
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different

CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
CC sequences derived from the 5' ends of mRNAs and even in those cases where  
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors

SQ Sequence 142 AA;

Query Match 100.0%; Score 32; DB 3; Length 142;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|||  
DB 22 DYDMH 26

RESULT 6  
ABG20497  
ID ABG20497 standard; protein, 144 AA.  
XX  
AC ABG20497;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #20488.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
DR N-PSDB; AAS84684.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

PS Claim 20; SEQ ID NO 50856; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AB000010-AB030377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 144 AA;

Query Match 100.0%; Score 32; DB 4; Length 144;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|||  
DB 26 DYDMH 30

RESULT 7  
ABU70539  
ID ABU70539 standard; protein, 180 AA.  
XX  
AC ABU70539;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Human adipocyte Selected Interacting domain, SID, #170.  
XX  
KW Human; prey; adipocyte; SID; selected interacting domain; anorectic;  
KW antidiabetic; protein-protein interaction; diabetes;  
KW yeast 2-hybrid assay; metabolic disorder; obesity.  
XX  
OS Homo sapiens.  
XX  
PN WO200286122-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 14-MAR-2002; 2002WO-EP003768.  
XX  
PR 14-MAR-2001; 2001US-0275734P.  
XX  
PA (HYBR-) HYBRIGENICS.  
XX  
PI Legrain P, Davlet L;  
XX  
DR WPI; 2003-103412/09.  
DR N-PSDB; ACA57083.  
XX  
PT New complex between two interacting proteins in adipocyte cells, useful  
PT for identifying selected interacting domains that modulate protein  
PT interactions, or for preventing or treating metabolic disorders such as  
PT obesity or diabetes.

PS Claim 6; Page 163; 382pp; English.

CC The invention relates to a complex between two interacting proteins in  
CC adipocyte cells, given in the specification. The proteins are identified  
CC by selecting a bait protein from a known adipocyte marker and then  
CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by  
CC members of an adipocyte cDNA library. The proteins are designated SID  
CC (RIM) (selected interacting domains) proteins. Also included are a  
CC polynucleotide encoding a polypeptide in the adipocyte cells, a  
CC recombinant host cell expressing at least one of the interacting  
CC polypeptides of the complex, selecting a modulating compound in adipocyte  
CC cells, a SID (RIM) polypeptide comprising any of the 738 amino acid  
CC sequences given in the specification (including its fragment or variant),  
CC a SID (RIM) polynucleotide comprising any of the 738 nucleotide sequences  
CC given in the specification (including its fragment or variant), a vector  
CC comprising the SID (RIM) polynucleotide, a recombinant host cell  
CC comprising the vector, a protein chip comprising the polypeptides and a

CC record comprising all or part of the data, listed in the specification.  
CC The complex, polypeptides, polynucleotides and compounds are useful for  
CC preventing or treating metabolic disorders such as obesity or diabetes.  
CC The polynucleotides are useful as probes or primers. The complex is  
CC particularly useful for identifying selected interacting domains (SID  
CC (RMM)) for screening drugs that modulate the protein interaction, thus  
CC exhibiting the therapeutic effect. The present sequence represents a SID  
CC (prey) protein of the invention  
XX  
SQ Sequence 180 AA;  
Query Match 100.0%; Score 32; DB 6; Length 180;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYDMH 5  
DB 22 DYDMH 26  
RESULT 8  
ADS09256  
ID ADS09256 standard; protein; 253 AA.  
AC ADS09256;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human c-Met protein tyrosine kinase antibody, FG1A-2-A4.  
XX  
KW c-Met; tyrosine kinase antibody; antigen binding; cytostatic;  
KW ophthalmological; antiinflammatory; analgesic; vasotropic; antipsoriatic;  
KW osteopathic; cancer; tumour; ophthalmic disease; glaucoma; retinitis;  
KW retinopathy; uveitis; ocular photophobia; macular degeneration; pain;  
KW acute injury; eye; hyperproliferative disorder; restenosis; angioplasty;  
KW psoriasis; HGF; osteoporosis; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004072117-A2.  
XX  
PD 26-AUG-2004.  
XX  
PF 11-FEB-2004; 2004WO-1B000503.  
XX  
PR 13-FEB-2003; 2003US-0447073P.  
XX  
PA (PHMA ) PHARMACIA CORP.  
XX  
PI Morton PA, Arbuckle JA, Evans ML, Joy WD, Kahn LB, Shieh JU;  
XX  
DR MPI: 2004-616044/59.  
XX  
DR N-PSDB; ADS09316.  
XX  
PT Novel c-Met protein tyrosine kinase antibody or its antigen-binding  
PT portion specifically binding to c-Met, useful for manufacture of  
PT medicament for treating cancer or tumor for treatment of ophthalmic  
PT diseases such as glaucoma.  
XX  
PS Claim 1; SEQ ID NO 18; 303pp; English.  
XX  
XX The invention relates to a novel c-Met protein tyrosine kinase antibody  
CC or its antigen binding portion that specifically binds to c-Met. The c-  
CC Met antibody comprises any one of 1-60 fully defined sequence of 238,  
CC 244, 240, 250, 251, 242, 245, 247, 246, 253, 249, 243, 241, etc., amino  
CC acids as given in the specification, or its fragment. The invention  
CC further comprises: a pharmaceutical composition comprising the c-Met  
CC protein tyrosine kinase antibody and a carrier; an isolated cell that  
CC produces the c-Met protein tyrosine kinase antibody; and an isolated  
CC nucleic acid molecule that comprises a nucleic acid sequence that encodes  
CC a heavy chain or its antigen-binding portion or light chain or its  
CC antigen-binding portion of the c-Met protein tyrosine kinase antibody.  
CC The c-Met protein tyrosine kinase antibody has cytostatic.

CC ophthalmological, antiinflammatory, analgesic, vasotropic, antipsoriatic,  
CC and osteopathic activities. The c-Met protein tyrosine kinase antibody is  
CC useful for the manufacture of medicament for the treatment of cancer or  
CC tumour. The c-Met protein tyrosine kinase antibody is useful for  
CC diagnosing the presence or ligand of c-Met expressing tissue. The c-Met  
CC protein tyrosine kinase antibody is useful for detecting c-Met in a  
CC biological sample in vitro or in vivo. The c-Met protein tyrosine kinase  
CC antibody is also useful in the treatment or prevention of ophthalmic  
CC diseases such as glaucoma, retinitis, retinopathies (e.g., diabetic  
CC retinopathy), uveitis, ocular photophobia, macular degeneration and pain  
CC associated with acute injury to the eye. The pharmaceutical composition  
CC is useful for the treatment of hyperproliferative disorders such as  
CC restenosis after angioplasty, and psoriasis, and for the treatment of  
CC animals that lack sufficient HGF, e.g. osteoporosis and cancer. This  
CC sequence represents the protein of a phage display generated human c-Met  
CC antibody of the invention.  
XX  
SQ Sequence 253 AA;  
Query Match 100.0%; Score 32; DB 8; Length 253;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYDMH 5  
DB 31 DYDMH 35  
RESULT 9  
ADS44811  
ID ADS44811 standard; protein; 319 AA.  
AC ADS44811;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #23241.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
XX US2003233675-A1.  
XX  
PN 18-DEC-2003.  
XX  
PD 20-FEB-2003; 2003US-00369493.  
XX  
PF 21-FEB-2002; 2002US-0360039P.  
XX  
PR (CAOY/) CAO Y.  
XX  
PA (HINK/) HINKLE G J.  
XX  
PA (SLAT/) SLATER S C.  
XX  
PA (CHEN/) CHEN X.  
XX  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX  
DR MPI: 2004-061375/06.  
XX  
PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 23241; 122pp; English.  
XX  
XX The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition. Improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 319 AA;

Query Match 100.0%; Score 32; DB 8; Length 319;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5

Db 195 DYDMH 199

RESULT 10

ABM68679 standard; protein; 341 AA.

XX ABM68679;

XX 20-NOV-2003 (first entry)

XX Photorhabdus luminescens protein sequence #1776.

XX Antibiacterial; fungicide; insecticide; polymorphism; genetic analysis;

XX detection; food; gene expression; plant; animal; microorganism; toxin;

XX antibiotic; bioplastic; virulence factor; disease model; plague;

XX whooping cough.

XX Photorhabdus luminescens.

XX MO200294867-A2.

XX 28-NOV-2002.

XX 07-FEB-2002; 2002MO-IB003040.

XX 07-FEB-2001; 2001FR-00001659.

XX (INSP ) INST PASTEUR.

XX (CNRS ) CNRS CENT NAT RECH SCT.

XX Duchaud E, Taourit S, Glaeser P, Frangeul L, Kunet F, Danchin A;

XX Buchrieser C;

XX WPI; 2003-148459/14.

XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,

XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX Claim 2; SEQ ID NO 1776; 1205bp; French.

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CC The invention relates to the isolation of genes and their encoded  
CC proteins from Photorhabdus luminescens. The isolated sequences are  
CC sources of probes and primers for detecting the genome of P. luminescens  
CC and related species; to study polymorphisms, for gene analysis and for  
CC detection/amplification of the genes. Antibodies (Ab) raised against the  
CC polypeptides encoded by the genes are used for detection/identification  
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that  
CC carry a gene-containing vector are used to select compounds that  
CC modulate, regulate, induce or inhibit expression of the genes in plants,  
CC animals or microorganisms other than P. luminescens and are able to alter  
CC response or sensitivity to toxins and antibiotics produced by P.  
CC luminescens. Cells transformed to express the genes are useful for  
CC recombinant production of the proteins, particularly toxins and  
CC antibacterials useful as insecticides, bactericides and fungicides. The  
CC genes, proteins, vectors containing the genes and Ab are also useful  
CC therapeutically (to treat microbial infection by bacteria or fungi that  
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as  
CC biopesticides. Other uses of the genes and the proteins are as virulence  
CC factors and for identifying targets of human diseases for which P.  
CC luminescens is a model (particularly plague and whooping cough). This  
CC sequence represents one of the isolated P. luminescens proteins

XX Sequence 341 AA;

Query Match 100.0%; Score 32; DB 6; Length 341;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5

Db 194 DYDMH 198

RESULT 11

ADS41979 standard; protein; 457 AA.

XX ADS41979;

XX 02-DEC-2004 (first entry)

XX Bacterial polypeptide #20409.

XX Recombinant DNA construct; transformed plant; improved plant property;

XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;

XX pathogen tolerance; pest tolerance; plant disease resistance;

XX cell cycle pathway modification; plant growth regulator;

XX homologous recombination; seed oil yield; protein yield; carbohydrate;

XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

XX bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI, 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide

XX for expression of a polynucleotide encoding a polypeptide from a

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XX

FT microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 20409; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 457 AA;

Query Match 100.0%; Score 32; DB 8; Length 457;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYDNH 5  
Db 235 DYDNH 239

RESULT 12

ID ADN18693 standard; protein; 465 AA.

XX AC ADN18693;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #1346.

KM Recombinant DNA construct; transformed plant; improved plant property;  
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KM pathogen tolerance; pest tolerance; plant disease resistance;  
KM cell cycle pathway modification; plant growth regulator;  
KM homologous recombination; seed oil yield; protein yield; carbohydrate;  
KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KM bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX (CAO Y.  
XX (HINKLE G J.  
XX (SLATER S C.  
XX (CHEN X.  
XX (GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX DR WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide  
XX for expression of a polynucleotide encoding a polypeptide from a  
XX microbial source, useful for producing plants with improved properties.  
XX Claim 1; SEQ ID NO 1346; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 465 AA;

Query Match 100.0%; Score 32; DB 8; Length 465;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYDNH 5  
Db 241 DYDNH 245

RESULT 13

ID ABB92826 standard; protein; 473 AA.

XX AC ABB92826;

XX DT 31-MAY-2002 (first entry)

XX DE Herbicidally active polypeptide SEQ ID NO 2037.

XX OS Herbicidal; plant; agriculture; herbicide.

XX PN Arabidopsis thaliana.

XX PD WO200210210-A2.

XX PF 07-FEB-2002.

XX PR 26-AUG-2001; 2001WO-BP009892.

XX (FARB ) BAYER AG.

XX Tietjen K, Weidner M;

DR WPI; 2002-269010/31.  
XX  
XX Identifying plant target proteins for herbicidally active compounds,  
PT comprising aligning and comparing nucleic acid or amino acid sequences  
PT from plant with nucleic acid or amino acid sequences from non-plant  
PT organisms.  
XX  
XX Claim 5; SEQ ID NO 2037; 261pp + Sequence Listing; English.  
PS  
CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
CC for herbicidally active compounds, comprising aligning and comparing  
CC nucleic acid or amino acid sequences from plant with nucleic acid or  
CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
CC herbicides  
XX  
XX Sequence 473 AA;  
SQ  
Query Match 100.0%; Score 32; DB 5; Length 473;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYDMH 5  
DB 62 DYDMH 66  
RESULT 14  
AAAG3283  
ID AAM93283 standard; protein: 493 AA.  
AC AAM93283;  
DT 06-NOV-2001 (first entry)  
XX  
XX Human polypeptide, SEQ ID NO: 2764.  
DE  
XX Human, full length cDNA; cDNA synthesis; oligo-capping.  
XX  
XX Homo sapiens.  
OS  
XX EPI130094-A2.  
PN  
XX  
XX 05-SEP-2001.  
PD  
XX 07-JUL-2000; 2000EP-00114089.  
PF  
XX 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183765.  
XX  
XX (HELI-) HELIX RES INST.  
PA  
XX  
XX Oca T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
PI WPI; 2001-524255/58.  
XX  
XX N-PSDB; AAK94202.  
DR  
XX 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
PT  
XX  
XX Disclosure; SEQ ID NO 2764; 1380pp + Sequence Listing; English.  
PS  
CC The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
CC been determined. Primers for synthesizing the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA

CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a polypeptide provided in the  
CC specification. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in CD-ROM format directly  
CC from EPO  
XX  
XX Sequence 493 AA;  
SQ  
Query Match 100.0%; Score 32; DB 4; Length 493;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYDMH 5  
DB 50 DYDMH 54  
RESULT 15  
ADL30731  
ID ADL30731 standard; protein: 493 AA.  
AC ADL30731;  
DT 20-MAY-2004 (first entry)  
XX  
XX Human protein encoded by a full length cDNA clone seqid 2764.  
DE  
XX human, medicine; signal transduction; glycoprotein; transcription;  
KW oligo-capping method.  
KW  
XX Homo sapiens.  
OS  
XX EPI136543-A2.  
PN  
XX 10-MAR-2004.  
PD  
XX 07-JUL-2000; 2003EP-00025638.  
PF  
XX 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183865.  
PR 07-JUL-2000; 2000EP-00114089.  
XX  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
PA  
XX  
XX Oca T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
PI WPI; 2004-204755/20.  
XX  
XX N-PSDB; ADL30730.  
DR  
XX New oligonucleotide primers (830 cDNAs) Useful for synthesizing full  
PT length human cDNAs.  
PT  
XX  
XX Example 1; SEQ ID NO 2764; 1340pp; English.  
PS  
XX This invention relates to a novel primer useful for synthesizing full  
CC length cDNA molecules that encode human proteins. Specifically, it refers  
CC to secretory or membrane proteins that are potential therapeutic agents/  
CC target molecules in the field of medicine, and in particular genes  
CC encoding proteins that are associated with signal transduction,  
CC glycoproteins and transcription. The present invention describes a method  
CC for efficiently cloning a full length human cDNA from both the 5' and 3'  
CC ends using the oligo-capping method. This polypeptide sequence is a full  
CC length human protein of the invention.  
XX  
XX Sequence 493 AA;  
SQ  
Query Match 100.0%; Score 32; DB 8; Length 493;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DYDWH	5
Db	50	DYDWH	54

Search completed: November 21, 2005, 12:20:05  
Job time : 8.69414 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 ; Search time 1.21795 Seconds  
(without alignments)  
394.995 Million cell updates/sec

Title: US-10-632-706-159

Perfect score: 32

Sequence: 1 DYDMH 5

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	93	2 A37263	Ig heavy chain V r
2	32	100.0	101	2 I37262	Ig heavy chain V r
3	32	100.0	319	2 A69675	6-phosphofructokin
4	32	100.0	465	2 F71213	probable H(+)-tran
5	32	100.0	473	2 D85041	hypothetical prote
6	32	100.0	984	2 AB0290	insecticidal toxin
7	29	90.6	284	2 T04491	hypothetical prote
8	29	90.6	286	2 A84797	hypothetical prote
9	29	90.6	301	2 AH3431	cobalt-zinc-cadmium
10	29	90.6	495	2 A26396	T-cell surface gly
11	29	90.6	824	2 T36818	probable secreted
12	29	90.6	825	2 A59296	alpha-L-arabinofur
13	29	90.6	986	2 A65116	hypothetical prote
14	29	90.6	1016	2 T25433	hypothetical prote
15	29	90.6	1266	2 AF0911	probable exported
16	29	90.6	1266	2 A85989	hypothetical prote
17	29	90.6	1266	2 F91143	hypothetical prote
18	28	87.5	80	2 PH1166	Ig heavy chain V r
19	28	87.5	149	2 AB0812	conserved hypotet
20	28	87.5	266	2 A85114	hypothetical prote
21	28	87.5	266	2 B97983	hypothetical prote
22	28	87.5	273	2 H70849	hypothetical prote
23	28	87.5	279	2 G97143	probable membrane
24	28	87.5	298	1 WMLJLK	bel-1 protein - 81
25	28	87.5	298	1 A28260	chromosomal protei
26	28	87.5	311	2 S18740	bell protein - sim
27	28	87.5	321	2 B98200	hypothetical prote
28	28	87.5	321	2 AG3086	formyltetrahydrofo
29	28	87.5	327	2 AC1615	glycine betaine/ca

30	28	87.5	328	2 AE1252	glycine betaine/ca
31	28	87.5	354	2 A75087	acetyl ornithine d
32	28	87.5	367	2 E87340	Rieske 2Fe-2S fami
33	28	87.5	368	2 S40627	hypothetical prote
34	28	87.5	371	2 T18558	probable mitochond
35	28	87.5	409	2 A48890	transcription acti
36	28	87.5	448	2 AB2740	acetyl-CoA carboxy
37	28	87.5	448	2 H97520	biotin carboxylase
38	28	87.5	459	2 A13384	biotin carboxylase
39	28	87.5	473	2 H69762	two-component sens
40	28	87.5	498	2 F88359	protein Y51HA.5 f
41	28	87.5	499	2 S74396	hypothetical prote
42	28	87.5	500	2 B83364	poveridine biosynt
43	28	87.5	511	2 G90455	acid phosphatase
44	28	87.5	517	2 T27101	hypothetical prote
45	28	87.5	544	2 S24915	gene 18 protein -

#### ALIGNMENTS

##### RESULT 1

A37263  
Ig heavy chain V region (4A9) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Aug-1991 #sequence\_revision 03-Apr-1992 #text\_change 16-Aug-1996

C/Accession: A37263

R/Goshorn, S.C.; Retzel, E.; Jemerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A/Title: Common structural features among monoclonal antibodies binding the same antigen

A/Reference number: A38601; MUID:91115823; PMID:1703527

A/Accession: A37263

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-93 <GOS>

A/Cross-references: UNIPARC:UPI0000176AE0; GB:M57996

A/Note: the authors translated the codon CNA for residue 38 as His, AGA for residue 39 as

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 93;  
Best Local Similarity 100.0%; Pred. No. 3.5;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|||||  
DB 15 DYDMH 19

##### RESULT 2

I37262  
Ig heavy chain V region (1G1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Aug-1991 #sequence\_revision 30-Aug-1991 #text\_change 23-Jul-1999

C/Accession: I37262

R/Goshorn, S.C.; Retzel, E.; Jemerson, R.

J. Biol. Chem. 266, 2134-2142, 1991

A/Title: Common structural features among monoclonal antibodies binding the same antigen

A/Reference number: A38601; MUID:91115823; PMID:1703527

A/Accession: I37262

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-101 <GOS>

A/Cross-references: UNIPARC:UPI0000115185; GB:M57995; NID:G195375; PIDD:AAA6334.1; PID:G

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|||||

Db 23 DYDMH 27

RESULT 3  
A69675 6-phosphofructokinase pfk - Bacillus subtilis

C/Species: Bacillus subtilis

C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C/Accession: A69675

C/Kunitz: F.; Ogatawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C./ Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A./ Shilich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gallie

tech, J.; Harwood, C.R.; Hentz, A.; Hilbert, H.; Holappel, S.; Hosono, S.; Hullo, M.F.

koetter, P.; Koningsreth, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A/Authors: Lauber, U.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maues

Y., M.; Ogawa, K.; Ogatawara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli

Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A/Authors: Schleicher, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, Y.; Sekowska, A.; Serot

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A/Authors: Yoshikawa, H.F.; Zumbstein, B.; Yoshikawa, H.; Datchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: A69675

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-319 <KUN>

A/Cross-references: UNIPROT:O34529; UNIPARC:UP100000608C0; GB:Z99118; GB:AL009126; NID:G

A/Experimental source: strain 168

C/Genetics:

A/Gene: pfk

C/Superfamily: ATP-dependent phosphofructokinase, prokaryotic type; 6-phosphofructokinase

F/4-278/Domain: 6-phosphofructokinase I homology <BPF1>

Query Match 100.0%; Score 32; DB 2; Length 319;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5

Db 195 DYDMH 199

RESULT 4

F71213 Probable H(+)-transporting ATP synthase subunit B - Pyrococcus horikoshii

C/Species: Pyrococcus horikoshii

C/Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 31-Dec-2004

C/Accession: F71213

R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatake, Y.; Hino, Y.; Yamamoto, S.; Seki

M.; Ohnaka, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A/Reference number: A71000; MUID:98344137; PMID:9679194

A/Accession: F71213

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-465 <KAM>

A/Cross-references: UNIPROT:O57729; UNIPARC:UP10000138167; GB:AP000007; NID:G3236134; PI

A/Experimental source: strain OT3

A/Note: this accession replaces an interim accession for a sequence replaced by Genbank

C/Genetics:

A/Gene: PH1974

C/Superfamily: H(+)-transporting ATP synthase

F/183-354/Domain: H+-transporting ATP synthase alpha chain homology <AP>

Query Match 100.0%; Score 32; DB 2; Length 465;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5

Db 241 DYDMH 245

RESULT 5  
D85041 Hypothetical protein AT4g03260 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C/Accession: D85041

R/anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A/Reference number: A85001; MUID:20083488; PMID:10617198

A/Accession: D85041

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-473 <STO>

A/Cross-references: UNIPROT:Q92R05; UNIPARC:UP100000488F1; GB:NC\_001268; NID:G7270196; P

C/Genetics:

A/Gene: AT4g03260

A/Map position: 4

Query Match 100.0%; Score 32; DB 2; Length 473;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5

Db 62 DYDMH 66

RESULT 6

AE0290 Insecticidal toxin [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis

C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C/Accession: AE0290

R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibbali, R.W.; Holden, M.T.G.; Prentice, M.B.;

deno-Terraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, E

Nature 413, 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AE0290

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-984 <KUR>

A/Cross-references: UNIPROT:Q8ZE10; UNIPARC:UP100000CD8FE; GB:AL590842; PIDN:CAC91185.1;

C/Genetics:

A/Gene: sepc

Query Match 100.0%; Score 32; DB 2; Length 984;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5

Db 834 DYDMH 838

RESULT 7

T04491 Hypothetical protein FER16.60 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004

C/Accession: T04491

R/Beyan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hohenberg, J.; Mewer

submitted to the Protein Sequence Database, April 1998

A/Reference number: Z15375

A/Accession: T04491

A/Molecule type: DNA

A/Residues: 1-204 <BEV>

A:Cross-references: UNIPROT:O49574; UNIPARC:UPI00000A96C5; EMBL:AL021633  
A:Experimental source: cultivar Columbia; BAC clone F8F16  
C:Genetics:  
A:Map position: 4  
A:Note: F8F16.60

Query Match 90.6%; Score 29; DB 2; Length 204;  
Best Local Similarity 80.0%; Pred. No. 39;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
DB 188 DYDLH 192

## RESULT 8

A84797  
hypothetical protein At2g37780 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C:Accession: A84797

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffett, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.;  
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84797

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-286 <STD>

A:Cross-references: UNIPROT:O7XUP2; UNIPARC:UPI00001623D2; GB:AE002093; NID:G4895206; PI

A:Genetics:  
A:Gene: At2g37780  
A:Map position: 2

Query Match 90.6%; Score 29; DB 2; Length 286;  
Best Local Similarity 80.0%; Pred. No. 56;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
DB 45 DYDLH 49

## RESULT 9

AH3431  
cobalt-zinc-cadmium resistance protein czcd [imported] - Brucella melitensis (strain 16M

C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004

C:Accession: AH3431

R:DeVechio, V.G.; Kaprat, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,  
J.; Manur, M.; Goldstein, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessé

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD325; PMID:11756688

A:Accession: AH3431

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-301 <KUR>

A:Cross-references: UNIPROT:O8YPT2; UNIPARC:UPI0000058084; GB:AE008917; PIDN:AAL52619.1;  
A:Experimental source: strain 16M

C:Genetics:  
A:Gene: BME11438  
A:Map position: 1

C:Superfamily: zinc transporter Znt-2

Query Match 90.6%; Score 29; DB 2; Length 301;  
Best Local Similarity 80.0%; Pred. No. 60;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
DB 111:1

DB 279 DYDLH 283

## RESULT 10

A26396  
T-cell surface glycoprotein CD5 precursor [validated] - human

N:Alternate names: T1/Lew-1 antigen

C:Species: Homo sapiens (man)  
C:Date: 17-Sep-1987 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004

C:Accession: A26396

R:Jones, N.H.; Clabby, M.L.; Dialyna, D.P.; Huang, H.J.S.; Herzenberg, L.A.; Strominger,  
Nature 323, 346-349, 1986

A:Title: Isolation of complementary DNA clones encoding the human lymphocyte glycoprotein

A:Reference number: A26396; MUID:87014786; PMID:3093892

A:Accession: A26396

A:Molecule type: mRNA

A:Residues: 1-495 <JON>

A:Cross-references: UNIPROT:P06127; UNIPARC:UPI0000012AD; GB:X04391; NID:G37186; PIDN:C

A:Experimental source: lymphoblastoid tumor cell line HPB-ALL

A:Note: parts of this sequence, including the amino end of the mature protein, were confi

C:Genetics:  
A:Gene: GDB:CD5; LEU1

A:Cross-references: GDB:120579; OMIM:153340

A:Map position: 11q13.1-11q13.1

C:Superfamily: T-cell surface glycoprotein CD5; scavenger receptor cysteine-rich domain }  
C:Keywords: duplication; glycoprotein; T-cell; transmembrane protein  
F/1-24/Domains: signal sequence #status predicted <SIG>  
F/25-495/Product: T-cell surface glycoprotein CD5 #status experimental <MAT>  
F/25-371/Domains: extracellular #status predicted <EXT>  
F/32-133/Domains: scavenger receptor cysteine-rich domain homology <SRC1>  
F/158-268/Domains: scavenger receptor cysteine-rich domain homology #status atypical <SRC>  
F/273-368/Domains: scavenger receptor cysteine-rich domain homology <SRC3>  
F/377-402/Domains: transmembrane #status predicted <TM>  
F/403-495/Domains: intracellular #status predicted <CYT>  
F/116,241/Binding site: carbohydrate (Asn) (dovalent) #status predicted

Query Match 90.6%; Score 29; DB 1; Length 495;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
DB 486 DYDLH 490

## RESULT 11

T36818

probable secreted arabinosidase - Streptomyces coelicolor

C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T36818

R:Oliver, K.; Harris, D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, September 1998

A:Reference number: Z21615

A:Accession: T36818

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-824 <OLA>

A:Cross-references: UNIPROT:O88043; UNIPARC:UPI00000DAD66; EMBL:AL031541; PIDN:CAA20794.1;  
A:Experimental source: strain AJ(2)

C:Genetics:  
A:Gene: SCODB:SC135.05C

C:Superfamily: Streptomyces alpha-L-arabinofuranosidase SC135.05C

Query Match 90.6%; Score 29; DB 2; Length 824;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
DB 634 DYDLH 638

## RESULT 12

A/Species: Streptomyces chartreusis  
C/Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
C/Accession: A59296  
R/Matsu, N.; Kaneko, S.; Kuroki, A.; Kobayashi, H.; Kusakabe, I.  
Biochem. J. 346, 9-15, 2000  
A/Title: Purification, characterization and gene cloning of two alpha-L-arabinofuranosidase  
A/Reference number: A59296; MUID:20125575; PMID:1055733  
A/Accession: A59296  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-825 <MAT>  
A/Cross-references: UNIPROT:P82593; UNIPARC:UPI0000125127; GB:AB023625; PIDD:BA90771.1  
C/Superfamily: Streptomyces alpha-L-arabinofuranosidase SC135.05c

Query Match 90.6%; Score 29; DB 2; Length 825;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
DB 635 DYDLH 639

## RESULT 13

G65116  
hypothetical protein b3245 - Escherichia coli (strain K-12)  
C/Species: Escherichia coli  
C/Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C/Accession: G65116  
R/Battnner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Ch.  
A.; Rose, D.J.; Mau, B.; Siao, Y.  
Science 277, 1453-1462, 1997  
A/Title: The complete genome sequence of Escherichia coli K-12.  
A/Reference number: A64720; MUID:9742617; PMID:9278503  
A/Accession: G65116  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-986 <BLAT>  
A/Cross-references: UNIPROT:P46474; UNIPARC:UPI0000131619; GB:AE000403; GB:U00096; NID:G  
C/Superfamily: Escherichia coli hypothetical protein yhdP

Query Match 90.6%; Score 29; DB 2; Length 986;  
Best Local Similarity 80.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
DB 804 DYDLH 808

## RESULT 14

T25433  
hypothetical protein ZK524.4 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T25433; T27888  
R/McMurray, A.  
submitted to the EMBL Data Library, May 1996  
A/Reference number: Z20033

A/Accession: T25433  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1016 <WIL>  
A/Cross-references: UNIPROT:Q22855; UNIPARC:UPI000007F2B3; EMBL:Z72517; PIDD:CAA96698.1;  
A/Experimental source: clone T28F4  
R/Gardner, A.  
submitted to the EMBL Data Library, June 1996  
A/Reference number: Z20435  
A/Accession: T27888

A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1016 <WIL>  
A/Cross-references: UNIPARC:UPI000007F2B3; EMBL:Z73912; PIDD:CAA98148.1; GSPDB:GN00019; C  
C/Experimental source: clone ZK524  
C/Accession: T25433  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-825 <MAT>  
A/Cross-references: UNIPROT:P82593; UNIPARC:UPI0000125127; GB:AB023625; PIDD:BA90771.1  
C/Superfamily: Streptomyces alpha-L-arabinofuranosidase SC135.05c

Query Match 90.6%; Score 29; DB 2; Length 1016;  
Best Local Similarity 80.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
DB 107 DYDLH 111

## RESULT 15

AF0911  
probable exported protein [imported] - Salmonella enterica subsp. enterica serovar Typh  
C/Species: Salmonella enterica subsp. enterica serovar Typh  
A/Note: this species has also been called Salmonella typhi  
C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C/Accession: AF0911  
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dord, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A/Reference number: AB0502; MUID:21534947; PMID:11677608  
A/Accession: AF0911  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1266 <PAR>  
A/Cross-references: UNIPARC:UPI00000CDBA6; GB:AL51382; PIDD:CAD07884.1; PIDD:G16504431; C  
C/Superfamily: Escherichia coli hypothetical protein yhdP

Query Match 90.6%; Score 29; DB 2; Length 1266;  
Best Local Similarity 80.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
DB 1084 DYDLH 1088

Search completed: November 21, 2005, 12:22:17  
Job time : 3.21795 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:45:55 ; Search time 7.39927 Seconds  
(without alignments)  
476.756 Million cell updates/sec

Title: US-10-632-706-159  
Perfect score: 32  
Sequence: 1 DYDMH 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	100.0	123	Q4GYZ8_TRYRYP	Q4GYZ8 trypanosoma
2	100.0	129	Q4GYZ5_TRYRYP	Q4GYZ5 trypanosoma
3	100.0	276	Q5B0Z9_TRENTI	Q5B0Z9 aspergillus
4	100.0	287	Q5NH60_PPRAT	Q5NH60 francisella
5	100.0	319	K6PF_BACGU	Q4529 bacillus su
6	100.0	326	Q4IH26_GIBZE	Q4IH26 gibberella
7	100.0	340	Q7N656_PHOUL	Q7N656 photorhabdu
8	100.0	462	VATB_PYRPU	Q8U445 pyrococcus
9	100.0	465	VATB_PYRHO	Q57729 pyrococcus
10	100.0	473	Q9ZRD5_ARATH	Q9ZRD5 arabidopsis
11	100.0	493	Q8KCL6_HUMAN	Q8KCL6 homo sapien
12	100.0	521	Q64B03_SARCH	Q64B03 uncultured
13	100.0	562	Q6B878_XENTR	Q6B878 xenopus tro
14	100.0	564	IF31_HUMAN	Q9Y262 homo sapien
15	100.0	564	Q5QTR1_HUMAN	Q5QTR1 homo sapien
16	100.0	564	Q53H01_HUMAN	Q53H01 homo sapien
17	100.0	564	Q53HT4_HUMAN	Q53HT4 homo sapien
18	100.0	564	Q5T115_HUMAN	Q5T115 homo sapien
19	100.0	564	Q91YE4_MOUSE	Q91YE4 mus musculu
20	100.0	564	Q8QZY1_MOUSE	Q8QZY1 m eukaryoti
21	100.0	564	Q5F428_CHICK	Q5F428 gallus gall
22	100.0	607	Q6ICD2_HUMAN	Q6ICD2 homo sapien
23	100.0	637	Q53LNU_ORISA	Q53LNU oryza sativ
24	100.0	641	Q53LNU_ORISA	Q53LNU oryza sativ
25	100.0	677	Q8GJ05_ARATH	Q8GJ05 arabidopsis
26	100.0	796	Q38354_BRLIH	Q38354 lactococcus
27	100.0	858	Q9VR06_DROME	Q9VR06 drosophila
28	100.0	973	Q9P9Z0_GENTR	Q9P9Z0 serralia ps
29	100.0	982	Q66A38_YEERS	Q66A38 yersinia ps
30	100.0	984	Q8ZE10_YEERS	Q8ZE10 yersinia pe
31	100.0	1697	Q7RTE2_PLAYO	Q7RTE2 plasmidium

32	100.0	2320	Q9XYM9_TRIYA	Q9XYM9 trichomonas
33	90.6	99	Q53IF4_ORISA	Q53IF4 oryza sativ
34	90.6	131	Q4G346_EMRU	Q4G346 emiliania h
35	90.6	176	Q7QX88_GIALA	Q7QX88 giardia lam
36	90.6	204	Q49574_ARATH	Q49574 arabidopsis
37	90.6	282	Q5XD57_STRP4	Q5XD57 streptococc
38	90.6	282	Q9A0V2_STRP4	Q9A0V2 streptococc
39	90.6	282	Q7CNP3_STRP6	Q7CNP3 streptococc
40	90.6	282	Q8P1X2_STRP3	Q8P1X2 streptococc
41	90.6	286	Q7XJP2_ARATH	Q7XJP2 arabidopsis
42	90.6	297	Q8G236_BRUSU	Q8G236 bruceella su
43	90.6	300	Q4PSA6_ARATH	Q4PSA6 arabidopsis
44	90.6	301	Q8YFT2_BRIME	Q8YFT2 bruceella me
45	90.6	305	Q4TML7_9SPRN	Q4TML7 erythrobact

## ALIGNMENTS

RESULT 1  
Q4GYZ8\_TRYRYP PRELIMINARY; PRT; 123 AA.  
ID Q4GYZ8\_TRYRYP PRELIMINARY;  
AC Q4GYZ8;  
DT 13-SEP-2005 (TREMBLrel. 31, Created)  
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE Calpain-like protein, putative.  
GN ORFNames=Ib927.1.2230;  
OS Trypanosoma brucei.  
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
CX NCBI\_TaxID=5691;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=927/4 GUTa10.1;  
RA Hall N., Berriman M., Lennard N.J., Harris B.R., Hertz-Fowler C.,  
RA Bart-delebase E.N., Gerrard C.S., Atkid R.J., Barron A.J., Bowman S.,  
RA Bray-Allen S.P., Bringaud F., Clark L.N., Corton C.H., Cronin A.,  
RA Davies R., Doggett J., Fraser A., Gruter E., Hall S., Harper A.D.,  
RA Kay M.P., Leech V., Mayes R., Price C., Quail M.A., Rabinowitch B.,  
RA Reiter C., Rutherford K., Saase J., Sharp S., Showkeen R.,  
RA Macleod A., Taylor S., Tweedie A., Turner C.M.R., Tait A., Gull K.,  
RA Barrell B., Melville S.E.;  
RT "The DNA sequence of chromosome I of an African trypanosome: gene  
content, chromosome organization, recombination and polymorphism";  
RL Nucleic Acids Res. 31:4864-4873(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=927/4 GUTa10.1;  
RA Hertz-Fowler C., Berriman M.,  
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL929603; CAJ16331.1; -; Genomic DNA.  
SQ SEQUENCE 123 AA; 13535 MW; 26D0156E593594F7 CRC64;  
Query Match 100.0%; Score 32; DB 2; Length 123;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYDMH 5  
DB 55 DYDMH 59  
RESULT 2  
Q4GYZ5\_TRYRYP PRELIMINARY; PRT; 129 AA.  
AC Q4GYZ5;  
DT 13-SEP-2005 (TREMBLrel. 31, Created)  
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE Calpain-like protein, putative.  
GN ORFNames=Ib927.1.2260;  
OS Trypanosoma brucei.  
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

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OX NCBI_TaxID=5691;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=927/4 GUTACT10.1;
RA Hall N., Berriman M., Lennard N.J., Harris B.R., Hertz-Fowler C.,
RA Bart-Delabesse B.N., Gerre C.S., Atkin R.J., Barron A.J., Bowman S.,
RA Bray-Allen S.P., Brington F., Clark L.N., Corcoran C.H., Cronin A.D.,
RA Davies R., Doggett J., Fraser A., Gruter E., Hall S., Harper A.D.,
RA Kay M.P., Leech V., Mayes R., Price C., Quail M.A., Rabinowitch B.,
RA Ralston C., Rutherford K., Sasse J., Sharp S., Showman R.,
RA Macleod A., Taylor S., Turner A., Turner C.M.R., Tait A., Gull K.,
RA Barrett B., Melville S.E.;
RT "The DNA sequence of chromosome I of an African trypanosome: gene
RT content, chromosome organisation, recombination and polymorphism.";
RL Nucleic Acids Res. 31:4864-4873(2003).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=927/4 GUTACT10.1;
RA Hertz-Fowler C., Berriman M.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL, AJ299603, CAJ16336.1; -; Genomic DNA.
SQ SEQUENCE 129 AA; 14030 MW; 91C28ECF31609A1A CRC64;

Query Match 100.0%; Score 32; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 54 DYDMH 58

RESULT 3
ID Q5B029 EMENI PRELIMINARY; PRT; 276 AA.
OS Q5B029;
DT 10-MAY-2005 (TREMblrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMblrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMblrel. 30, Last annotation update)
DE Hypothetical protein.
OS ORFNames=AN5781.2;
GN Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Biren B., Nisbaum C., Abouneillel A., Allen N., Anderson S.,
RA Archchi H.M., Barnes N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Develiano K.,
RA Diaz J.S., Dodge S., Doolay K., Dorris L., Ekins T., Engels R.,
RA Erickson J., Fato S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gherre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karakas A.,
RA Kelle C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Menais L.,
RA Mihova T., Mienna V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkiang P., Pierre R., Rise R., Rogov P.,
RA Rachupka A., Ramasamy U., Raymond C., Rella R., Ruse S., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkatarman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RL "Genome Sequence of Aspergillus nidulans.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an

```

```

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL, AACD01000098, EAA62874.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 276 AA; 31803 MW; 9C1E24C76A107E74 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 92 DYDMH 96

RESULT 4
ID Q5NH60 FRATT PRELIMINARY; PRT; 287 AA.
OS Q5NH60;
DT 01-FEB-2005 (TREMblrel. 29, Created)
DT 01-FEB-2005 (TREMblrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMblrel. 29, Last annotation update)
DE Beta-lactamase (EC 3.5.2.6).
OS OrderedLocNames=FTT061ic;
GN Francisella tularensis (subsp. tularensis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
OC Francisellaceae; Francisella.
OX NCBI_TaxID=119856;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Schu S4 / Schu 4;
RX PubMed=15640799; DOI=10.1038/ng1499;
RA Larsson P., Oyston P.C.F., Chain P., Chu M.C., Duffield M.,
RA Fuxelius H.-H., Garcia E., Haeiltoip G., Johansson D., Isherwood K.E.,
RA Karp P.D., Larsson E., Liu Y., Mitchell S., Prior J., Prior R.,
RA Malfatti S., Sjoestedt A., Svensson K., Thompson N., Verges L.,
RA Wagg J.K., Wren B.W., Lindler L.E., Andersson S.G.E., Foreman M.,
RA Tibball R.W.;
RT "The complete genome sequence of Francisella tularensis, the causative
RT agent of tularemia."
RL Nat. Genet. 37:153-159(2005).
DR EMBL, AJ749949; CAG45244.1; -; Genomic DNA.
DR GO; GO:0008800; F:beta-lactamase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030655; P:beta-lactam antibiotic catabolism; IEA.
DR GO; GO:0046677; P:response to antibiotic; IEA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR InterPro; IPR000008; C2.
DR Pfam; PF00144; Beta-lactamase; 1.
DR PRINTS; PRO0116; BLACTAMASEA.
DR PRINTS; PRO0360; C2DOMAIN.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 287 AA; 31982 MW; 93FC6A24A1C0383A CRC64;

Query Match 100.0%; Score 32; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 73 DYDMH 77

RESULT 5
ID K6PF_BACSU STANDARD; PRT; 319 AA.
AC 034539;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)

```

(phosphohexokinase).  
 GN Name=pfkA; Synonyms=pfk; Ordered locusNames=BSU29190;  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OK NCBI\_TaxID=1423;  
 RN NCULEOTIDE SEQUENCE.  
 RC STRAIN=168;  
 RX MEDLINE=8048467; PubMed=9387221;  
 RT Lapidus A., Galleron N., Sorokin A., Ehrlich S.-D.;  
 "sequencing and functional annotation of the Bacillus subtilis genes  
 in the 200 kb rnb-dnaB region";  
 RL Microbiology 143:3431-3441(1997).  
 [2]  
 RP NCULEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=168;  
 RX MEDLINE=8044033; PubMed=9384377; DOI=10.1038/36786;  
 RA Kunst F., Ogatawara N., Moszer I., Albertini A.M., Alloni G.,  
 Aaevedo V., Berteiro M.G., Besieres P., Bolotin A., Borchert S.,  
 Borries R., Boursier L., Brans A., Braun M., Brigelli S.C., Bron S.,  
 Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 Choi S.-K., Codani J.-J., Comerion I.F., Cummings N.J., Daniel R.A.,  
 Entian K.-D., Errington J., Fabret C., Ferrati E., Foulger D.,  
 Frits C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,  
 Gilm S.-Y., Glaeser P., Goffeau A., Gollightly B.J., Grandi G.,  
 Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 Hilbert H., Holtepel S., Hosono S., Hulio M.-F., Itaya M.,  
 Jones L.-M., Joris B., Karamata D., Kasahara Y., Kaefer-Blanchard M.,  
 Klein C., Kobayashi Y., Koetter P., Kontingstein G., Krohn S.,  
 Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,  
 Lagreche V., Lee S.-M., Levine A., Liu H., Maeda S., Manuel C.,  
 Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,  
 Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,  
 Park S.-H., Parro V., Pohl T.M., Portetelle D., Portwollk S.,  
 Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,  
 Rey M., Reynolds S., Rieger M., Rivolta C., Rocha B., Roche B.,  
 Rose M., Sadale Y., Sato T., Scanlan B., Schleich S., Schroeter R.,  
 Scoffone P., Sekiguchi J., Sekowska A., Seror S.J., Serron P.,  
 Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,  
 Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpeira P.,  
 Tognoni A., Tosato V., Uchiyama S., Vandenberg M., Vandler F.,  
 Vassarotti A., Viali A., Wambuit R., Wedler H.,  
 Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,  
 Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumbstein B.,  
 Yoshikawa H., Zurchin A.,  
 RA The complete genome sequence of the Gram-positive bacterium Bacillus  
 subtilis.  
 RT Nature 390:249-256(1997).  
 RL Nature 390:249-256(1997).  
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-  
 fructose 1,6-bisphosphate.  
 CC -1- PATHWAY: Key control step of glycolysis.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: Belongs to the phosphofructokinase family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 CC EMBL, AF008220; AAC00343.1; -; Genomic DNA.  
 CC EMBL, Z99118; CAB14879.1; -; Genomic DNA.  
 CC F1R, A69675; A69675.  
 CC HSP, P00512; 3PEK.  
 CC SMR, O34529; 1-319.  
 CC Subtilin; BG12644; pfkA.  
 CC HAMAP, MF\_00339; -; 1.  
 CC InterPro, IPR012003; ATP\_PFK\_prok.  
 CC InterPro, IPR012828; pfkA\_ATP.  
 CC InterPro, IPR000023; pfkfructinase.  
 CC PANTHER, PTHR13697; pfkfructinase; 1.

DR pfam, PF00365; PFK; 1.  
 DR PIRSF, PIRSF000532; ATP\_PFK\_prok; 1.  
 DR PRINTS, PR00476; PFRCTKINASE.  
 DR ProDom, PD000707; Pfrctkinase; 1.  
 DR TIGRFAMs, TIGR02482; PFKA\_ATP; 1.  
 DR PROSITE, PS00433; PHOSPHOFRUCTOKINASE; 1.  
 KW Allosteric enzyme, ATP-binding, Complete proteome, Glycolysis, Kinase,  
 Magnesium, Metal-binding, Nucleotide-binding, Transferase.  
 KW NP\_BIND 21 25  
 FT NP\_BIND 154 158 ATP (By similarity).  
 FT NP\_BIND 171 187 ATP (By similarity).  
 FT ACT\_SITE 127 127 Proton acceptor (By similarity).  
 FT METAL 185 185 Magnesium (via carbonyl oxygen) (By  
 similarity).  
 FT METAL 187 187 Magnesium (By similarity).  
 FT BINDING 162 162 Substrate (By similarity).  
 FT BINDING 243 243 Substrate (By similarity).  
 FT BINDING 249 249 Substrate (By similarity).  
 FT BINDING 252 252 Substrate (By similarity).  
 SQ SEQUENCE 319 AA; 34254 MW; 706C8C7F9BCFCDC CRC64;  
 Query Match 100.0%; Score 32; DB 1; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYDMH 5  
 Db 195 DYDMH 199  
 RESULT 6  
 Q41H26 GIBZE PRELIMINARY; PRT; 326 AA.  
 ID Q41H26 GIBZE PRELIMINARY; PRT; 326 AA.  
 AC Q41H26;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 OS ORFNames=FG03162.1;  
 GN Gibberella zeae PH-1.  
 CC Gibberellales; Hypocerales; Nectriaceae; Gibberella.  
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 CC Hypocerales; Nectriaceae; Gibberella.  
 OK NCBI\_TaxID=229533;  
 RN [1]  
 RP NCULEOTIDE SEQUENCE.  
 RC STRAIN=PH-1;  
 RA Archchi H.M., Barna N., Bastien V., Bidom T., Boguslavsky L.,  
 Bouhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,  
 Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Darelilano K.,  
 Diaz J.S., Dodge S., Dooley K., Dorris U., Elkins T., Engels R.,  
 Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,  
 Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,  
 Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,  
 Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,  
 Kelle C., Landers T., Levine R., Lindblad-Toh K., Liu G., Liu A.,  
 Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,  
 Matthews C., Mauceli B., McCarthy M., Meldrum J., Menus L.,  
 Mihova T., Miene V., Murphy T., Naylor J., Nguyen C., Nicol R.,  
 Nielsen C.B., Nochu C., O'Connor T., O'Donnell P., O'Neill D.,  
 Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,  
 Rachung A., Ramasamy U., Raymond C., Reta R., Rise K., Rogov P.,  
 Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Shtromov S.,  
 Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,  
 Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,  
 Vasiliev H., Venkatarman V.S., Viel R., Vo A., Wang S., Wilson B.,  
 Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,  
 Lander E.;  
 RA "Fusarium graminearum genome sequence";  
 RT Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.



```

DR EMBL: AACM01000148; EAA72902.1; -; genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 326 AA; 35576 MW; F211C78983428339 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 2; Length 326;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 292 DYDMH 296

RESULT 7
Q7N656_PHOHL
ID Q7N656_PHOHL PRELIMINARY; PRT; 340 AA.
AC Q7N656;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Similarities with C-terminal region of insecticidal toxin.
GN OrderedLocustNames=Plu1712;
OS Photobacterium luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photobacterium.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TF01;
RC MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rustiok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Teourt S., Bocs S., Bouraux-Eude C., Chandler M., Charles J.-F.,
RA Dasse E., Daroche R., Derzelle S., Freydisse G., Gaudreau S.,
RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,
RA Zouine M., Glaeser P., Boemare N., Danchin A., Kunst F.,
RT "The genome sequence of the entomopathogenic bacterium Photobacterium
RT luminescens."
RT Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL: BX571864; CAEL4005.1; -; Genomic_DNA.
DR Photobacterium plu1712; -.
KM Complete proteome.
SQ SEQUENCE 340 AA; 37562 MW; 4CFDA1FDA20BC91B CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 2; Length 340;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 194 DYDMH 198

RESULT 8
VATB_PYRFU
ID VATB_PYRFU STANDARD; PRT; 462 AA.
AC OBU4A5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE V-type ATP synthase beta chain (EC 3.6.3.14) (V-type ATPase subunit
DE B).
GN Name=atpB; OrderedLocustNames=PF0183;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.,
RT "The complete sequence of the Pyrococcus furiosus genome."
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Produces ATP from ADP in the presence of a proton

```

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CC gradient across the membrane. The archaeal beta chain is a
CC regulatory subunit.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AE010144; AAL80307.1; -; Genomic_DNA.
CC HAMAP: MF_00310; -; 1.
CC DR InterPro: IPR005724; ATP_synth_B.
CC DR InterPro: IPR000793; ATPase_a/b_C.
CC DR InterPro: IPR004100; ATPase_a/b_N.
CC DR InterPro: IPR000194; ATPase_a/bcentre.
CC DR Pfam: PF00006; ATP-synt_ab; 1.
CC DR Pfam: PF00306; ATP-synt_ab; 1.
CC DR Pfam: PF02874; ATP-synt_ab_N; 1.
CC DR TIGRfam: TIGR01041; ATP_syn_B_arch; 1.
CC DR PROSITE: PS00152; ATPase_ALPHA_BETA; 1.
CC KM ATP synthesis; Complete proteome; Hydrogen ion transport; Hydrolase;
CC ion transport; Transport.
SQ SEQUENCE 462 AA; 51915 MW; 5AB9F8AFA2C86283 CRC64;

Query Match
Best Local Similarity 100.0%; Score 32; DB 1; Length 462;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 238 DYDMH 242

RESULT 9
VATB_PYRHO
ID VATB_PYRHO STANDARD; PRT; 465 AA.
AC 057729;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE V-type ATP synthase beta chain (EC 3.6.3.14) (V-type ATPase subunit
DE B).
GN Name=atpB; OrderedLocustNames=PH1974;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=OT3;
RC MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosooyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kusihide N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.,
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RT DNA Res. 5:55-76(1998).
CC -1- FUNCTION: Produces ATP from ADP in the presence of a proton
CC gradient across the membrane. The archaeal beta chain is a
CC regulatory subunit.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC EMBL; BA000001; BAA31101.1; -, Genomic\_DNA.

DR EMBL; F71213; F71213.

DR HAMAP; MF\_00310; -, 1.

DR InterPro; IPR005724; ATP\_synthA\_B.

DR InterPro; IPR000793; ATPase\_a/b\_C.

DR InterPro; IPR004100; ATPase\_a/b\_N.

DR InterPro; IPR000194; ATPase\_a/bcentre.

DR Pfam; PF00006; ATP-synt\_ab; 1.

DR Pfam; PF00306; ATP-synt\_ab\_C; 1.

DR Pfam; PF02874; ATP-synt\_ab\_N; 1.

DR TIGRFAMs; TIGR01041; ATP\_syn\_B\_arch; 1.

DR PROSITE; PS00152; ATPase\_ALPHA\_BETA; 1.

DR ATP synthase; Complete proteome; Hydrogen ion transport; Hydrolase; ion transport; Transport.

KW SEQUENCE 465 AA; 52265 MW; EDAPDFAD74C2A54 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 465;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|||||  
Db 241 DYDMH 245

RESULT 10  
Q9ZRO5 ARATH PRELIMINARY; PRT; 473 AA.

AC Q9ZRO5; (TIGR005724, 10, Created)

DT 01-MAY-1999 (TIGR005724, 10, Last sequence update)

DT 01-MAY-1999 (TIGR005724, 10, Last sequence update)

DE Hypothetical protein P4C21.19 (Hypothetical protein AT4903260).

GN Name=P4C21.19; Synonyms=AT4903260;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RA Habermann K., de la Bastide M., Huang B.N., Gnoj L., Schutz K., Preston R., Calma C., Martensen R., Parnell L.D., Dedhia N., McCombie W.R.; "Arabidopsis thaliana BAC P4C21 from chromosome IV near 17 cM." RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

RL [2]

RN NUCLEOTIDE SEQUENCE.

RA Parnell L.D.; Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RP [3]

RN NUCLEOTIDE SEQUENCE.

RA Spiegel L.A., Huang B.N., Nascimiento L.U., de la Bastide M., Vil D.M., Preston R.R., Maturo A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Wewes H.W., Lemcke K., Mayer K.F.X.; RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RL [4]

RN NUCLEOTIDE SEQUENCE.

RA EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RL EMBL; AC005275; AAD1454.1; -, Genomic\_DNA.

DR EMBL; AL161496; CAB7811.1; -, Genomic\_DNA.

DR PIR; D85041; D85041.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR007092; LRR\_SD822.

DR Pfam; PF00560; LRR\_1\_4.

DR PRINTS; PR00019; LEURICRPT.

DR Hypothetical protein; Leucine-rich repeat; Repeat.

KW SEQUENCE 473 AA; 52344 MW; 02EF2385906D5C40 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 473;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|||||  
Db 62 DYDMH 66

RESULT 11  
O8NCL6 HUMAN  
ID O8NCL6\_HUMAN PRELIMINARY; PRT; 493 AA.

AC O8NCL6; (TIGR005724, 22, Created)

DT 01-OCT-2002 (TIGR005724, 22, Last sequence update)

DT 01-OCT-2002 (TIGR005724, 22, Last sequence update)

DE 01-MAR-2004 (TIGR005724, 26, Last annotation update)

DR CDNA F130170.f1s, clone MAMMA1000370, highly similar to Ig alpha-1 chain C region.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RA [1]

RN NUCLEOTIDE SEQUENCE.

RC TISSUE=Mammary gland;

RA Otsuki T., Ota T., Nishikawa T., Hayashi K., Suzuki Y., Yamamoto J., Wakamatsu A., Kimura K., Sakamoto K., Hatanaka N., Kawai Y., Ishii S., Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Nagai K., Sugano S., Ito T.; RT "Signal Sequence and Keyword Trap in silico for Selection of Full-length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-RT Capped cDNA Libraries." RT DNA Res. 12:117-126(2005).

DR EMBL; AK074651; BAC1114.1; -, mRNA.

DR HSSP; P01876; 10M0.

DR SMR; O8NCL6; 263-471.

DR InterPro; IPR007110; Ig-1Lk.

DR InterPro; IPR003597; Ig\_C1.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF07654; C1-sect; 2.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Immunoglobulin domain.

SW SEQUENCE 493 AA; 53224 MW; 12EC07B094777101 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 493;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|||||  
Db 50 DYDMH 54

RESULT 12  
Q64BJ3\_9ARCH  
ID Q64BJ3\_9ARCH PRELIMINARY; PRT; 521 AA.

AC Q64BJ3; (TIGR005724, 28, Created)

DT 25-OCT-2004 (TIGR005724, 28, Last sequence update)

DT 25-OCT-2004 (TIGR005724, 28, Last sequence update)

DE Hypothetical protein.

GN ORFNames=G277A8\_54; ZF05277A8.

OS Uncultured archaean GZ05277A8.

OC Archaea; environmental samples.

OX NCBI\_TaxID=285382;

RN [1]

RN NUCLEOTIDE SEQUENCE.

Query Match	Similarity	Score	DB	Length
Best Local	100.0%	100.0%	Pred. No. 2.2e+02	
Matches	5	Conservative	0	Mismatches 0; Indels 0; Gaps 0
DB	247	DYDMH	251	
Qy	1	DYDMH	5	
Db	247	DYDMH	251	
RESULT 13				
Q6P878	XENTR	PRELIMINARY	PR1	562 AA.
AC	Q6P878			
DT	05-JUL-2004	(TRENBLREL. 27, Created)		
DT	05-JUL-2004	(TRENBLREL. 27, Last sequence update)		
DE	05-JUL-2004	(TRENBLREL. 27, Last annotation update)		
DR	Hypothetical protein MGC75896.			
GN	Name=MGC75896			
OS	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;			
OC	Xenopodina; Xenopus; Silurana.			
OX	NCBI_TaxID=8364;			
NP	[1]			
NP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Embryo;			
RC	MEBLIN=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marulna K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carlini P., Prange C.,			
RA	Rata S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Vallatou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Helton B., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,			
RA	Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalski R., Smallus D.E.,			
RA	Schmerer A., Schein J.E., Jones J.W., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RP	NUCLEOTIDE SEQUENCE.			
RP	TISSUE=Embryo;			
RC	Klein S., Gerhard D.S.;			
RL	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC061351; AA061351.1; -; mRNA.			
DR	Hypothetical protein.			
SO	SEQUENCE 562 AA; 59736 MW; 248BDDF08E8DE1F CRC64;			

07 1 DYDMH 5  
 |||||  
 Db 20 DYDMH 24

RESULT 14  
 IF31\_HUMAN  
 ID IF31\_HUMAN STANDARD; PRT; 564 AA.  
 AC O9Y2F;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Eukaryotic translation initiation factor 3 subunit 6 interacting  
 DE protein.  
 GN Name=EIF3S61P; ORFNames=HSPC021, HSPC025;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 CX NCBI\_TaxID=9606;  
 [1]  
 NP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RP TISSUE=Umbilical cord blood;  
 RC MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;  
 RA Zhang Q.-H., Ye M., Xu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
 RT "Cloning and functional analysis of cDNAs with open reading frames for  
 RT 300 previously undefined genes expressed in CD34+ hematopoietic  
 RT stem/progenitor cells.";  
 RL Genome Res. 10:1546-1560(2000).  
 [2]  
 NP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RP TISSUE=Brain, Cervix, and Colon;  
 RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Dichtenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA StACPeton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein W.J., Udell T.B., Tomshylyki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McGraw P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska S., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 -1- INTERACT:  
 O9H0DB:XEN2; NDExp=1; IntAct=EBI-373b19, EBI-372110;  
 -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; AF077207; AAD27002.1; -; mRNA.  
 CC EMBL; AF083243; AAD39841.1; -; mRNA.  
 CC EMBL; BC001101; AA040101.1; -; mRNA.  
 CC EMBL; BC007510; AA076510.1; -; mRNA.  
 CC EMBL; BC029265; AA029265.1; -; mRNA.  
 CC IntAct; O9Y2F; -;  
 CC Ensemble; ENSG00000100129; Homo sapiens.  
 CC HGNC; HGNC:18138; EIF3S61P.

DR InterPro; IPR011990; TPR-like\_helical.  
 KM Protein biosynthesis.  
 SQ SEQUENCE 564 AA; 66727 MW; ECBDD32192D96E3FE CRC64;

Query Match 100.0%; Score 32; DB 1; Length 564  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
 |||||  
 Db 22 DYDMH 26

## RESULT 15

OSQTRL HUMAN  
 ID OSQTRL\_HUMAN PRELIMINARY; PRT; 564 AA.  
 AC OSQTRL;  
 DT 01-FEB-2005 (TRENBLrel. 29, Created)  
 DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)  
 DE MSTRP005.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Arter;.  
 RA Hui R.T., Liu Y.Q., Liu B., Zhao B., Meng X.M., Sheng H., Xu Y.Y.,  
 RA Wang X.Y., Ye J., Song L., Gao Y., Wei Y.J., Zhang C.L., Zhang J.,  
 RA Chai M.Q., Chen J.Z., Sun Y.H., Zhou X.L., Jiang Y.X., Zhao X.W.,  
 RA Liu S., Cao H.Q., Zhao Y., Liu D.Q., Ding J.F., Liu L.S., Gao R.L.,  
 RA Wu Q.Y., Qiang B.Q., Yuan J.G., Liew C.C., Zhao M.S.;  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF109359; AAQ13507.1; -; mRNA.  
 SQ SEQUENCE 564 AA; 66739 MW; 415F13C1FEB8C4DB CRC64;

Query Match 100.0%; Score 32; DB 2; Length 564;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
 |||||  
 Db 22 DYDMH 26

Search completed: November 21, 2005, 12:04:14  
 Job time : 9.39927 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:31 / Search time 1.88645 Seconds  
(without alignments)  
219.131 Million cell updates/sec

Title: US-10-632-706-159  
Perfect score: 32  
Sequence: 1 DYDMH 5

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PCUTS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	93	2	US-09-621-976-5904
2	32	100.0	142	2	US-09-513-999C-5024
3	32	100.0	149	2	US-09-621-976-5116
4	32	100.0	150	2	US-09-621-976-5112
5	32	100.0	150	2	US-09-621-976-5117
6	32	100.0	160	2	US-09-621-976-5115
7	32	100.0	161	2	US-09-621-976-5114
8	32	100.0	176	2	US-09-621-976-5113
9	32	100.0	163	2	US-09-621-976-5111
10	29	90.6	20	2	US-09-688-017-216
11	29	90.6	528	2	US-09-543-681A-6551
12	29	90.6	1019	2	US-09-902-540-15997
13	29	90.6	1279	2	US-09-489-039A-13602
14	28	87.5	60	2	US-09-331-930A-27
15	28	87.5	94	2	US-09-270-767-60718
16	28	87.5	120	2	US-10-092-246-9
17	28	87.5	120	2	US-10-096-246A-9
18	28	87.5	156	2	US-09-270-767-45241
19	28	87.5	205	2	US-09-270-767-58924
20	28	87.5	231	2	US-09-328-352-4910
21	28	87.5	262	2	US-09-583-110-5208
22	28	87.5	266	2	US-09-134-000C-5984
23	28	87.5	433	2	US-09-270-767-43555
24	28	87.5	446	2	US-09-543-681A-7270
25	28	87.5	517	2	US-09-252-991A-25364
26	28	87.5	527	2	US-09-270-767-45390
27	27	84.4	97	2	US-09-534-717-615

28	27	84.4	99	2	US-09-270-767-60648	Sequence 60648, A
29	27	84.4	116	1	US-07-634-278-56	Sequence 56, Appl
30	27	84.4	116	1	US-07-634-278-57	Sequence 57, Appl
31	27	84.4	116	1	US-07-634-278-73	Sequence 73, Appl
32	27	84.4	116	1	US-08-477-728-56	Sequence 56, Appl
33	27	84.4	116	1	US-08-477-728-57	Sequence 57, Appl
34	27	84.4	116	1	US-08-477-728-73	Sequence 73, Appl
35	27	84.4	116	1	US-08-474-040-56	Sequence 56, Appl
36	27	84.4	116	1	US-08-474-040-57	Sequence 57, Appl
37	27	84.4	116	1	US-08-474-040-73	Sequence 73, Appl
38	27	84.4	116	1	US-08-487-200-56	Sequence 56, Appl
39	27	84.4	116	1	US-08-487-200-57	Sequence 57, Appl
40	27	84.4	116	1	US-08-487-200-73	Sequence 73, Appl
41	27	84.4	116	2	US-08-545-809A-101	Sequence 101, Appl
42	27	84.4	116	2	US-08-484-537-56	Sequence 56, Appl
43	27	84.4	116	2	US-08-484-537-57	Sequence 57, Appl
44	27	84.4	116	2	US-08-484-537-73	Sequence 73, Appl
45	27	84.4	116	2	US-09-515-697-101	Sequence 101, Appl

## ALIGNMENTS

```
RESULT 1
US-09-621-976-5904
; Sequence 5904, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5904
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -82...-1
US-09-621-976-5904

Query Match      100.0%; Score 32; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 DYDMH 5
Db      22 DYDMH 26

RESULT 2
US-09-513-999C-5024
; Sequence 5024, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2,REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5024
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/ LENGTH: 142  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-513-999C-5024

Query Match 100.0%; Score 32; DB 2; Length 142;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|||  
Db 22 DYDMH 26

RESULT 3  
US-09-621-976-5116  
/ Sequence 5116, Application US/09621976  
/ Patent No. 6639063  
/ GENERAL INFORMATION:  
/ APPLICANT: Dumas Milne Edwards, J.B.  
/ APPLICANT: Jobert, S.  
/ APPLICANT: Giordano, J.Y.  
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
/ FILE REFERENCE: GENSET.054PR2  
/ CURRENT APPLICATION NUMBER: US/09/621,976  
/ CURRENT FILING DATE: 2000-07-21  
/ NUMBER OF SEQ ID NOS: 19335  
/ SOFTWARE: Patent.pm  
/ SEQ ID NO 5116  
/ LENGTH: 149  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-621-976-5116

Query Match 100.0%; Score 32; DB 2; Length 149;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|||  
Db 22 DYDMH 26

RESULT 4  
US-09-621-976-5112  
/ Sequence 5112, Application US/09621976  
/ Patent No. 6639063  
/ GENERAL INFORMATION:  
/ APPLICANT: Dumas Milne Edwards, J.B.  
/ APPLICANT: Jobert, S.  
/ APPLICANT: Giordano, J.Y.  
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
/ FILE REFERENCE: GENSET.054PR2  
/ CURRENT APPLICATION NUMBER: US/09/621,976  
/ CURRENT FILING DATE: 2000-07-21  
/ NUMBER OF SEQ ID NOS: 19335  
/ SOFTWARE: Patent.pm  
/ SEQ ID NO 5112  
/ LENGTH: 150  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-621-976-5112

Query Match 100.0%; Score 32; DB 2; Length 150;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|||  
Db 22 DYDMH 26

RESULT 5

US-09-621-976-5117  
/ Sequence 5117, Application US/09621976  
/ Patent No. 6639063  
/ GENERAL INFORMATION:  
/ APPLICANT: Dumas Milne Edwards, J.B.  
/ APPLICANT: Jobert, S.  
/ APPLICANT: Giordano, J.Y.  
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
/ FILE REFERENCE: GENSET.054PR2  
/ CURRENT APPLICATION NUMBER: US/09/621,976  
/ CURRENT FILING DATE: 2000-07-21  
/ NUMBER OF SEQ ID NOS: 19335  
/ SOFTWARE: Patent.pm  
/ SEQ ID NO 5117  
/ LENGTH: 150  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: UNSURE  
/ LOCATION: 134  
/ OTHER INFORMATION: Xaa = Asp,Glu  
/ NAME/KEY: UNSURE  
/ LOCATION: 66  
/ OTHER INFORMATION: Xaa = Leu,Met  
US-09-621-976-5117

Query Match 100.0%; Score 32; DB 2; Length 150;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|||  
Db 22 DYDMH 26

RESULT 6  
US-09-621-976-5115  
/ Sequence 5115, Application US/09621976  
/ Patent No. 6639063  
/ GENERAL INFORMATION:  
/ APPLICANT: Dumas Milne Edwards, J.B.  
/ APPLICANT: Jobert, S.  
/ APPLICANT: Giordano, J.Y.  
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
/ FILE REFERENCE: GENSET.054PR2  
/ CURRENT APPLICATION NUMBER: US/09/621,976  
/ CURRENT FILING DATE: 2000-07-21  
/ NUMBER OF SEQ ID NOS: 19335  
/ SOFTWARE: Patent.pm  
/ SEQ ID NO 5115  
/ LENGTH: 160  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-621-976-5115

Query Match 100.0%; Score 32; DB 2; Length 160;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|||  
Db 22 DYDMH 26

RESULT 7  
US-09-621-976-5114  
/ Sequence 5114, Application US/09621976  
/ Patent No. 6639063  
/ GENERAL INFORMATION:  
/ APPLICANT: Dumas Milne Edwards, J.B.  
/ APPLICANT: Jobert, S.  
/ APPLICANT: Giordano, J.Y.  
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
US-09-621-976-5114

FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621.976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 5114  
LENGTH: 161  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-621-976-5114

Query Match 100.0%; Score 32; DB 2; Length 161;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 22 DYDMH 26

RESULT 8  
US-09-621-976-5113  
Sequence 5113, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621.976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 5113  
LENGTH: 163  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: UNSURB  
LOCATION: 148  
OTHER INFORMATION: Xaa = His, Pro  
US-09-621-976-5113

Query Match 100.0%; Score 32; DB 2; Length 163;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 22 DYDMH 26

RESULT 9  
US-09-621-976-5111  
Sequence 5111, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621.976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 5111  
LENGTH: 176  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-621-976-5111

Query Match 100.0%; Score 32; DB 2; Length 176;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 22 DYDMH 26

RESULT 10  
US-09-688-017-216  
Sequence 216, Application US/09688017  
Patent No. 6942881  
GENERAL INFORMATION:  
APPLICANT: Lu, Peter S.  
APPLICANT: Rabinowitz, Joshua D.  
APPLICANT: Schweitzer, Johannes  
APPLICANT: Arbor Vita Corporation  
TITLE OF INVENTION: Molecular Interactions in Hematopoietic  
TITLE OF INVENTION: Cells  
FILE REFERENCE: 020054-001110US  
CURRENT APPLICATION NUMBER: US/09/688.017  
CURRENT FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 60/134,114  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US 60/134,117  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US 60/134,118  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US 60/160,860  
PRIOR FILING DATE: 1999-10-21  
PRIOR APPLICATION NUMBER: US 60/162,498  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 60/170,453  
PRIOR FILING DATE: 1999-12-13  
PRIOR APPLICATION NUMBER: US 60/176,195  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: US 60/182,296  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: US 60/196,267  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: US 60/196,460  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: US 60/196,527  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: US 60/196,528  
PRIOR FILING DATE: 2000-04-11  
NUMBER OF SEQ ID NOS: 383  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 216  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: AA49L CDS PL peptide  
US-09-688-017-216

Query Match 90.6%; Score 29; DB 2; Length 20;  
Best Local Similarity 80.0%; Pred. No. 13;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 11 DYDLH 15

RESULT 11  
US-09-543-681A-6551  
Sequence 6551, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543.681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 6551  
LENGTH: 528  
TYPE: PRT  
ORGANISM: *Proteus mirabilis*  
US-09-543-681A-6551

Query Match 90.6%; Score 29; DB 2; Length 528;  
Best Local Similarity 80.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 231 DYDLH 235

RESULT 12  
US-09-502-540-15897  
Sequence 15897, Application US/0902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/502,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 15897  
LENGTH: 1019  
TYPE: PRT  
ORGANISM: *Myxococcus xanthus*  
US-09-502-540-15897

Query Match 90.6%; Score 29; DB 2; Length 1019;  
Best Local Similarity 80.0%; Pred. No. 7.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 658 DYDLH 662

RESULT 13  
US-09-489-039A-13602  
Sequence 13602, Application US/09489039A  
Patent No. 6610835  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *KLEBSIELLA*  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 13602  
LENGTH: 1279  
TYPE: PRT  
ORGANISM: *Klebsiella pneumoniae*  
US-09-489-039A-13602

Query Match 90.6%; Score 29; DB 2; Length 1279;  
Best Local Similarity 80.0%; Pred. No. 9.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 1097 DYDLH 1101

RESULT 14  
US-09-331-930A-27  
Sequence 27, Application US/09331930A  
Patent No. 6436670  
GENERAL INFORMATION:  
APPLICANT: ZIMMET, PAUL Z.  
APPLICANT: COLLIER, GREGORY  
TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
FILE REFERENCE: 22975-20007.00  
CURRENT APPLICATION NUMBER: US/09/331,930A  
CURRENT FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: PCT/AU98/00902  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: AU PP0117/97  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: AU PP0323/97  
PRIOR FILING DATE: 1997-11-11  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 27  
LENGTH: 60  
TYPE: PRT  
ORGANISM: *Arabidopsis thaliana*  
US-09-331-930A-27

Query Match 87.5%; Score 28; DB 2; Length 60;  
Best Local Similarity 80.0%; Pred. No. 63;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 49 DYDLH 53

RESULT 15  
US-09-270-767-60718  
Sequence 60718, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 60718  
LENGTH: 94  
TYPE: PRT  
ORGANISM: *Drosophila melanogaster*  
US-09-270-767-60718

Query Match 87.5%; Score 28; DB 2; Length 94;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 35 DYDLH 39

Search completed: November 21, 2005, 12:07:40  
Job time : 2.88645 secs





; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 163  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-163

Query Match 100.0%; Score 32; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
Db 1 DYDMH 5

RESULT 3  
US-10-632-706-167  
; Sequence 167; Application US/10632706  
; Publication No. US20040175385A1  
; GENERAL INFORMATION:  
; APPLICANT: MARKS, JAMES D.  
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
; FILE REFERENCE: 407T-895120US  
; CURRENT APPLICATION NUMBER: US/10/632,706  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US 60/400,721  
; PRIOR FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: US 09/144,806  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 167  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-167

Query Match 100.0%; Score 32; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
Db 1 DYDMH 5

RESULT 4  
US-10-632-706-171  
; Sequence 171; Application US/10632706  
; Publication No. US20040175385A1  
; GENERAL INFORMATION:  
; APPLICANT: MARKS, JAMES D.  
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
; FILE REFERENCE: 407T-895120US  
; CURRENT APPLICATION NUMBER: US/10/632,706  
; CURRENT FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: US 60/400,721  
; PRIOR FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: US 09/144,806  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 278  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 171  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-171

Query Match 100.0%; Score 32; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
Db 1 DYDMH 5

RESULT 5  
US-10-424-599-176475  
; Sequence 176475; Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovacic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 176475  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1) - (73)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_130375C.1.pep  
US-10-424-599-176475

Query Match 100.0%; Score 32; DB 4; Length 73;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
Db 47 DYDMH 51

RESULT 6  
US-10-450-763-50856  
; Sequence 50856; Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 50856  
; LENGTH: 144

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-450-763-50856

Query Match 100.0%; Score 32; DB 5; Length 144;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
Db 26 DYDMH 30

RESULT 7  
US-10-779-461-18  
Sequence 18, Application US/10779461  
Publication NO. US20040166544A1  
GENERAL INFORMATION:  
APPLICANT: Morton, Philip A  
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS  
FILE REFERENCE: 00980/1  
CURRENT APPLICATION NUMBER: US/10/779,461  
CURRENT FILING DATE: 2004-02-13  
PRIOR APPLICATION NUMBER: 60/447,073  
PRIOR FILING DATE: 2003-02-13  
NUMBER OF SEQ ID NOS: 161  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 18  
LENGTH: 253  
TYPE: PRT  
ORGANISM: artificial  
FEATURE:  
OTHER INFORMATION: phage display generated human antibody  
US-10-779-461-18

Query Match 100.0%; Score 32; DB 4; Length 233;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
Db 31 DYDMH 35

RESULT 8  
US-10-369-493-23241  
Sequence 23241, Application US/10369493  
Publication NO. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 23241  
LENGTH: 319  
TYPE: PRT  
ORGANISM: Bacillus subtilis  
US-10-369-493-23241

Query Match 100.0%; Score 32; DB 4; Length 319;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5

Db 195 DYDMH 199

RESULT 9  
US-10-369-493-20409  
Sequence 20409, Application US/10369493  
Publication NO. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 20409  
LENGTH: 457  
TYPE: PRT  
ORGANISM: Pyrococcus horikoshii  
US-10-369-493-20409

Query Match 100.0%; Score 32; DB 4; Length 457;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
Db 235 DYDMH 239

RESULT 10  
US-10-369-493-1346  
Sequence 1346, Application US/10369493  
Publication NO. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 1346  
LENGTH: 465  
TYPE: PRT  
ORGANISM: Pyrococcus horikoshii  
US-10-369-493-1346

Query Match 100.0%; Score 32; DB 4; Length 465;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
Db 241 DYDMH 245

RESULT 11  
US-10-514-150-10  
Sequence 10, Application US/10514150

```
/ Publication No. US20050233957A1
/ GENERAL INFORMATION:
/ APPLICANT: UNIVERSITY COLLEGE LONDON
/ APPLICANT: Kenji OKUSE
/ APPLICANT: Mark BAKER
/ APPLICANT: Louise POON
/ APPLICANT: John Nicholas WOOD
/ APPLICANT: Mubash Malik-Hall
/ TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS
/ FILE REFERENCE: 117-528 / N.88745B GCM
/ CURRENT APPLICATION NUMBER: US/10/514,150
/ PRIOR FILING DATE: 2004-11-12
/ PRIOR APPLICATION NUMBER: PCT/GB03/02225
/ PRIOR FILING DATE: 2003-05-22
/ PRIOR APPLICATION NUMBER: GB 0211833.9
/ PRIOR FILING DATE: 2002-05-22
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 10
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-514-150-10
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```
Query Match          100.0%; Score 32; DB 5; Length 564;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYDMH 5
        |||||
DB      22 DYDMH 26
```

```
RESULT 12
US-09-925-302-801
/ Sequence 801, Application US/09925302
/ Patent No. US20020044941A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA104
/ CURRENT APPLICATION NUMBER: US/09/925,302
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05918
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ PRIOR FILING DATE: 1999-03-12
/ NUMBER OF SEQ ID NOS: 896
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 801
/ LENGTH: 581
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: SITE
/ LOCATION: (1)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-801
```

```
Query Match          100.0%; Score 32; DB 3; Length 581;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 DYDMH 5
        |||||
DB      39 DYDMH 43
```

```
RESULT 13
US-09-925-302-801
/ Sequence 801, Application US/09925302
/ Publication No. US20030064072A9
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA104
/ CURRENT APPLICATION NUMBER: US/09/925,302
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05918
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ PRIOR FILING DATE: 1999-03-12
/ NUMBER OF SEQ ID NOS: 896
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 801
/ LENGTH: 581
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: SITE
/ LOCATION: (1)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-801
```

```
Query Match          100.0%; Score 32; DB 5; Length 581;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYDMH 5
        |||||
DB      39 DYDMH 43
```

```
RESULT 14
US-10-450-763-42152
/ Sequence 42152, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP3/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ PRIOR FILING DATE: 2003-06-11
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO 42152
/ LENGTH: 585
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(585)
/ OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-42152
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Query Match          100.0%; Score 32; DB 5; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 DYDMH 5
        |||||
DB      22 DYDMH 26
```

```
RESULT 15
US-10-450-763-34775
/ Sequence 34775, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
```

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIP3/US  
CURRENT APPLICATION NUMBER: US/10/450,763  
CURRENT FILING DATE: 2003-06-11  
PRIOR APPLICATION NUMBER: PCT/US01/08631  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 60736  
SOFTWARE: Custom  
SEQ ID NO 34775  
LENGTH: 596  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(596)  
OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
US-10-450-763-34775

Query Match 100.0%; Score 32; DB 5; Length 596;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DYDMH 5  
|||  
Db 22 DYDMH 26

Search completed: November 21, 2005, 12:33:39  
Job time : 8.19048 secs

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GenCore version 5.1.6  
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OM protein - protein search, using BW model

Run on: November 21, 2005, 12:04:27 / Search time 0.0915751 Seconds  
(without alignments)  
61.686 Million cell updates/sec

Title: US-10-632-706-159  
Perfect score: 32  
Sequence: 1 DYDMH 5

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
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8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	78.1	153	1	US-10-522-883-2
2	25	78.1	173	1	US-10-522-883-19
3	25	78.1	173	1	US-10-522-883-23
4	25	78.1	177	1	US-10-522-883-4
5	25	78.1	177	1	US-10-522-883-13
6	25	78.1	179	1	US-10-522-883-17
7	25	78.1	179	1	US-10-522-883-21
8	25	78.1	179	1	US-10-522-883-17
9	25	78.1	552	1	US-10-131-826A-332
10	24	75.0	503	7	US-11-082-389-290
11	23	71.9	275	1	US-10-510-386-100
12	23	71.9	278	1	US-10-131-826A-136
13	23	71.9	293	1	US-10-131-826A-456
14	23	71.9	296	7	US-11-179-977-8
15	23	71.9	628	7	US-11-074-176-244
16	23	71.9	634	1	US-10-632-150-26
17	23	71.9	937	7	US-11-057-058-55
18	22	68.8	106	7	US-11-144-248-26
19	22	68.8	213	7	US-11-172-320-4
20	22	68.8	213	7	US-11-172-320-8
21	22	68.8	213	7	US-11-174-186-42
22	22	68.8	227	1	US-10-986-501-136
23	22	68.8	236	7	US-11-144-248-47
24	22	68.8	236	7	US-11-144-248-48
25	22	68.8	236	7	US-11-144-248-51
26	22	68.8	236	7	US-11-144-248-51
27	22	68.8	236	7	US-11-144-248-51
28	22	68.8	236	7	US-11-144-248-51
29	22	68.8	236	7	US-11-144-248-51
30	22	68.8	236	7	US-11-144-248-51
31	22	68.8	236	7	US-11-144-248-51
32	22	68.8	236	7	US-11-144-248-51
33	22	68.8	236	7	US-11-144-248-51
34	22	68.8	236	7	US-11-144-248-51
35	22	68.8	236	7	US-11-144-248-51
36	22	68.8	236	7	US-11-144-248-51
37	22	68.8	236	7	US-11-144-248-51
38	22	68.8	236	7	US-11-144-248-51
39	22	68.8	236	7	US-11-144-248-51
40	22	68.8	236	7	US-11-144-248-51
41	22	68.8	236	7	US-11-144-248-51
42	22	68.8	236	7	US-11-144-248-51
43	22	68.8	236	7	US-11-144-248-51
44	22	68.8	236	7	US-11-144-248-51
45	22	68.8	236	7	US-11-144-248-51

26	22	68.8	239	7	US-11-074-176-198	Sequence 198, App
27	22	68.8	329	1	US-10-510-386-36	Sequence 36, App
28	22	68.8	330	1	US-10-510-386-196	Sequence 196, App
29	22	68.8	444	1	US-10-131-826A-498	Sequence 498, App
30	22	68.8	902	7	US-11-057-058-64	Sequence 64, App
31	22	68.8	1827	7	US-11-057-058-62	Sequence 62, App
32	22	68.8	1841	7	US-11-057-058-63	Sequence 63, App
33	22	68.8	1857	7	US-11-057-058-60	Sequence 60, App
34	22	68.8	1857	7	US-11-057-058-61	Sequence 61, App
35	22	68.8	1857	7	US-11-057-058-61	Sequence 61, App
36	21	65.6	13	1	US-10-509-170-3	Sequence 3, App
37	21	65.6	138	7	US-11-008-727-2	Sequence 2, App
38	21	65.6	204	1	US-10-131-826A-288	Sequence 288, App
39	21	65.6	234	1	US-10-997-697-47	Sequence 47, App
40	21	65.6	296	1	US-10-510-386-58	Sequence 58, App
41	21	65.6	304	7	US-11-074-176-262	Sequence 262, App
42	21	65.6	316	1	US-10-131-826A-80	Sequence 80, App
43	21	65.6	420	7	US-11-074-176-48	Sequence 48, App
44	21	65.6	468	1	US-10-131-826A-90	Sequence 90, App
45	21	65.6	470	7	US-11-008-727-20	Sequence 20, App
46	21	65.6	476	1	US-10-997-697-29	Sequence 29, App

## ALIGNMENTS

RESULT 1  
US-10-522-883-2  
Sequence 2, Application US/10522883  
Publication No. US20050249701A1  
GENERAL INFORMATION:  
APPLICANT: CYTHERIS  
TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
FILE REFERENCE: B0131W0  
CURRENT APPLICATION NUMBER: US/10/522,883  
CURRENT FILING DATE: 2005-02-02  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 153  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: r-hil-7 cDNA  
US-10-522-883-2

Query Match 78.1%, Score 25; DB 1; Length 153;  
Best Local Similarity 60.0%, Pred. No. 6.1;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 75 DFIDLH 79

RESULT 2  
US-10-522-883-19  
Sequence 19, Application US/10522883  
Publication No. US20050249701A1  
GENERAL INFORMATION:  
APPLICANT: CYTHERIS  
TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
FILE REFERENCE: B0131W0  
CURRENT APPLICATION NUMBER: US/10/522,883  
CURRENT FILING DATE: 2005-02-02  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 19  
LENGTH: 173  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: HM338PS-r-hil-7 cDNA  
US-10-522-883-19

Query Match 78.1%; Score 25; DB 1; Length 173;  
Best Local Similarity 60.0%; Pred. No. 7;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|:|:|  
Db 95 DFDLH 99

RESULT 3  
US-10-522-883-23  
; Sequence 23, Application US/10522883  
; Publication No. US20050249701A1  
; GENERAL INFORMATION:

; APPLICANT: CYTHERIS  
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
; FILE REFERENCE: B0131WO  
; CURRENT APPLICATION NUMBER: US/10/522,883  
; CURRENT FILING DATE: 2005-02-02

; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 173

; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: HMM38PS-sIL-7

US-10-522-883-23

Query Match 78.1%; Score 25; DB 1; Length 173;  
Best Local Similarity 60.0%; Pred. No. 7;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|:|:|  
Db 95 DFDLH 99

RESULT 4  
US-10-522-883-4  
; Sequence 4, Application US/10522883  
; Publication No. US20050249701A1  
; GENERAL INFORMATION:

; APPLICANT: CYTHERIS  
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
; FILE REFERENCE: B0131WO  
; CURRENT APPLICATION NUMBER: US/10/522,883  
; CURRENT FILING DATE: 2005-02-02

; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 177

; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: r-hIL-7 cDNA

US-10-522-883-4

Query Match 78.1%; Score 25; DB 1; Length 177;  
Best Local Similarity 60.0%; Pred. No. 7.1;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|:|:|  
Db 99 DFDLH 103

RESULT 5  
US-10-522-883-13  
; Sequence 13, Application US/10522883  
; Publication No. US20050249701A1  
; GENERAL INFORMATION:

; APPLICANT: CYTHERIS  
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
; FILE REFERENCE: B0131WO  
; CURRENT APPLICATION NUMBER: US/10/522,883  
; CURRENT FILING DATE: 2005-02-02

; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 177

; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: PS-sIL-7 cDNA

US-10-522-883-13

Query Match 78.1%; Score 25; DB 1; Length 177;  
Best Local Similarity 60.0%; Pred. No. 7.1;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|:|:|  
Db 99 DFDLH 103

RESULT 6  
US-10-522-883-17  
; Sequence 17, Application US/10522883  
; Publication No. US20050249701A1  
; GENERAL INFORMATION:

; APPLICANT: CYTHERIS  
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
; FILE REFERENCE: B0131WO  
; CURRENT APPLICATION NUMBER: US/10/522,883  
; CURRENT FILING DATE: 2005-02-02

; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 179

; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: EPOPS-r-hIL-7 cDNA

US-10-522-883-17

Query Match 78.1%; Score 25; DB 1; Length 179;  
Best Local Similarity 60.0%; Pred. No. 7.2;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
|:|:|  
Db 101 DFDLH 105

RESULT 7  
US-10-522-883-21  
; Sequence 21, Application US/10522883  
; Publication No. US20050249701A1  
; GENERAL INFORMATION:

; APPLICANT: CYTHERIS  
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.  
; FILE REFERENCE: B0131WO  
; CURRENT APPLICATION NUMBER: US/10/522,883  
; CURRENT FILING DATE: 2005-02-02

; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 179

; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: EPOPS-sIL-7 cDNA

US-10-522-883-21



Query Match 78.1%; Score 25; DB 1; Length 179;  
Best Local Similarity 60.0%; Pred. No. 7.2;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDM 5  
DB 101 DYDM 105

## RESULT 8

US-10-131-826A-332  
Sequence 332, Application US/10131826A  
Publication No. US20050245730A1

GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunes, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C128  
CURRENT FILING DATE: 2002-04-24  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 332  
LENGTH: 552  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-131-826A-332

Query Match 78.1%; Score 25; DB 1; Length 552;  
Best Local Similarity 60.0%; Pred. No. 24;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDM 5  
DB 268 DYDM 272

## RESULT 9

US-11-082-389-290  
Sequence 290, Application US/11082389  
Publication No. US20050244935A1

GENERAL INFORMATION:  
APPLICANT: Pompeius, Markus  
APPLICANT: Kroger, Burkhard  
APPLICANT: Schröder, Hartwig  
APPLICANT: Zelder, Oskar  
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
FILE REFERENCE: BGI-131CPCN  
CURRENT FILING DATE: 2005-03-16  
CURRENT FILING DATE: 2005-03-16  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 60/141031  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: US 60/143262  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: US 60/151281  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: DE 19930487.4  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: DE 19930489.0  
PRIOR FILING DATE: 1999-07-01  
PRIOR APPLICATION NUMBER: DE 19931549.3  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19931550.7  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19932134.5  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19941379.7  
PRIOR FILING DATE: 1999-08-31  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 446  
SEQ ID NO 290  
LENGTH: 503  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-11-082-389-290

Query Match 75.0%; Score 24; DB 7; Length 503;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDM 4  
DB 400 DYDM 403

## RESULT 10

US-10-510-386-100  
Sequence 100, Application US/10510386  
Publication No. US20050244932A1

GENERAL INFORMATION:  
APPLICANT: Andersen, Jens Tonne  
APPLICANT: Clausen, Ib Steen  
APPLICANT: Jorgensen, Peter Troels  
APPLICANT: Olsen, Peter Bjarke  
APPLICANT: Rasmussen, Michael Dolberg  
TITLE OF INVENTION: Improved Bacillus Host Cell  
FILE REFERENCE: 10294.204-US  
CURRENT FILING DATE: US/10/510,386  
CURRENT FILING DATE: 2004-10-04  
NUMBER OF SEQ ID NOS: 248  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 100  
LENGTH: 275  
TYPE: PRT  
ORGANISM: Bacillus licheniformis

US-10-510-386-100

Query Match 71.9%; Score 23; DB 1; Length 275;  
Best Local Similarity 60.0%; Pred. No. 31;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 86 DYDLY 90

## RESULT 11

US-10-131-826A-136  
; Sequence 136, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 136  
; LENGTH: 278  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-131-826A-136

Query Match 71.9%; Score 23; DB 1; Length 278;  
Best Local Similarity 60.0%; Pred. No. 31;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 109 DYSLH 113

## RESULT 12

US-10-131-826A-456  
; Sequence 456, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 456  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-131-826A-456

Query Match 71.9%; Score 23; DB 1; Length 293;  
Best Local Similarity 80.0%; Pred. No. 32;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYDMH 5  
Db 72 DCDMH 76

## RESULT 13

US-11-179-977-8  
; Sequence 8, Application US/11179977  
; Publication No. US20050249789A1  
; GENERAL INFORMATION:  
; APPLICANT: Genencor International, Inc.  
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes

FILE REFERENCE: GC511-PCT  
CURRENT APPLICATION NUMBER: US/11/179,977  
CURRENT FILING DATE: 2005-07-12  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 8  
LENGTH: 296  
TYPE: PRT  
ORGANISM: Bacillus  
US-11-179-977-8

Query Match 71.9%; Score 23; DB 7; Length 296;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 3; Conservative 1; Mismatches 0; Gaps 0;

QY 2 YDMH 5  
DB 190 YDLH 193

RESULT 14  
US-11-074-176-244  
Sequence 244, Application US/11074176  
Publication No. US20050250135A1  
GENERAL INFORMATION:  
APPLICANT: Kjaerhammer, Todd R.  
APPLICANT: Russell, William M.  
APPLICANT: Altermann, Eric  
APPLICANT: McAuliffe, Olivia  
APPLICANT: Perill, Andrea Azcarate  
TITLE OF INVENTION: Nucleic Acid Sequences Encoding  
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore  
FILE REFERENCE: 5051-694  
CURRENT APPLICATION NUMBER: US/11/074,176  
CURRENT FILING DATE: 2005-03-07  
PRIOR APPLICATION NUMBER: 60/551,161  
PRIOR FILING DATE: 2004-03-08  
NUMBER OF SEQ ID NOS: 381  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 244  
LENGTH: 628  
TYPE: PRT  
ORGANISM: Lactobacillus acidophilus  
US-11-074-176-244

Query Match 71.9%; Score 23; DB 7; Length 628;  
Best Local Similarity 60.0%; Pred. No. 74;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5  
DB 145 DHDH 149

RESULT 15  
US-10-632-150-26  
Sequence 26, Application US/10632150  
Publication No. US20050251871A1  
GENERAL INFORMATION:  
APPLICANT: Chlaui, D.  
APPLICANT: Pagano, M.  
APPLICANT: Latres, E.  
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS  
FILE REFERENCE: 5914-081  
CURRENT APPLICATION NUMBER: US/10/632,150  
CURRENT FILING DATE: 2003-07-30  
PRIOR APPLICATION NUMBER: US/09/385,219  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: 60/098,355  
PRIOR FILING DATE: 1998-08-28  
PRIOR APPLICATION NUMBER: 60/118,568  
PRIOR FILING DATE: 1999-02-03  
PRIOR APPLICATION NUMBER: 60/124,449

PRIOR FILING DATE: 1999-03-15  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 26  
LENGTH: 634  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: all Xaa positions  
OTHER INFORMATION: Xaa=unknown amino acid residue  
US-10-632-150-26

Query Match 71.9%; Score 23; DB 1; Length 634;  
Best Local Similarity 75.0%; Pred. No. 75;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YDMH 5  
DB 621 YDLH 624

Search completed: November 21, 2005, 12:33:52  
Job time : 0.191575 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:32 ; Search time 42.8425 Seconds  
(without alignments)  
328.182 Million cell updates/sec

Title: US-10-632-706-196

Perfect score: 155  
Sequence: 1 RPTSRDMSKNTLFLQMSLRADPTAVYCAR 32

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: Geneseq\_21: \*  
2: Geneseqp1980s: \*  
3: Geneseqp1990s: \*  
4: Geneseqp2000s: \*  
5: Geneseqp2001s: \*  
6: Geneseqp2002s: \*  
7: Geneseqp2003s: \*  
8: Geneseqp2004s: \*  
9: Geneseqp2005s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165	100.0	32	8	ADR38791 Mouse hea
2	165	100.0	32	8	ADR38794 Mouse hea
3	165	100.0	32	8	ADR38797 Mouse hea
4	165	100.0	32	8	ADR38800 Mouse hea
5	162	98.2	113	4	ADU02529 Antl-adip
6	162	98.2	116	5	ABG30486 Human ant
7	162	98.2	117	5	ABG30484 Human ant
8	162	98.2	118	5	ADW08865 IGF-IR an
9	162	98.2	126	4	AAg93640 Human ant
10	162	98.2	126	6	ABO27447 Antl-Rh(D
11	162	98.2	127	4	AAg93627 Human ant
12	162	98.2	127	6	ABO27434 Antl-Rh(D
13	162	98.2	127	7	ADG30422 Human GMB
14	161	97.6	115	8	ADP22238 Human ant
15	161	97.6	121	8	ADG36356 Intracell
16	161	97.6	121	8	ADG75229 Immunoglo
17	161	97.6	122	8	ADG22252 Human ant
18	161	97.6	122	8	ADP22308 Human ant
19	161	97.6	123	7	ADL91339 VH chain
20	161	97.6	463	3	AAV93701 The heavy
21	161	97.6	463	3	AAV93727 The heavy
22	161	97.6	463	3	AAV93728 The heavy
23	161	97.6	463	6	AAE35882 Human 4.1
24	161	97.6	463	6	AAE35883 Human 4.1

25	159	96.4	120	4	AAU02508	AAU02508 Antl-adip
26	158	95.8	32	2	AAE87051	AAE87051 Human gro
27	158	95.8	32	5	AAE19693	AAE19693 Human gro
28	158	95.8	32	5	AAU70472	AAU70472 Human hea
29	158	95.8	32	8	ADL93533	ADL93533 Human CD4
30	158	95.8	32	8	ADL93671	ADL93671 Human CD4
31	158	95.8	32	8	ADQ90726	ADQ90726 Antl-VEGFR
32	158	95.8	32	9	ADW96725	ADW96725 Antl-EGFR
33	158	95.8	32	9	ADW96738	ADW96738 Antl-EGFR
34	158	95.8	32	9	ADW80310	ADW80310 Human ant
35	158	95.8	32	9	ADW80297	ADW80297 Human ant
36	158	95.8	32	9	ADX27039	ADX27039 Human gro
37	158	95.8	32	9	ADY31524	ADY31524 Human ant
38	158	95.8	32	9	ADY31503	ADY31503 Human ant
39	158	95.8	32	9	ADY31398	ADY31398 Human ant
40	158	95.8	32	9	ADY31371	ADY31371 Human ant
41	158	95.8	32	9	ADY31506	ADY31506 Human ant
42	158	95.8	32	9	ADY31392	ADY31392 Human ant
43	158	95.8	32	9	ADY31374	ADY31374 Human ant
44	158	95.8	32	9	ADY31530	ADY31530 Human ant
45	158	95.8	32	9	AEA21479	AEA21479 Human ant

#### ALIGNMENTS

RESULT 1  
ID ADR38791 standard; peptide; 32 AA.  
AC ADR38791;  
DT 02-DEC-2004 (first entry)  
DE Mouse heavy chain anti-BONT-antibody framework 3 seqid 193.  
XX antihbacterial; antibody; botulinum neurotoxin type A; BONT/A;  
KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KM toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
KM framework 3.  
XX  
OS Mus sp.  
XX  
FN US2004175385-A1.  
XX  
PD 09-SEP-2004.  
XX  
PP 01-AUG-2003; 2003US-00632706.  
XX  
PR 31-AUG-1998; 98US-00144886.  
PR 01-AUG-2002; 2002US-0400721P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX Marks JD, Amersdorfer P;  
XX WPI, 2004-652009/63.  
XX  
PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
XX  
PS Example 4; SEQ ID NO 193; 110pp; English.  
XX  
CC The invention describes an isolated antibody (I) that specifically binds  
CC to an epitope specifically bound by an antibody expressed by a specific  
CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone  
CC S25, C35, C39, 1C6, 3D12, B4, 1F3, huc25, A1, Ar2, WRI(V), WRI(T), 3-1,  
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum  
CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
CC comprising BONT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I) and a composition (II) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I) and a kit comprising (I). (I) is useful for neutralising  
CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain anti-BONT-antibody framework region 3.  
XX  
SQ Sequence 32 AA;  
Query Match 100.0%; Score 165; DB 8; Length 32;  
Best Local Similarity 100.0%; Pred. No. 9.9e-16;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32  
Db 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32  
RESULT 2  
ID ADR38794 standard; peptide; 32 AA.  
XX  
AC ADR38794;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Mouse heavy chain anti-BONT-antibody framework 3 seqid 196.  
XX  
KM antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KM toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
KM framework 3.  
XX  
OS Mus sp.  
XX  
PN US2004175385-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 01-AUG-2003; 2003US-00632706.  
XX  
PR 31-AUG-1998; 98US-00144886.  
PR 01-AUG-2002; 2002US-0400721P.  
XX  
PA (REGC ) UNITV CALIFORNIA.  
XX  
PI Marks JD, Amerdorfer P;  
PI WPI; 2004-652009/63.  
XX  
PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
XX  
PS Example 4; SEQ ID NO 196; 110pp; English.  
XX  
CC The invention describes an isolated antibody (I) that specifically binds  
CC to an epitope specifically bound by an antibody expressed by a specific  
CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone  
CC S25, C25, C39, IC6, 3D12, B4, 1F3, huC25, A1, A2, WR1(V), WR1(T), 3-1,  
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum  
CC

CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)  
CC comprising BONT/A neutralising epitope having an epitope that is  
CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC ; producing (I) and a composition (II) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surplus. The following are disclosed: a pharmaceutical composition  
CC comprising (I) and a kit comprising (I). (I) is useful for neutralising  
CC BONT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surplus. (I) is useful for diagnosing the botulism  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)  
CC enables rapid detection or diagnosis of botulism. This is the amino acid  
CC sequence of mouse heavy chain anti-BONT-antibody framework region 3.  
XX  
SQ Sequence 32 AA;  
Query Match 100.0%; Score 165; DB 8; Length 32;  
Best Local Similarity 100.0%; Pred. No. 9.9e-16;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32  
Db 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32  
RESULT 3  
ID ADR38797 standard; peptide; 32 AA.  
XX  
AC ADR38797;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Mouse heavy chain anti-BONT-antibody framework 3 seqid 199.  
XX  
KM antibacterial; antibody; botulinum neurotoxin type A; BONT/A;  
KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
KM toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
KM framework 3.  
XX  
OS Mus sp.  
XX  
PN US2004175385-A1.  
XX  
PD 09-SEP-2004.  
XX  
PF 01-AUG-2003; 2003US-00632706.  
XX  
PR 31-AUG-1998; 98US-00144886.  
PR 01-AUG-2002; 2002US-0400721P.  
XX  
PA (REGC ) UNITV CALIFORNIA.  
XX  
PI Marks JD, Amerdorfer P;  
PI WPI; 2004-652009/63.  
XX  
PT New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.  
XX  
PS Example 4; SEQ ID NO 199; 110pp; English.  
XX  
CC The invention describes an isolated antibody (I) that specifically binds  
CC to an epitope specifically bound by an antibody expressed by a specific  
CC clone where (I) binds to and neutralises botulinum neurotoxin type A  
CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone  
CC

CC 525, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
CC comprising BoNT/A neutralising epitope having an epitope that is  
CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC / producing (I) and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surpluss. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising a botulinum neurotoxin which  
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surpluss, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surpluss. (I) is useful for diagnosing the botulinum  
CC or for treating pathologies associated with botulinum neurotoxin (I)  
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
CC enables rapid detection or diagnosis of botulinism. This is the amino acid  
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 3.

## SQ Sequence 32 AA;

Query Match 100.0%; Score 165; DB 8; Length 32;  
Best Local Similarity 100.0%; Pred. No. 9.9e-16;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTSRDSSKNTLFLQMSLRADPTAVYYCAR 32  
Db 1 RFTSRDSSKNTLFLQMSLRADPTAVYYCAR 32

## RESULT 4

ADR38800 standard; peptide: 32 AA.

ADR38800;

02-DEC-2004 (first entry)

Mouse heavy chain anti-BoNT-antibody framework 3 seqid 202.

antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;  
BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;  
toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;  
framework 3.

Mus sp.

US2004175385-A1.

09-SEP-2004.

01-AUG-2003; 2003US-00632706.

31-AUG-1998; 98US-00144886.

01-AUG-2002; 2002US-0400721P.

(REGC ) UNIV CALIFORNIA.

Marks JD, Amerdorter P.

WPI; 2004-652009/63.

New isolated antibody that neutralizes botulinum neurotoxin type A,  
PT useful for diagnosing botulinism or for treating pathologies associated  
PT with botulinum neurotoxin poisoning.

Example 4; SEQ ID NO 202; 110p; English.

The invention describes an isolated antibody (I) that specifically binds  
CC to an epitope specifically bound by an antibody expressed by a specific  
CC clone where (I) binds to and neutralises botulinum neurotoxin type A

CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope  
CC specifically bound by an antibody expressed by a clone chosen from clone  
CC 525, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,  
CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum  
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)  
CC comprising BoNT/A neutralising epitope having an epitope that is  
CC specifically bound by an antibody expressed by clones as mentioned in (I)  
CC / producing (I) and a composition (III) comprising several anti-  
CC botulinum neurotoxin antibodies, where each antibody is specific for a  
CC different epitope of a botulinum neurotoxin and the combination of  
CC antibodies shows greater toxin neutralisation than the single antibodies  
CC in surpluss. The following are disclosed: a pharmaceutical composition  
CC comprising (I); and a kit comprising a botulinum neurotoxin which  
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which  
CC involves contacting neurotoxin with (I) in surpluss, where each of (I) is  
CC specific for a different epitope of the botulinum neurotoxin and the  
CC combination of antibodies shows greater toxin neutralisation than the  
CC single antibodies in surpluss. (I) is useful for diagnosing the botulinum  
CC or for treating pathologies associated with botulinum neurotoxin  
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)  
CC enables rapid detection or diagnosis of botulinism. This is the amino acid  
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 3.

## SQ Sequence 32 AA;

Query Match 100.0%; Score 165; DB 8; Length 32;  
Best Local Similarity 100.0%; Pred. No. 9.9e-16;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTSRDSSKNTLFLQMSLRADPTAVYYCAR 32  
Db 1 RFTSRDSSKNTLFLQMSLRADPTAVYYCAR 32

## RESULT 5

AAU02529 standard; protein: 113 AA.

AAU02529;

29-AUG-2001 (first entry)

Anti-adipocyte monoclonal antibody heavy chain, FAT 19.

Antibody; adipocyte; heavy chain; light chain; obesity; fat;  
heart disease; complementarity determining region; CDR.

Homo sapiens.

WO200127279-A1.

19-APR-2001.

11-OCT-2000; 2000WO-GB003900.

12-OCT-1999; 99US-0158812P.

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Edwards BM, Main SH, Vaughan TV;

WPI; 2001-282031/29.

N-PSDB; AAS03429.

Panel of specific binding members of antibody molecules which bind to  
PT whole adipocytes is used in the treatment of obesity and obesity related  
PT diseases.

Claim 1; Page 111; 182p; English.

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid  
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,  
CC and heavy chain complementarity determining regions (CDR) of the

CC invention. The antibodies can be used in the treatment of obesity and  
 CC obesity related diseases. The antibodies can be used to deliver drugs or  
 CC pro-drugs directly to the fat mass of an obese patient or the antibody  
 CC can be used as a therapeutic itself. Antibodies binding specifically to  
 CC adipocytes can be used to activate the immune system to destroy the cells  
 CC by complement mediated lysis. The antibodies may be labeled with a  
 CC detectable label such as radiolabel, fluorescent or chemical group and  
 CC used in methods of diagnosis in human subjects e.g. to determine the  
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or  
 CC determine the presence or level of adipocytes in a cell or tissue sample.  
 CC The antibodies can be used as an alternative means of treatment for obese  
 CC patients other than undergoing surgery to remove excess fat. Antibodies  
 CC for different types of fat deposits can also be produced e.g. intra-  
 CC abdominal fat associated with heart disease

XX Sequence 113 AA;  
 SQ

Query Match 98.2%; Score 162; DB 4; Length 113;  
 Best Local Similarity 96.9%; Pred. No. 1.1e-14;  
 Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLYLQWNSLRADDTAVYYCAR 32  
 DB 67 RFTISRDNKNTLYLQWNSLRADDTAVYYCAR 98

RESULT 6  
 ABG30486 ID ABG30486 standard; protein; 116 AA.  
 XX  
 AC ABG30486;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Human anti-CD40 monoclonal antibody 12D9 heavy chain #1.  
 XX  
 XX Human; heavy chain; CD40; autoimmune disease; multiple sclerosis;  
 KM systemic lupus erythematosus; psoriasis; inflammatory bowel disease;  
 KM Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;  
 KM non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;  
 KM proliferation.  
 XX  
 XX Homo sapiens.  
 OS  
 XX MO200228904-A2.  
 PN  
 XX 11-APR-2002.  
 PD  
 XX 02-OCT-2001; 2001WO-US030857.  
 PF  
 XX 02-OCT-2000; 2000US-0237556P.  
 PR  
 XX (CHIR ) CHIRON CORP.  
 PA  
 PI Chu K, Wang C, Yoshihara C, Donnelly JY;  
 XX WPI; 2002-405169/43.  
 DR  
 XX  
 XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting  
 PT proliferation, growth or differentiation of a normal human B cells and  
 PT treating autoimmune disease such as rheumatoid arthritis or systemic  
 PT lupus erythematosus.  
 XX  
 XX Claim 8; Fig 6; 75pp; English.  
 PS  
 XX The invention relates to a human monoclonal antibody or fragment capable  
 CC of specifically binding to a human CD40 antigen (a glycoprotein expressed  
 CC on the surface of human B cells), where the antibody or fragment is free  
 CC of significant agonistic activity when it binds to the CD40 antigen, and  
 CC the growth or differentiation is inhibited. The fragments comprise the  
 CC complementarily determining region (CDR) of the light and heavy chains of  
 CC the monoclonal antibodies secreted by a hybridoma consisting of 15B8,  
 CC 20C4, 12D9, 9F7 and 13B4. Also included are the nucleic acids encoding

CC the antibody (or fragments). The antibodies or fragments are used for  
 CC inhibiting proliferation, growth or differentiation of a normal human B  
 CC cells and to inhibit antibody production by B cells. They may also be  
 CC useful for treating autoimmune diseases, such as systemic lupus  
 CC erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease  
 CC (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-  
 CC Hodgkin's lymphoma). The present sequence represents the antibody 12D9  
 CC heavy chain

XX Sequence 116 AA;  
 SQ

Query Match 98.2%; Score 162; DB 5; Length 116;  
 Best Local Similarity 96.9%; Pred. No. 1.2e-14;  
 Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLYLQWNSLRADDTAVYYCAR 32  
 DB 66 RFTISRDNKNTLYLQWNSLRADDTAVYYCAR 97

RESULT 7  
 ABG30484 ID ABG30484 standard; protein; 117 AA.  
 XX  
 AC ABG30484;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Human anti-CD40 monoclonal antibody 9F7 heavy chain #1.  
 XX  
 XX Human; heavy chain; CD40; autoimmune disease; multiple sclerosis;  
 KM systemic lupus erythematosus; psoriasis; inflammatory bowel disease;  
 KM Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;  
 KM non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;  
 KM proliferation.  
 XX  
 XX Homo sapiens.  
 OS  
 XX MO200228904-A2.  
 PN  
 XX 11-APR-2002.  
 PD  
 XX 02-OCT-2001; 2001WO-US030857.  
 PF  
 XX 02-OCT-2000; 2000US-0237556P.  
 PR  
 XX (CHIR ) CHIRON CORP.  
 PA  
 PI Chu K, Wang C, Yoshihara C, Donnelly JY;  
 XX WPI; 2002-405169/43.  
 DR  
 XX  
 XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting  
 PT proliferation, growth or differentiation of a normal human B cells and  
 PT treating autoimmune disease such as rheumatoid arthritis or systemic  
 PT lupus erythematosus.  
 XX  
 XX Claim 6; Fig 6; 75pp; English.  
 PS  
 XX The invention relates to a human monoclonal antibody or fragment capable  
 CC of specifically binding to a human CD40 antigen (a glycoprotein expressed  
 CC on the surface of human B cells), where the antibody or fragment is free  
 CC of significant agonistic activity when it binds to the CD40 antigen, and  
 CC the growth or differentiation is inhibited. The fragments comprise the  
 CC complementarily determining region (CDR) of the light and heavy chains of  
 CC the monoclonal antibodies secreted by a hybridoma consisting of 15B8,  
 CC 20C4, 12D9, 9F7 and 13B4. Also included are the nucleic acids encoding  
 CC the antibody (or fragments). The antibodies or fragments are used for  
 CC inhibiting proliferation, growth or differentiation of a normal human B  
 CC cells and to inhibit antibody production by B cells. They may also be  
 CC useful for treating autoimmune diseases, such as systemic lupus  
 CC erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease  
 CC (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-





QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32  
 DB 67 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 98

## RESULT 10

ID ABO27447 standard; protein; 126 AA.

XX ABO27447;

DT 12-SEP-2003 (first entry)

XX Anti-Rh(D) heavy chain SH54.

XX Human; RH(D) binding protein; blood typing; blood product; antibody;  
 KM magnetically activated cell sorting.

XX Homo sapiens.

XX US2003040605-A1.

XX 27-FEB-2003.

PF 04-MAY-2001; 2001US-00848798.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PR 29-JAN-1999; 99US-00240274.

XX (UTPR-) UNIV PENNSYLVANIA.

XX S1egel DL;

XX WPI; 2003-512273/48.

XX N-PSDB; ACDA5361.

XX New human Rh(D)-binding protein useful for various diagnostic and  
 PT therapeutic applications, including typing of blood or blood products.

XX Claim 4; Page 49; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein  
 CC can be used for magnetically activated cell sorting. The protein is  
 CC useful in various diagnostic and therapeutic applications in humans,  
 CC including typing of blood or blood products. The present sequence  
 CC represents the amino acid sequence of a human anti-Rh(D) chain

XX Sequence 126 AA;

Query Match 98.2%; Score 162; DB 6; Length 126;  
 Best Local Similarity 96.9%; Pred. No. 1.3e-14;

Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32

DB 67 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 98

## RESULT 11

ID AAG93627 standard; protein; 127 AA.

XX AAG93627;

DT 14-SEP-2001 (first entry)

XX Human anti-Rh(D) antibody clone SH10 protein sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;  
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.

XX Homo sapiens.  
 OS US6255455-B1.

XX 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

XX (UTPR-) UNIV PENNSYLVANIA.

XX S1egel DL;

XX WPI; 2001-388931/41.

XX N-PSDB; AAH68684.

XX Claim 1; Col 65; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,  
 CC preferably a human antibody, (I) having an amino acid sequence comprising  
 CC one of the sequences (S) given in AAG93558 to AAG93659. (I) has  
 CC immunostimulant activity, and can be used as an immune system stimulant.

CC (2) can be used in diagnostic and therapeutic medicine. The antibodies  
 CC are used in diagnostics that require human antibodies instead of animal  
 CC antibodies, such as determine the Rh phenotype of human red blood cells.

CC AAH68615 to AAH68726 represent the nucleotide sequence which encode  
 CC AAG93558 to AAG93659. AAG93670 to AAG93697 represent anti-Rh(D) heavy  
 CC chain CDR3 amino acid sequences which are given in the exemplification of  
 CC the present invention

XX Sequence 127 AA;

Query Match 98.2%; Score 162; DB 4; Length 127;  
 Best Local Similarity 96.9%; Pred. No. 1.3e-14;

Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32

DB 68 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 99

## RESULT 12

ID ABO27434 standard; protein; 127 AA.

XX ABO27434;

DT 12-SEP-2003 (first entry)

XX Anti-Rh(D) heavy chain SH10.

XX Human; RH(D) binding protein; blood typing; blood product; antibody;  
 KM magnetically activated cell sorting.

XX Homo sapiens.

XX US2003040605-A1.

XX 27-FEB-2003.

PF 04-MAY-2001; 2001US-00848798.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PR 29-JAN-1999; 99US-00240274.  
XX (UYPR-) UNIV PENNSYLVANIA.  
XX  
XX Slegel DL;  
XX WPI; 2003-512273/48.  
XX N-PSDB; ACD45348.  
XX  
XX New human Rh(D)-binding protein useful for various diagnostic and  
PT therapeutic applications, including typing of blood or blood products.  
XX  
XX Claim 4; Page 48; 187pp; English.  
XX  
XX The invention relates to an isolated Rh(D) binding protein. The protein  
CC can be used for magnetically activated cell sorting. The protein is  
CC useful in various diagnostic and therapeutic applications in humans,  
CC including typing of blood or blood products. The present sequence  
CC represents the amino acid sequence of a human anti-Rh(D) chain  
XX  
SQ Sequence 127 AA;  
XX  
Query Match 98.2%; Score 162; DB 6; Length 127;  
Best Local Similarity 96.9%; Pred. No. 1.3e-14;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
CY 1 RFTISRDNKNTLFLQNNSLRADPTAVYYCAR 32  
Db 68 RFTISRDNKNTLYLQNNSLRADPTAVYYCAR 99  
XX  
RESULT 13  
ADG30422  
ID ADG30422 standard; protein; 244 AA.  
XX  
AC ADG30422;  
XX  
XX 26-FEB-2004 (first entry)  
XX  
XX Human GMB619 scFv protein.  
XX  
XX GMB619; VH; CDR; complementarity determining region; VL; scFv;  
XX single chain antibody; antidiabetic; type II diabetes; human; GMB619.  
XX  
XX Homo sapiens.  
XX  
XX WO2003085093-A2.  
XX  
XX 16-OCT-2003.  
XX  
XX 28-MAR-2003; 2003WO-US009625.  
XX  
XX 01-APR-2002; 2002US-0368813P.  
XX  
XX (HUMA-) HUMA GENOME SCI INC.  
XX  
XX Baker KP, Albert VR, Chowdhury P;  
XX WPI; 2003-804305/75.  
XX N-PSDB; ADG30519.  
XX  
XX New antibody that specifically binds to GMB polypeptide, useful for  
PT diagnosing, monitoring, treating, preventing or ameliorating type II  
PT diabetes.  
XX  
XX Claim 2; SEQ ID NO 55; 410pp; English.  
XX  
XX The invention relates to a novel antibody that specifically binds to a  
CC GMB polypeptide comprising a first amino acid sequence that is at least  
CC 95% identical to a second amino acid sequence of a VH CDR  
CC (complementarity determining region) or VL CDR of an scFv (single chain  
CC antibody molecule). The antibody of the invention demonstrates  
CC antidiabetic activity and may be useful for diagnosing, monitoring,

CC treating, preventing or ameliorating type II diabetes. The current  
CC sequence is that of the human scFv protein of the invention.  
XX  
XX Sequence 244 AA;  
XX  
Query Match 98.2%; Score 162; DB 7; Length 244;  
Best Local Similarity 96.9%; Pred. No. 2.7e-14;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
XX  
CY 1 RFTISRDNKNTLFLQNNSLRADPTAVYYCAR 32  
Db 67 RFTISRDNKNTLYLQNNSLRADPTAVYYCAR 98  
XX  
RESULT 14  
ADP22238  
ID ADP22238 standard; protein; 115 AA.  
XX  
XX ADP22238;  
XX  
XX 09-SEP-2004 (first entry)  
XX  
XX Human anti-TNFA antibody light chain variable region SEQ ID NO:144.  
XX  
XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;  
XX anti-TNFA antibody; antibody; antiarteriosclerotic; antiarthritic;  
XX antibacterial; antiinflammatory; antipapillary; antithrombotic;  
XX eating-disorder; immunomodulator; immunosuppressive; nephrotoxic;  
XX neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;  
XX TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;  
XX bladder cancer; lung cancer; glioblastoma; stomach cancer;  
XX endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;  
XX prostate cancer; immuno-mediated inflammatory disease;  
XX rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;  
XX restenosis; autoimmune disease; Crohn's disease; graft-host reaction;  
XX septic shock; cachexia; anorexia; multiple sclerosis.  
XX  
XX Homo sapiens.  
XX  
XX WO2004050683-A2.  
XX  
XX 17-JUN-2004.  
XX  
XX 02-DEC-2003; 2003WO-US038281.  
XX  
XX 02-DEC-2002; 2002US-0430729P.  
XX  
XX (ABGE-) ABGENIX INC.  
XX  
XX Babcock JS, Kang JS, Poord O, Green U, Peng X, Klakamp S;  
XX Haek-Frendscho W, Rathnaswami P, Pigott C, Liang ML, Lee R;  
XX Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;  
XX WPI; 2004-480601/45.  
XX N-PSDB; ADP22237.  
XX  
XX New recombinant human monoclonal antibody that specifically binds to  
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such  
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid  
PT arthritis.  
XX  
XX Example 10; SEQ ID NO 144; 213pp; English.  
XX  
XX The present invention describes a human monoclonal antibody (I) that  
CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:  
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the  
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);  
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid  
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying  
CC (M1) the level of TNFA in a patient sample, comprising contacting with  
CC (I), and detecting the level of binding between the antibody and TNFA in  
CC the sample; (2) a composition comprising the antibody or its functional  
CC fragment and a carrier; (3) treating (M2) an animal suffering from a

CC neoplastic, or an immuno-mediated inflammatory disease by selecting an  
CC animal in need of treatment for the disease by administering the human  
CC monoclonal antibody of (1); and (4) inhibiting (M3) TNF $\alpha$  induced  
CC apoptosis in an animal by selecting an animal in need of treatment for  
CC TNF $\alpha$  induced apoptosis by administering the human monoclonal antibody of  
CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,  
CC antidiabetic, antiinflammatory, antihypertensive, antirheumatic, eating-  
CC disorders, immunomodulator, immunosuppressive, nephrotropic, and  
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used  
CC as a TNF $\alpha$  antagonist. The antibody (1) is useful in the preparation of  
CC medicament for treating TNF induced apoptosis, neoplastic disease such as  
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,  
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,  
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory  
CC diseases such as rheumatoid arthritis, glomerulonephritis,  
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's  
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and  
CC multiple sclerosis. The present sequence represents a human anti-TNF $\alpha$   
CC antibody light chain variable region, which is used in the  
CC exemplification of the present invention.

SQ Sequence 115 AA;

Query Match 97.6%; Score 161; DB 8; Length 115;  
Best Local Similarity 96.9%; Pred. No. 1.6e-14;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSSKNTLFLQNSISLRADDTAVYYCAR 32  
Db 66 RFTISRDNSSKNTLFLQNSISLRADDTAVYYCAR 97

RESULT 15  
ADO36356 standard; protein; 121 AA.

AC ADO36356;  
XX  
XX 26-AUG-2004 (first entry)  
XX  
XX Intracellular interaction-related scfv protein SeqID20.  
XX DE  
XX Immunoglobulin single domain; intracellular environment;  
XX KM intracellular interaction; immunoglobulin domain; scfv;  
XX KW single chain variable fragment.  
XX  
XX Unidentified.  
XX OS  
XX PN WO2004046185-A2.  
XX  
XX PD 03-JUN-2004.  
XX  
XX PF 14-NOV-2003; 2003WO-GB004942.  
XX  
XX PR 15-NOV-2002; 2002GB-00026729.  
XX  
XX (MED1-) MEDICAL RES COUNCIL.  
XX PA  
XX Rabbits TH, Tanaka T;  
XX PI  
XX WPI, 2004-431946/40.  
XX  
XX  
XX PT Determining the ability of an immunoglobulin single domain to bind to a  
XX PT target in an intracellular environment by assessing the intracellular  
XX PT interaction between the immunoglobulin domain and the target by  
XX PT monitoring the signal.  
XX  
XX  
XX PS Disclosure; SEQ ID NO 20; 66pp; English.  
XX  
XX This invention relates to a novel method of determining the ability of an  
XX CC immunoglobulin single domain to bind to a target in an intracellular  
XX CC environment comprising assessing the intracellular interaction between  
XX CC the immunoglobulin domain and the target by monitoring the signal. The

CC method comprises providing a first molecule and a second molecule, where  
CC stable interaction of the first and second molecules leads to the  
CC generation of a signal; providing a single intracellular immunoglobulin  
CC domain which is associated with the first molecule, where the single  
CC immunoglobulin domain is free of complementary immunoglobulin domains;  
CC providing an intracellular target which is associated with the second  
CC molecule, such that association of the immunoglobulin domain and the  
CC target leads to stable interaction of the first and second molecules and  
CC generation of the signal; and assessing the intracellular interaction  
CC between the immunoglobulin domain and the target by monitoring the  
CC signal. The methods are useful for determining the ability of an  
CC immunoglobulin single domain to bind to a target in an intracellular  
CC environment. The present sequence is that of a single chain variable  
CC fragment (scfv) protein which was used to illustrate the method of the  
CC invention.

SQ Sequence 121 AA;

Query Match 97.6%; Score 161; DB 8; Length 121;  
Best Local Similarity 96.9%; Pred. No. 1.7e-14;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSSKNTLFLQNSISLRADDTAVYYCAR 32  
Db 67 RFTISRDNSSKNTLFLQNSISLRADDTAVYYCAR 98

Search completed: November 21, 2005, 12:20:06  
Job time : 43.8425 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using BW model

Run on: November 21, 2005, 11:49:36 / Search time 7.79487 Seconds  
(without alignments)  
394.995 Million cell updates/sec

Title: US-10-632-706-196

Perfect score: 165  
Sequence: 1 RFTISRDNKNTLFLQNMNLSRADPTAVYYCAR 32

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	158	95.8	97	2	S26935 Ig heavy chain V r
2	158	95.8	97	2	S46462 Ig heavy chain V r
3	158	95.8	98	2	S29546 Ig heavy chain V r
4	158	95.8	105	2	S24249 Ig heavy chain V r
5	158	95.8	108	2	PH1642 Ig heavy chain V r
6	158	95.8	109	2	PH1646 Ig heavy chain V r
7	158	95.8	109	2	PH1644 Ig heavy chain V r
8	158	95.8	111	2	PH1645 Ig heavy chain V r
9	158	95.8	114	2	S46390 Ig heavy chain V r
10	158	95.8	114	2	S46391 Ig heavy chain V r
11	158	95.8	114	2	S46392 Ig heavy chain V r
12	158	95.8	116	2	B28966 Ig heavy chain pre
13	158	95.8	119	2	S31111 Ig heavy chain - h
14	158	95.8	121	2	F36005 Ig heavy chain V r
15	158	95.8	121	2	G36005 Ig heavy chain V r
16	158	95.8	122	2	S31117 Ig heavy chain - h
17	158	95.8	122	2	E36005 Ig heavy chain V r
18	158	95.8	123	2	S38493 Ig heavy chain - h
19	158	95.8	128	2	S48797 Ig heavy chain V r
20	158	95.8	130	2	S31601 Ig heavy chain V r
21	158	95.8	133	2	A49028 Ig heavy chain V-I
22	158	95.8	134	2	S31679 Ig heavy chain V r
23	158	95.8	140	2	S70442 Ig heavy chain pre
24	157	95.2	133	2	S31510 Ig heavy chain - h
25	155	93.9	52	2	S21591 Ig heavy chain V r
26	155	93.9	76	2	S31592 Ig heavy chain V r
27	155	93.9	98	2	S26889 Ig heavy chain V-I
28	155	93.9	98	2	PL0121 Ig heavy chain V-I
29	155	93.9	98	2	PL0116 Ig heavy chain V-I

30	155	93.9	98	2	S29545 Ig heavy chain V r
31	155	93.9	98	2	S29543 Ig heavy chain V r
32	155	93.9	98	2	S26896 Ig heavy chain V r
33	155	93.9	99	2	S24259 Ig heavy chain V r
34	155	93.9	100	2	S24258 Ig heavy chain V r
35	155	93.9	101	2	S24257 Ig heavy chain V r
36	155	93.9	102	2	S24256 Ig heavy chain V r
37	155	93.9	104	2	S24255 Ig heavy chain V r
38	155	93.9	106	2	S24256 Ig heavy chain V r
39	155	93.9	108	2	PH1648 Ig heavy chain V r
40	155	93.9	109	2	PH1649 Ig heavy chain V r
41	155	93.9	111	2	PH1643 Ig heavy chain V r
42	155	93.9	112	2	PH1647 Ig heavy chain V r
43	155	93.9	117	1	H3H026 Ig heavy chain pre
44	155	93.9	117	2	A45953 Ig heavy chain pre
45	155	93.9	117	2	A34964 Ig heavy chain pre

## ALIGNMENTS

## RESULT 1

S26935  
Ig heavy chain V region (DP-42) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S26935  
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Ulewelyn, M.B.; Winter, G.  
J. Mol. Biol. 227, 776-798, 1992  
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V.  
A/Reference number: S26885; MUID:93021117; PMID:1404388  
A/Accession: S26935  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-97 <TOM>  
A/Cross-references: UNIPARC:UPI0000116408; EMBL:Z12342; NID:G32905; PIDN:CAA78212.1; PID:  
C/Species: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotetramer; Immunoglobulin  
F,15-97/Domain: Immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 97;  
Best Local Similarity 93.8%; Pred. No. 9.6e-15;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMNLSRADPTAVYYCAR 32  
Db 66 RFTISRDNKNTLFLQNMNLSRADPTAVYYCAR 97

## RESULT 2

S46462  
Ig heavy chain V region (YAC-5) - human  
C/Species: Homo sapiens (man)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C/Accession: S46462  
R/Tomlinson, I.M.; Walter, G.; Rietman, H.; Carter, N.P.; Bulwela, L.; Wint  
R/Cook, G.P.; Tomlinson, I.M.; Walter, G.; Rietman, H.; Carter, N.P.; Bulwela, L.; Wint  
Nature Genet. 7, 162-168, 1994  
A/Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telome  
A/Reference number: S46460; MUID:95004581; PMID:7920635  
A/Accession: S46462  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-97 <COO>  
A/Cross-references: UNIPARC:UPI0000116509; EMBL:Z27504; NID:G505430; PIDN:CAA81824.1; PIT  
C/Species: Immunoglobulin V region; Immunoglobulin homology  
C/Keywords: heterotetramer; Immunoglobulin  
F,15-97/Domain: Immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 97;  
Best Local Similarity 93.8%; Pred. No. 9.6e-15;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMNLSRADPTAVYYCAR 32

Db 66 RFTISRDNKNTLYLQNSLRADTAVYYCAR 97

## RESULT 3

S29546

Ig heavy chain V region (COS-8 / DP-46) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-Jan-1994 #sequence\_revision 17-Nov-1995 #text\_change 23-Jul-1999

C/Accession: S29546; S26888

R/Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.

Submitted to the EMBL Data Library, October 1992

A/Reference number: S29543

A/Accession: S29546

A/Molecule type: DNA

A/Residues: 1-98 &lt;TOM&gt;

A/Cross-references: UNIPARC:UPI000002DD16; EMBL:Z17394; NID:932843; PIDD:CAA78997.1; PII

A/Note: designated COS-8

R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A/Reference number: S26885; MUID:93021117; PMID:11404388

A/Accession: S26888

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-98 &lt;TOM&gt;

A/Note: designated DP-46

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 95.8%; Score 158; DB 2; Length 98;

Best Local Similarity 93.8%; Pred. No. 9.7e-15;

Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 67 RFTISRDNKNTLYLQNSLRADTAVYYCAR 98

## RESULT 4

S24249

Ig heavy chain V region (VH26-DN1-DXPI-JH4) - human

C/Species: Homo sapiens (man)

C/Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 30-May-1997

C/Accession: S24249

R/Stewart, A.K.; Huang, C.; Scollard, B.D.; Schwartz, R.S.

Submitted to the EMBL Data Library, June 1992

A/Description: A single VH gene predominates in the rearranged and expressed human B cell

A/Reference number: S24247

A/Accession: S24249

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-105 &lt;STW&gt;

A/Cross-references: UNIPARC:UPI0000176E3E; EMBL:X67070

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/10-92/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 95.8%; Score 158; DB 2; Length 105;

Best Local Similarity 93.8%; Pred. No. 1e-14;

Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 61 RFTISRDNKNTLYLQNSLRADTAVYYCAR 92

## RESULT 5

PH1642

Ig heavy chain V region (clone 5A10) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 31-Dec-2004

C/Accession: PH1642

R/Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Saaso, E.H.

J. Exp. Med. 178, 331-336, 1993

A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc

A/Reference number: PH1642; MUID:93301610; PMID:8315388

A/Accession: PH1642

A/Molecule type: mRNA

A/Residues: 1-108 &lt;HIL&gt;

A/Cross-references: UNIPROT:Q8WUX1; UNIPARC:UPI0000176B78

C/Superfamily: immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/7-90/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 95.8%; Score 158; DB 2; Length 108;

Best Local Similarity 93.8%; Pred. No. 1.1e-14;

Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 59 RFTISRDNKNTLYLQNSLRADTAVYYCAR 90

## RESULT 6

PH1646

Ig heavy chain V region (clone 6H12) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 31-Dec-2004

C/Accession: PH1646

R/Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Saaso, E.H.

J. Exp. Med. 178, 331-336, 1993

A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc

A/Reference number: PH1642; MUID:93301610; PMID:8315388

A/Accession: PH1646

A/Molecule type: mRNA

A/Residues: 1-109 &lt;HIL&gt;

A/Cross-references: UNIPROT:Q8WUX1; UNIPARC:UPI0000176B7C

C/Superfamily: immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/7-90/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 95.8%; Score 158; DB 2; Length 109;

Best Local Similarity 93.8%; Pred. No. 1.1e-14;

Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 59 RFTISRDNKNTLYLQNSLRADTAVYYCAR 90

## RESULT 7

PH1644

Ig heavy chain V region (clone 5D11) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 31-Dec-2004

C/Accession: PH1644

R/Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Saaso, E.H.

J. Exp. Med. 178, 331-336, 1993

A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc

A/Reference number: PH1642; MUID:93301610; PMID:8315388

A/Accession: PH1644

A/Molecule type: mRNA

A/Residues: 1-109 &lt;HIL&gt;

A/Cross-references: UNIPROT:Q8WUX1; UNIPARC:UPI0000176B7A

C/Superfamily: immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/7-90/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 95.8%; Score 158; DB 2; Length 109;

Best Local Similarity 93.8%; Pred. No. 1.1e-14;

Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 RFTISRDNKNTLYLQNSLRADTAVYYCAR 32

Db 59 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 90

## RESULT 8

PH1645  
Ig heavy chain V region (clone 6C8) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 31-Dec-2004  
C:Accession: PH1645  
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasse, B.H.  
J. Exp. Med. 178, 331-336, 1993  
A>Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphylococcal protein A  
A:Reference number: PH1642; MUID:93301610; PMID:8315388  
A:Accession: PH1645  
A:Molecule type: mRNA  
A:Residues: 1-111 <H1>  
A:Cross-references: UNIPROT:Q8WTK1; UNIPARC:UPI0000176B7B  
C:Superfamily: Immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 111;  
Best Local Similarity 93.8%; Pred. No. 1.1e-14;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 32  
Db 59 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 90

## RESULT 9

S46390  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C>Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S46390  
R:Figini, M.; Marke, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A>Title: In vitro assembly of repertoires of antibody chains on the surface of phage by phage display  
A:Reference number: S46390; MUID:94254092; PMID:8196048  
A:Accession: S46390  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-114 <FIG>  
A:Cross-references: UNIPARC:UPI000011663F; EMBL:Z31686; NID:G509782; PIDN:CAA83493.1; PII  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 114;  
Best Local Similarity 93.8%; Pred. No. 1.1e-14;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 32  
Db 67 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 98

## RESULT 10

S46391  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C>Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S46391  
R:Figini, M.; Marke, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A>Title: In vitro assembly of repertoires of antibody chains on the surface of phage by phage display  
A:Reference number: S46390; MUID:94254092; PMID:8196048  
A:Accession: S46391  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-114 <FIG>

A:Cross-references: UNIPARC:UPI00001137D5; EMBL:Z31687; NID:G509784; PIDN:CAA83492.1; PII  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 114;  
Best Local Similarity 93.8%; Pred. No. 1.1e-14;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 32  
Db 67 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 98

## RESULT 11

S46392  
Ig heavy chain V region (VH-28) - human  
C:Species: Homo sapiens (man)  
C>Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S46392  
R:Figini, M.; Marke, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A>Title: In vitro assembly of repertoires of antibody chains on the surface of phage by phage display  
A:Reference number: S46390; MUID:94254092; PMID:8196048  
A:Accession: S46392  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-114 <FIG>  
A:Cross-references: UNIPARC:UPI00001137D6; EMBL:Z31688; NID:G499306; PIDN:CAA83493.1; PII  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 114;  
Best Local Similarity 93.8%; Pred. No. 1.1e-14;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 32  
Db 67 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 98

## RESULT 12

B28966  
Ig heavy chain precursor V-region chain 5A - human  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 16-Aug-1996  
C:Accession: B28966; A32782  
R:Wilson, M.R.; Middleton, D.; Warr, G.W.  
Proc. Natl. Acad. Sci. U.S.A. 85, 1566-1570, 1988  
A>Title: Immunoglobulin heavy chain variable region gene evolution: structure and family  
A:Reference number: A28966; MUID:88144476; PMID:3125551  
A:Accession: B28966  
A:Molecule type: DNA  
A:Residues: 1-116 <H1>  
A:Cross-references: UNIPARC:UPI000012CDE  
R:Wilson, M.R.; Middleton, D.; Warr, G.W.  
Proc. Natl. Acad. Sci. U.S.A. 86, 3276, 1989  
A:Reference number: A32782  
A:Contents: annotation; erratum  
A>Note: The authors note that this sequence is of higher primate (probably human) origin  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 116;  
Best Local Similarity 93.8%; Pred. No. 1.2e-14;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 32  
Db 85 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 116

## RESULT 13

G31111  
 Ig heavy chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
 C/Accession: G31111  
 R/Schroeder, P.M.; Timmers, B.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
 Eur. J. Immunol. 22, 247-251, 1992  
 A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement  
 A/Reference number: S31104; MUID:92111633; PMID:1730252  
 A/Accession: G31111  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-119 <RNA>  
 A/Cross-references: UNIPARC:UPI0000176DC2; EMBL:X62959  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 119;  
 Best Local Similarity 93.8%; Pred. No. 1.2e-14;  
 Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32  
 DB 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 98

## RESULT 14

F36005  
 Ig heavy chain V region (M49) - human  
 C/Species: Homo sapiens (man)  
 C/Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 31-Dec-2004  
 C/Accession: F36005  
 R/Schroeder Jr., H.W.; Wang, J.Y.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
 A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
 A/Reference number: A36005; MUID:9034577; PMID:2117273  
 A/Accession: F36005  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-119 <SCH>  
 A/Cross-references: UNIPROT:Q8WUK1, UNIPARC:UPI0000176C32; GB:M34026  
 C/Genetics:  
 A/Gene: GDB:IGH@; IGHDX1  
 A/Cross-references: GDB:118731; OMIM:146910  
 A/Map position: 14q32.33-14q32.33  
 C/Superfamily: immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 119;  
 Best Local Similarity 93.8%; Pred. No. 1.2e-14;  
 Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32  
 DB 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 98

## RESULT 15

G36005  
 Ig heavy chain V region (M74) - human  
 C/Species: Homo sapiens (man)  
 C/Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 31-Dec-2004  
 C/Accession: G36005  
 R/Schroeder Jr., H.W.; Wang, J.Y.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
 A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
 A/Reference number: A36005; MUID:9034577; PMID:2117273  
 A/Accession: G36005

A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-121 <SCH>  
 A/Cross-references: UNIPROT:Q8WUK1, UNIPARC:UPI0000176C2C; GB:M34031  
 C/Genetics:  
 A/Gene: GDB:IGH@; IGHDX1  
 A/Cross-references: GDB:118731; OMIM:146910  
 A/Map position: 14q32.33-14q32.33  
 C/Superfamily: immunoglobulin homology  
 C/Keywords: heterotrimer; immunoglobulin  
 F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 121;  
 Best Local Similarity 93.8%; Pred. No. 1.2e-14;  
 Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32  
 DB 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 98

Search completed: November 21, 2005, 12:22:17  
 Job time: 7.79487 secs



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:45:55 ; Search time 47.3553 Seconds  
(without alignments)  
476.756 Million cell updates/sec

Title: US-10-632-706-196  
Perfect score: 165  
Sequence: 1 RPTISRDNKNTLFLQNNSLRADPTAVYYCAR 32

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniProt\_sprot:\*  
2: uniProt\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	158	95.8	112 2 Q9UGP3_HUMAN	Q9UGP3 homo sapien
2	158	95.8	116 1 HV05_CARAU	P19181 carassius a
3	158	95.8	240 2 Q6SZC9_HUMAN	Q6SZC9 homo sapien
4	158	95.8	465 2 Q6TNT8_HUMAN	Q6TNT8 homo sapien
5	155	93.9	113 2 Q9UL90_HUMAN	Q9UL90 homo sapien
6	155	93.9	117 1 HV3C_HUMAN	P01764 homo sapien
7	155	93.9	613 2 Q8WUK1_HUMAN	Q8WUK1 homo sapien
8	153	92.7	118 2 Q9UL72_HUMAN	Q9UL72 homo sapien
9	151	91.5	112 2 Q9HCC1_HUMAN	Q9HCC1 homo sapien
10	151	91.5	118 2 Q9UL91_HUMAN	Q9UL91 homo sapien
11	151	91.5	470 2 Q6RJ44_HUMAN	Q6RJ44 homo sapien
12	151	91.5	478 2 Q6P181_HUMAN	Q6P181 homo sapien
13	151	91.5	494 2 Q96K68_HUMAN	Q96K68 homo sapien
14	151	91.5	606 2 Q6GMV2_HUMAN	Q6GMV2 homo sapien
15	150	90.9	116 2 Q9UL93_HUMAN	Q9UL93 homo sapien
16	150	90.9	122 1 HV3G_HUMAN	P01768 homo sapien
17	150	90.9	466 2 Q6N096_HUMAN	Q6N096 homo sapien
18	148	89.7	121 2 Q9UL71_HUMAN	Q9UL71 homo sapien
19	148	89.7	473 2 Q6MZV7_HUMAN	Q6MZV7 homo sapien
20	147	89.1	597 2 Q96BB9_HUMAN	Q96BB9 homo sapien
21	146	88.5	119 2 Q5F218_MOUSE	Q5F218 mus musculu
22	146	88.5	464 2 Q6MZU6_HUMAN	Q6MZU6 homo sapien
23	146	88.5	469 2 Q569P4_HUMAN	Q569P4 homo sapien
24	146	88.5	473 2 Q91Z05_MOUSE	Q91Z05 mus musculu
25	146	88.5	483 2 Q6MZK9_HUMAN	Q6MZK9 homo sapien
26	146	88.5	485 2 Q6PDB8_MOUSE	Q6PDB8 mus musculu
27	146	88.5	493 2 Q6GMX2_HUMAN	Q6GMX2 homo sapien
28	146	88.5	544 2 Q6P395_HUMAN	Q6P395 homo sapien
29	145	87.9	104 2 Q9UL87_HUMAN	Q9UL87 homo sapien
30	145	87.9	147 2 Q9Y509_HUMAN	Q9Y509 homo sapien
31	145	87.9	465 2 Q6PEC4_HUMAN	Q6PEC4 homo sapien

32	145	87.9	573 2 Q8WU38_HUMAN	Q8WU38 homo sapien
33	144	87.3	116 1 HV3T_HUMAN	P01781 homo sapien
34	144	87.3	121 1 HV3J_HUMAN	P01771 homo sapien
35	144	87.3	136 1 HV16_MOUSE	P01783 mus musculu
36	144	87.3	472 2 Q6N089_HUMAN	Q6N089 homo sapien
37	144	87.3	483 2 Q566J7_MOUSE	Q566J7 mus musculu
38	144	87.3	499 2 Q8NSK4_HUMAN	Q8NSK4 homo sapien
39	143	86.7	120 1 HV3B_HUMAN	P01766 homo sapien
40	143	86.7	126 1 HV3K_HUMAN	P01772 homo sapien
41	143	86.7	417 2 Q6N093_HUMAN	Q6N093 homo sapien
42	142	86.1	95 2 Q9ULB6_HUMAN	Q9ULB6 homo sapien
43	142	86.1	480 2 Q6N094_HUMAN	Q6N094 homo sapien
44	141	85.5	114 1 HV3B_HUMAN	P01763 homo sapien
45	141	85.5	115 1 HV3F_HUMAN	P01767 homo sapien

## ALIGNMENTS

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RESULT 1
Q9UGP3_HUMAN                                PRT; 112 AA.
ID Q9UGP3_HUMAN PRELIMINARY;
AC Q9UGP3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
GN Name=IGH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zafiroopoulos A., Kandiloglaniaki M., Dahlenborg C., Borrebaeck C.A.K.,
RA Krambovitis E.;
RL EMBL; AJ132560; CAB65078.1; -; mRNA.
DR HSSP; P01783; IIGC.
DR SMR; Q9UGP3; 1-105.
DR Ensembl; ENSG0000018443; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 112 AA; 12226 MW; 0A1F17082C7A8CE3 CRC64;
SQ
Query Match 95.8%; Score 158; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 4,7e-15;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPTISRDNKNTLFLQNNSLRADPTAVYYCAR 32
DB 50 RPTISRDNKNTLFLQNNSLRADPTAVYYCAR 81
RESULT 2
HV05_CARAU                                STANDARD; PRT; 116 AA.
ID HV05_CARAU
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
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RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=88144476; PubMed=3125551;  
RA Wilson M.R., Middleton D., Watt G.W.;  
RT "Immunoglobulin heavy chain variable region gene evolution: structure  
and family relationships of two genes and a pseudogene in a teleost  
fish";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).  
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
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CC HSP, P01783, 1IGC.  
DR SMR; P19181; 20-116.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
KM Immunoglobulin domain; Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 116 Ig heavy chain V region 5A.  
FT REGION 20 49 Framework-1.  
FT REGION 50 54 Complementarity-determining-1.  
FT REGION 55 68 Framework-2.  
FT REGION 69 84 Complementarity-determining-2.  
FT REGION 85 116 Framework-3.  
FT DISULFID 41 114 By similarity.  
FT NON\_TER 116 116  
SQ SEQUENCE 116 AA; 12808 MM; 9C2279E2DF199B12 CRC64;  
  
Query Match 95.8%; Score 158; DB 1; Length 116;  
Best Local Similarity 93.8%; Pred. No. 4.9e-15;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RFTISRDNKNTLFLQNSLRADTAAYYCAR 32  
Db 85 RFTISRDNKNTLFLQNSLRADTAAYYCAR 116  
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ID 065ZC9\_HUMAN PRELIMINARY; PRT; 240 AA.  
AC 065ZC9;  
DT 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE Single-chain Fv (Fragment).  
GN Name=scFv;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=C1g/7;  
RC MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;  
RA Komterman R.E., Wing M.G., Winter G.;  
RT "Complement recruitment using bispecific diabodies";  
RL Nat. Biotechnol. 15:629-631(1997).  
DR EMBL; Y13056; CAAT3499.1; -; mRNA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003596; IG\_v.  
DR SMART; SM00406; IG; 2.  
DR SMART; SM00409; IG; 2.  
DR PROSITE; PSS0835; IG\_LIKE; 2.  
FT NON\_TER 1 1  
FT NON\_TER 240 240  
SQ SEQUENCE 240 AA; 25569 MM; FDCFD3645F64B373 CRC64;

Query Match 95.8%; Score 158; DB 2; Length 240;  
Best Local Similarity 93.8%; Pred. No. 1.1e-14;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RFTISRDNKNTLFLQNSLRADTAAYYCAR 32  
Db 67 RFTISRDNKNTLFLQNSLRADTAAYYCAR 98  
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RESULT 4  
ID 06IN78\_HUMAN PRELIMINARY; PRT; 466 AA.  
AC 06IN78;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE IGHG1 protein.  
GN Name=IGHG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Peripheral Nervous System;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Bennett C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Musunna K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uebli T.B., Tomihata S., Carninci P., Prange C.J.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulvaney S.J.,  
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield V.S.N., Krzyzanski M.I., Skalka U., Smalley D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Peripheral Nervous System;  
RG NIH MGC Project;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC072419; AAH72419.1; -; mRNA.  
DR HSP; P01861; IADQ.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003597; IG\_cl.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-sect; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 4.  
DR PROSITE; PSS0290; IG\_MHC; UNKNOWN\_2.  
SQ SEQUENCE 466 AA; 50854 MM; 53EB0BCBDE81076E CRC64;  
  
Query Match 95.8%; Score 158; DB 2; Length 466;  
Best Local Similarity 93.8%; Pred. No. 2.3e-14;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 RFTISRDNKNTLFLQNSLRADTAAYYCAR 32  
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marisita K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshlyuk S., Carninci P., Prange C.,  
 RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Rahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallbone D.E.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,  
 RT "generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE-Primary B-Cells;  
 RG NIH MCC Project;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=2117273;  
 RA Schroeder H.W., Jr., Wang J.Y.,  
 RT "Preferential utilization of conserved immunoglobulin heavy chain  
 RT variable gene segments during human fetal life.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).  
 [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;  
 RA Cislinter A.M., Rumoux F., Fougereau M., Tommelle C.,  
 RT "IGM kappa/Lambda BBV human B cell clone: an early step of  
 RT differentiation of fetal B cells or a distinct B lineage?";  
 RL Mol. Immunol. 29:1363-1373(1992).  
 [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1730252;  
 RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,  
 RA Schuurman R.K.,  
 RT "Restricted utilization of germ-line VH3 genes and short diverse third  
 RT complementarity-determining regions (CDR3) in human fetal B lymphocyte  
 RT immunoglobulin heavy chain rearrangements.",  
 RL Eur. J. Immunol. 22:247-251(1992).  
 [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1904154;  
 RA Neale G.A., Kitchingman G.R.,  
 RT "mRNA transcripts initiating within the human immunoglobulin mu heavy  
 RT chain enhancer region contain a non-translatable exon and are  
 RT extremely heterogeneous at the 5' end.",  
 RL Nucleic Acids Res. 19:2427-2433(1991).  
 [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=2840480; DOI=10.1084/jem.168.1.229;  
 RA Bird U., Gallili N., Link W., Stiles D., Sklar J.,  
 RT "Continuing rearrangement but absence of somatic hypermutation in  
 RT immunoglobulin genes of human B cell precursor leukemia.",  
 RL J. Exp. Med. 168:229-245(1988).  
 [8]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=2538551; DOI=10.1084/jem.169.4.1391;  
 RA Nickerson K.G., Berman J., Glickman B., Chess L., Alt F.W.,  
 RT "Early human IGH gene assembly in Epstein-Barr virus-transformed fetal  
 RT B cell lines: Preferential utilization of the most 3H-proximal D  
 RT segment (DQ52) and two unusual VH-related rearrangements.",  
 RL J. Exp. Med. 169:1391-1403(1989).  
 [9]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93301610; PubMed=6315388; DOI=10.1084/jem.176.1.331;  
 RA Hiltson J.L., Karr N.S., Oppliger I.R., Mannik M., Sasso E.H.,

RT "The structural basis of germline-encoded VH3 immunoglobulin binding  
 RT to streptococcal protein A.",  
 RL J. Exp. Med. 178:331-336(1993).  
 DR EMBL/ BC020240; AAH20240.1; -, mRNA.  
 DR PIR/ F36005; F36005.  
 DR PIR/ G36005; G36005.  
 DR PIR/ PH1642; PH1642.  
 DR PIR/ PH1643; PH1643.  
 DR PIR/ PH1645; PH1645.  
 DR PIR/ PH1646; PH1646.  
 DR PIR/ P10098; P10098.  
 DR PIR/ P10120; P10120.  
 DR PIR/ S15590; S15590.  
 DR PIR/ S31116; S31116.  
 DR PIR/ S31119; S31119.  
 DR PIR/ S70442; S70442.  
 DR HSSP/ P01861; 1ADQ.  
 DR SMR/ Q8WOK1; 20-242.  
 DR Ensembl/ ENSG00000130076; Homo sapiens.  
 DR InterPro/ IPR007110; Ig\_1like.  
 DR InterPro/ IPR003597; Ig\_C1.  
 DR InterPro/ IPR003006; Ig\_MHC.  
 DR InterPro/ IPR003596; Ig\_V.  
 DR Pfam/ PF07654; C1-sect; 4.  
 DR SMART/ SM00406; IGV; 1.  
 DR PROSITE/ PS50835; IG\_LIKE; 5.  
 DR PROSITE/ PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Immunoglobulin domain.  
 SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 93.9%; Score 155; DB 2; Length 613;  
 Best Local Similarity 90.6%; Pred. No. 8,7e-14;  
 Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSKNTFLQMSLRADDTVYICAK 32  
 DB 86 RFTISRDNSKNTLYLQMSLRADDTVYICAK 117

RESULT 8  
 Q9UL72\_HUMAN  
 ID Q9UL72\_HUMAN PRELIMINARY; PRT; 118 AA.  
 AC Q9UL72;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernay S.M.,  
 RA Young D.C.,  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.",  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 [2]  
 RP PROTEIN SEQUENCE.  
 RX PubMed=1555592;  
 RA Makiya R., Stigbrand T.,  
 RT "Placental alkaline phosphatase has a binding site for the human  
 RT immunoglobulin-G Fc portion.",  
 RL Eur. J. Biochem. 205:341-345(1992).  
 DR EMBL/ AF035042; AAD56278.1; -, mRNA.  
 DR PIR/ S21205; S21205.  
 DR HSSP/ P01783; 1IGC.  
 DR SMR/ Q9UL72; 1-118.  
 DR InterPro/ IPR007110; Ig\_1like.



RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences." J.  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC NIH MGC Project.  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC018747; AA18747.1; -, mRNA.  
 DR HSSP; P01861; IADQ.  
 DR SMR; O6PJA4; 20-470.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;  
 Query Match 91.5%; Score 151; DB 2; Length 470;  
 Best Local Similarity 87.5%; Pred. No. 2.5e-13;  
 Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RFTISRDNKNTFLQNSLRADDTAVYYCAR 32  
 DB 86 RFTISRDNKNSLYLQNSLRADDTAVYYCAR 117  
 RESULT 12  
 Q6P181\_HUMAN PRELIMINARY; PRT; 478 AA.  
 AC Q6P181; 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE IGHM protein.  
 GN Name=IGHM;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RA MBLIME=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Dactchenko L., Mariani K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stajich E.M., Soares M.B., Donaldson M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueding T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hults S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heltan E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RG NIH MGC Project;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC041037; AA41037.1; -, mRNA.  
 DR HSSP; P01861; IADQ.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
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 Query Match 91.5%; Score 151; DB 2; Length 478;  
 Best Local Similarity 87.5%; Pred. No. 2.5e-13;  
 Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RFTISRDNKNTFLQNSLRADDTAVYYCAR 32  
 DB 86 RFTISRDNKNSLYLQNSLRADDTAVYYCAR 117  
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 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
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 GN Name=  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
 OC Homo.  
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 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Mammary gland;  
 RX PubMed=14702039; DOI=10.1038/ng1285;  
 RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RA Yamamoto J., Ii, Saito K., Kawai Y., Isono Y., Nakamura Y.,  
 RA Nagahara K., Murakami K., Yasuda T., Iwatsuki T., Magatsuna M.,  
 RA Shiratori A., Sudo H., Hosoki T., Kaku T., Kodaira H., Kondo H.,  
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
 RA Omura Y., Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa K.,  
 RA Yamazaki M., Niimura K., Ishibashi T., Yamashita H., Murakawa K.,  
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,  
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Horiuchi T.,  
 RA Kusano J., Kanehori K., Takahashi-Fuji A., Hara H., Tanase T.-O.,  
 RA Nomura Y., Togiyama S., Komai F., Hara R., Takeuchi K., Arita M.,  
 RA Iino N., Mutsaers K., Yuuki F., Hara R., Oshima A., Sasaki N., Aotsuka S.,  
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Tashiro H., Taniguchi A., Fujisawa T.,  
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirose M., Ohnori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuko Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 RT cDNAs";  
 RU Nat. Genet. 36:40-45(2004).  
 RN [2]  
 RP PROTEIN SEQUENCE.  
 RX PubMed=1555592;  
 RA Makiya R., Stigbrand T.;  
 RT "Placental alkaline phosphatase has a binding site for the human  
 RT immunoglobulin-G Fc portion";  
 RL Eur. J. Biochem. 205:341-345(1992).  
 DR EMBL; AK027379; BAB55072.1; -; mRNA.  
 DR PIR; S21205; S21205.  
 DR HSSP; P01876; 10M0.  
 DR SMR; Q96K68; 264-472.  
 DR InterPro; IPR007110; Ig-1like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; CI-sect; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
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 Best Local Similarity 87.5%; Pred. No. 2.6e-13;  
 Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 FFTSRDNRKNTLFLQNSLRADDTAVYYCAR 32  
 Db 86 FFTSRDNRKNTLFLQNSLRADDTAVYYCAR 117  
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 AC 06GMW2  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE IGHM protein.  
 DE Name=IGHM;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strusberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,  
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.B., Jones S.J.M., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Primary B-Cells;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073758; AAH73758.1; -; mRNA.  
 DR SKR; Q6GMW2; 20-256.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-1like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; CI-sect; 4.  
 DR SMART; SM00409; IGV; 2.  
 DR SMART; SM00407; IGV; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
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 Best Local Similarity 87.5%; Pred. No. 3.3e-13;  
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 Db 86 FFTSRDNRKNTLFLQNSLRADDTAVYYCAR 117  
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 AC 09UL93;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalish N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC PubMed=2840480;  
 RX Bird J., Gallili N., Link M., Stiles D., Sklar J.;  
 RA "Continuing rearrangement but absence of somatic hypermutation in  
 RT immunoglobulin genes of human B cell precursor leukemia";  
 RT J. Exp. Med. 181:229-245(1998).  
 RL EMBL; AF035021; AAD56257.1; -; mRNA.  
 DR PIR; PH1644; PH1644.  
 DR PIR; P01020; P01020.  
 DR HSSP; P01772; 2F84.  
 DR SMR; Q9UL93; 1-116.  
 DR InterPro; IPR007110; Ig-1like.  
 DR InterPro; IPR003596; Ig\_v.





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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:31 / Search time 12.0733 Seconds  
(without alignments)  
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Title: US-10-632-706-196

Perfect score: 165  
Sequence: 1 RFTISRDNKNTLFLQNNSLRADDTAVYYCAR 32

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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- 3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/PCITUS\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/RE\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	98.2	126	2	US-09-240-274-152 Sequence 152, App
2	162	98.2	126	2	US-09-848-798-152 Sequence 152, App
3	162	98.2	127	2	US-09-240-274-139 Sequence 139, App
4	162	98.2	127	2	US-09-848-798-139 Sequence 139, App
5	161	97.6	167	2	US-09-472-087-74 Sequence 74, Appl
6	161	97.6	463	2	US-09-472-087-11 Sequence 1, Appl
7	161	97.6	463	2	US-09-472-087-63 Sequence 63, Appl
8	161	97.6	463	2	US-09-472-087-64 Sequence 64, Appl
9	158	95.8	32	1	US-08-471-780C-82 Sequence 82, Appl
10	158	95.8	32	1	US-08-467-282B-82 Sequence 82, Appl
11	158	95.8	32	1	US-08-471-282A-82 Sequence 82, Appl
12	158	95.8	32	1	US-08-466-710C-82 Sequence 82, Appl
13	158	95.8	32	1	US-08-470-133-21 Sequence 21, Appl
14	158	95.8	32	1	US-08-468-739C-82 Sequence 82, Appl
15	158	95.8	32	2	US-09-347-061-21 Sequence 21, Appl
16	158	95.8	32	2	US-09-563-222C-142 Sequence 142, App
17	158	95.8	32	2	US-09-855-271-21 Sequence 21, Appl
18	158	95.8	32	2	US-09-293-769A-82 Sequence 82, Appl
19	158	95.8	32	2	US-08-537-871A-64 Sequence 64, Appl
20	158	95.8	89	2	US-09-472-087-72 Sequence 72, Appl
21	158	95.8	95	2	US-09-043-514-2 Sequence 2, Appl
22	158	95.8	97	2	US-10-194-975-29 Sequence 29, Appl
23	158	95.8	97	2	US-10-194-975-31 Sequence 31, Appl
24	158	95.8	97	2	US-09-534-717-616 Sequence 616, App
25	158	95.8	98	1	US-08-211-202-118 Sequence 118, App
26	158	95.8	98	1	US-10-194-975-24 Sequence 24, Appl
27	158	95.8	98	2	US-10-194-975-26 Sequence 26, Appl

28	158	95.8	98	2	US-10-194-975-30 Sequence 30, Appl
29	158	95.8	98	2	US-09-534-717-624 Sequence 624, App
30	158	95.8	98	2	US-09-534-717-625 Sequence 625, App
31	158	95.8	98	2	US-09-534-717-627 Sequence 627, App
32	158	95.8	98	2	US-09-534-717-628 Sequence 628, App
33	158	95.8	98	2	US-09-534-717-629 Sequence 629, App
34	158	95.8	98	2	US-09-534-717-630 Sequence 630, App
35	158	95.8	98	2	US-09-534-717-631 Sequence 631, App
36	158	95.8	98	2	US-09-534-717-632 Sequence 632, App
37	158	95.8	98	2	US-09-534-717-633 Sequence 633, App
38	158	95.8	98	2	US-09-534-717-634 Sequence 634, App
39	158	95.8	98	2	US-09-534-717-636 Sequence 636, App
40	158	95.8	98	2	US-09-534-717-641 Sequence 641, App
41	158	95.8	98	2	US-09-534-717-642 Sequence 642, App
42	158	95.8	98	2	US-09-534-717-643 Sequence 643, App
43	158	95.8	98	2	US-09-534-717-644 Sequence 644, App
44	158	95.8	98	2	US-09-534-717-646 Sequence 646, App
45	158	95.8	98	2	US-09-534-717-651 Sequence 651, App

## ALIGNMENTS

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RESULT 1
US-09-240-274-152
; Sequence 152, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rb(D)-BINDING PROTEIN AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THERMOF
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-152
Query Match 98.2% Score 162, DB 2, Length 126;
Best Local Similarity 96.9% Pred. No. 1e-15; 0, Indels 0, Gaps 0;
Matches 31, Conservative 1, Mismatches 98
CQ 1 RFTISRDNKNTLFLQNNSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLFLQNNSLRADDTAVYYCAR 98
RESULT 2
US-09-848-798-152
; Sequence 152, Application US/09848798
; Patent No. 6658719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rb(D)-BINDING PROTEIN AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THERMOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-152

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Best Local Similarity 96.9%; Pred. No. 1e-15;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-240-274-139
; Sequence 139, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH10
US-09-240-274-139

Query Match          98.2%; Score 162; DB 2; Length 127;
Best Local Similarity 96.9%; Pred. No. 1e-15;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
Db      68 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 99

RESULT 4
US-09-848-798-139
; Sequence 139, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH10
US-09-848-798-139

Query Match          98.2%; Score 162; DB 2; Length 127;
Best Local Similarity 96.9%; Pred. No. 1e-15;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
Db      68 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 99

RESULT 5
US-09-472-087-74
; Sequence 74, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-472-087-74

Query Match          97.6%; Score 161; DB 2; Length 167;
Best Local Similarity 96.9%; Pred. No. 1.9e-15;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
Db      58 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 89

RESULT 6
US-09-472-087-1
; Sequence 1, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-472-087-1

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Query Match 97.6%; Score 161; DB 2; Length 463;  
Best Local Similarity 96.9%; Pred. No. 6.1e-15;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTSRDMSKNTLFLQWNSLRADTAVYYCAR 32  
Db 86 RFTSRDMSKNTLFLQWNSLRADTAVYYCAR 117

RESULT 7  
US-09-472-087-63  
Sequence 63, Application US/09472087  
Patent No. 6682736  
GENERAL INFORMATION:  
APPLICANT: HANSON, DOUGLAS C.  
APPLICANT: NEVEU, MARK J.  
APPLICANT: MUELLER, EILEEN E.  
APPLICANT: HANKE, JEFFREY H.  
APPLICANT: GILMAN, STEVEN C.  
APPLICANT: DAVIS, C. GEOFFREY  
APPLICANT: CORVALLAN, JOSE R.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
FILE REFERENCE: ABX-PPI  
CURRENT APPLICATION NUMBER: US/09/472.087  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/113,647  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 63  
LENGTH: 463  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-472-087-63

Query Match 97.6%; Score 161; DB 2; Length 463;  
Best Local Similarity 96.9%; Pred. No. 6.1e-15;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTSRDMSKNTLFLQWNSLRADTAVYYCAR 32  
Db 86 RFTSRDMSKNTLFLQWNSLRADTAVYYCAR 117

RESULT 8  
US-09-472-087-64  
Sequence 64, Application US/09472087  
Patent No. 6682736  
GENERAL INFORMATION:  
APPLICANT: HANSON, DOUGLAS C.  
APPLICANT: NEVEU, MARK J.  
APPLICANT: MUELLER, EILEEN E.  
APPLICANT: HANKE, JEFFREY H.  
APPLICANT: GILMAN, STEVEN C.  
APPLICANT: DAVIS, C. GEOFFREY  
APPLICANT: CORVALLAN, JOSE R.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
FILE REFERENCE: ABX-PPI  
CURRENT APPLICATION NUMBER: US/09/472.087  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/113,647  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 64  
LENGTH: 463  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-472-087-64

Query Match 97.6%; Score 161; DB 2; Length 463;  
Best Local Similarity 96.9%; Pred. No. 6.1e-15;

Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTSRDMSKNTLFLQWNSLRADTAVYYCAR 32  
Db 86 RFTSRDMSKNTLFLQWNSLRADTAVYYCAR 117

RESULT 9  
US-08-471-780C-82  
Sequence 82, Application US/08471780C  
Patent No. 5759808  
GENERAL INFORMATION:  
APPLICANT: Castelman, Cecile  
APPLICANT: Hamers, Raymond  
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Flinnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471.780C  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/106,944  
FILING DATE: 17-AUG-1993  
APPLICATION NUMBER: FR 92402326.0  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 93401310.3  
FILING DATE: 21-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E.R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 04958.0008-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-780C-82

Query Match 95.8%; Score 158; DB 1; Length 32;  
Best Local Similarity 93.8%; Pred. No. 7.8e-16;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTSRDMSKNTLFLQWNSLRADTAVYYCAR 32  
Db 1 RFTSRDMSKNTLFLQWNSLRADTAVYYCAR 32

RESULT 10  
US-08-467-282B-82  
Sequence 82, Application US/08467282B  
Patent No. 5800988  
GENERAL INFORMATION:  
APPLICANT: Castelman, Cecile  
APPLICANT: Hamers, Raymond  
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains

```

NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,282B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-282B-82

Query Match          95.8%; Score 158; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 7.8e-16;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 32
DB 1 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 32

RESULT 11
US-08-471-282A-82
Sequence 82, Application US/08471282A
Patent No. 5840853
GENERAL INFORMATION:
APPLICANT: Casteleman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,282A
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-282A-82

Query Match          95.8%; Score 158; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 7.8e-16;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 32
DB 1 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 32

RESULT 12
US-08-466-710C-82
Sequence 82, Application US/08466710C
Patent No. 5874541
GENERAL INFORMATION:
APPLICANT: Casteleman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,710C
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-466-710C-82

Query Match 95.8%; Score 158; DB 1; Length 32;  
Best Local Similarity 93.8%; Pred. No. 7.8e-16;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSKNTLFLQNMSLRADDTAVYYCAR 32  
DB 1 RFTISRDNSKNTLYIQNMSLRADDTAVYYCAR 32

RESULT 13  
US-08-470-139-21  
Sequence 21, Application US/08470139  
Patent No. 5998586  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies  
NUMBER OF SEQUENCES: 28  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,139  
FILING DATE: 06 JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: TRUITILO, DOREEN YATKO  
REGISTRATION/DOCKET NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CARP-0044  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-470-139-21

Query Match 95.8%; Score 158; DB 1; Length 32;  
Best Local Similarity 93.8%; Pred. No. 7.8e-16;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSKNTLFLQNMSLRADDTAVYYCAR 32  
DB 1 RFTISRDNSKNTLYIQNMSLRADDTAVYYCAR 32

RESULT 14  
US-08-468-739C-82  
Sequence 82, Application US/08468739C  
Patent No. 6015695  
GENERAL INFORMATION:  
APPLICANT: Casterman, Cecile  
APPLICANT: Haney, Raymond  
TITLE OF INVENTION: Immunoglobulins devoid of light chains  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESS: Flinnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.

COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,739C  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/106,944  
FILING DATE: 17-AUG-1993  
APPLICATION NUMBER: FR 92402326.0  
FILING DATE: 21-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 93401310.3  
FILING DATE: 21-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pottery, Jane B.R.  
REGISTRATION/DOCKET NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 04958.0008-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-739C-82

Query Match 95.8%; Score 158; DB 2; Length 32;  
Best Local Similarity 93.8%; Pred. No. 7.8e-16;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSKNTLFLQNMSLRADDTAVYYCAR 32  
DB 1 RFTISRDNSKNTLYIQNMSLRADDTAVYYCAR 32

RESULT 15  
US-09-347-061-21  
Sequence 21, Application US/09347061  
Patent No. 6316227  
GENERAL INFORMATION:  
APPLICANT: Bodmer, Mark  
APPLICANT: Athwal, Diljeet Singh  
APPLICANT: Emtage, John Spencer  
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies  
FILE REFERENCE: CARP-0071  
CURRENT APPLICATION NUMBER: US/09/347,061  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 21  
LENGTH: 32  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Consensus  
US-09-347-061-21

Query Match 95.8%; Score 158; DB 2; Length 32;  
Best Local Similarity 93.8%; Pred. No. 7.8e-16;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSKNTLFLQNMSLRADDTAVYYCAR 32  
DB 1 RFTISRDNSKNTLYIQNMSLRADDTAVYYCAR 32

Db 1 RFTISRDNSKNTLYLQNNSLRAEPTAVYYCAR 32

Search completed: November 21, 2005, 12:07:40  
Job time : 12.0733 secs

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## OM protein - protein search, using sw model

Run on: November 21, 2005, 11:50:51, Search time 39.619 Seconds  
(without alignments)  
337,478 Million cell updates/sec

Title: US-10-632-706-196  
Perfect score: 165  
Sequence: 1 RFTISRDNKNTLFLQNMSLRADDTAVYYCAR 32

Scoring table:  
BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	165	100.0	32 4 US-10-632-706-193	Sequence 193, App
2	165	100.0	32 4 US-10-632-706-196	Sequence 196, App
3	165	100.0	32 4 US-10-632-706-199	Sequence 199, App
4	165	100.0	32 4 US-10-632-706-202	Sequence 202, App
5	162	98.2	118 5 US-10-886-838-3	Sequence 3, Appl
6	162	98.2	126 3 US-09-848-798-152	Sequence 152, App
7	162	98.2	127 3 US-09-848-798-139	Sequence 139, App
8	162	98.2	244 5 US-10-935-229-55	Sequence 55, Appl
9	161	97.6	115 5 US-10-727-155-144	Sequence 144, App
10	161	97.6	122 5 US-10-727-155-158	Sequence 158, App
11	161	97.6	122 5 US-10-727-155-214	Sequence 214, App
12	161	97.6	167 5 US-10-612-497-74	Sequence 74, Appl
13	161	97.6	167 5 US-10-776-649-74	Sequence 74, Appl
14	161	97.6	463 4 US-10-153-382-3	Sequence 3, Appl
15	161	97.6	463 4 US-10-153-382-5	Sequence 5, Appl
16	161	97.6	463 4 US-10-612-497-1	Sequence 63, Appl
17	161	97.6	463 5 US-10-612-497-63	Sequence 64, Appl
18	161	97.6	463 5 US-10-612-497-64	Sequence 1, Appl
19	161	97.6	463 5 US-10-776-649-1	Sequence 63, Appl
20	161	97.6	463 5 US-10-776-649-63	Sequence 64, Appl
21	161	97.6	463 5 US-11-085-368-3	Sequence 3, Appl
22	161	97.6	463 6 US-11-085-368-5	Sequence 5, Appl
23	161	97.6	463 6 US-11-085-368-41	Sequence 41, Appl
24	161	97.6	463 6 US-09-855-271-21	Sequence 21, App
25	158	95.8	32 3 US-09-949-559-123	Sequence 123, App
26	158	95.8	32 3 US-09-873-221A-123	Sequence 123, App
27	158	95.8	32 3 US-09-873-221A-123	Sequence 123, App

28	158	95.8	32 3 US-09-563-212-152	Sequence 152, App
29	158	95.8	32 4 US-10-663-244-28	Sequence 28, Appl
30	158	95.8	32 4 US-10-783-950-142	Sequence 142, Appl
31	158	95.8	32 5 US-10-764-418-30	Sequence 30, Appl
32	158	95.8	32 5 US-10-751-826-82	Sequence 82, Appl
33	158	95.8	32 5 US-10-728-4108-108	Sequence 108, App
34	158	95.8	32 5 US-10-923-068-203	Sequence 203, App
35	158	95.8	32 5 US-10-923-068-206	Sequence 206, App
36	158	95.8	32 5 US-10-923-068-224	Sequence 224, App
37	158	95.8	32 5 US-10-923-068-230	Sequence 230, App
38	158	95.8	32 5 US-10-923-068-335	Sequence 335, App
39	158	95.8	32 5 US-10-923-068-338	Sequence 338, App
40	158	95.8	32 5 US-10-923-068-356	Sequence 356, App
41	158	95.8	32 5 US-10-923-068-362	Sequence 362, App
42	158	95.8	32 5 US-10-914-015-108	Sequence 108, App
43	158	95.8	32 5 US-10-877-773-111	Sequence 111, App
44	158	95.8	32 5 US-10-877-773-124	Sequence 124, App
45	158	95.8	32 5 US-10-877-774-111	Sequence 111, App

## ALIGNMENTS

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RESULT 1
US-10-632-706-193
; Sequence 193, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSOBER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-193
Query Match      100.0%; Score 165, DB 4, Length 32;
Best local similarity 100.0%; Pred. No. 3, 4e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy      1 RFTISRDNKNTLFLQNMSLRADDTAVYYCAR 32
Db      1 RFTISRDNKNTLFLQNMSLRADDTAVYYCAR 32
RESULT 2
US-10-632-706-196
; Sequence 196, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSOBER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
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/ PRIOR FILING DATE: 1998-08-31  
/ NUMBER OF SEQ ID NOS: 278  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 196  
/ LENGTH: 32  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-196

Query Match 100.0%; Score 165; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.4e-15;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32  
Db 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32

RESULT 3  
US-10-632-706-199  
/ Sequence 199, Application US/10632706  
/ Publication No. US2004015385A1  
/ GENERAL INFORMATION:  
/ APPLICANT: MARKS, JAMES D.  
/ APPLICANT: AMERSORFER, PETER  
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
/ FILE REFERENCE: 407T-895120US  
/ CURRENT APPLICATION NUMBER: US/10/632,706  
/ PRIOR FILING DATE: 2003-08-01  
/ PRIOR APPLICATION NUMBER: US 60/400,721  
/ PRIOR FILING DATE: 2002-08-01  
/ PRIOR APPLICATION NUMBER: US 09/144,806  
/ PRIOR FILING DATE: 1998-08-31  
/ NUMBER OF SEQ ID NOS: 278  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 199  
/ LENGTH: 32  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-199

Query Match 100.0%; Score 165; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.4e-15;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32  
Db 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32

RESULT 4  
US-10-632-706-202  
/ Sequence 202, Application US/10632706  
/ Publication No. US2004015385A1  
/ GENERAL INFORMATION:  
/ APPLICANT: MARKS, JAMES D.  
/ APPLICANT: AMERSORFER, PETER  
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM  
/ FILE REFERENCE: 407T-895120US  
/ CURRENT APPLICATION NUMBER: US/10/632,706  
/ PRIOR FILING DATE: 2003-08-01  
/ PRIOR APPLICATION NUMBER: US 60/400,721  
/ PRIOR FILING DATE: 2002-08-01  
/ PRIOR APPLICATION NUMBER: US 09/144,806  
/ PRIOR FILING DATE: 1998-08-31  
/ NUMBER OF SEQ ID NOS: 278  
/ SOFTWARE: PatentIn version 3.2

/ SEQ ID NO 202  
/ LENGTH: 32  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ OTHER INFORMATION: single chain antibody fragment  
US-10-632-706-202

Query Match 100.0%; Score 165; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.4e-15;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32  
Db 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32

RESULT 5  
US-10-886-838-3  
/ Sequence 3, Application US/10886838  
/ Publication No. US20050008642A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Hoffmann-La Roche Inc.  
/ TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses  
/ FILE REFERENCE: 21695  
/ CURRENT APPLICATION NUMBER: US/10/886,838  
/ PRIOR FILING DATE: 2004-07-08  
/ PRIOR APPLICATION NUMBER: EP 03015526  
/ PRIOR FILING DATE: 2003-07-10  
/ NUMBER OF SEQ ID NOS: 8  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 3  
/ LENGTH: 118  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-886-838-3

Query Match 98.2%; Score 162; DB 5; Length 118;  
Best Local Similarity 96.9%; Pred. No. 3.6e-14;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32  
Db 67 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 98

RESULT 6  
US-09-848-798-152  
/ Sequence 152, Application US/09848798  
/ Publication No. US20030040605A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Siegel, Donald L.  
/ TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
/ FILE REFERENCE: 09596-42U2  
/ CURRENT APPLICATION NUMBER: US/09/848,798  
/ PRIOR FILING DATE: 2001-05-04  
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
/ PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
/ NUMBER OF SEQ ID NOS: 224  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 152  
/ LENGTH: 126  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ OTHER INFORMATION: anti-Rh(D) antibody clone SH54  
US-09-848-798-152

Query Match 98.2%; Score 162; DB 3; Length 126;



Best Local Similarity 96.9%; Pred. No. 3.9e-14;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32  
Db 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 98

## RESULT 7

US-09-848-798-139  
; Sequence 139, Application US/09848798  
; Publication No. US20030040605A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/848,798  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 139  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) antibody clone SH10  
US-09-848-798-139

Query Match 98.2%; Score 162; DB 3; Length 127;  
Best Local Similarity 96.9%; Pred. No. 3.9e-14;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32  
Db 68 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 99

## RESULT 8

US-10-935-290-55  
; Sequence 55, Application US/10935290  
; Publication No. US20050069542A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker et al.  
; TITLE OF INVENTION: Antibodies that Specifically Bind to GMD  
; FILE REFERENCE: PFS64P1  
; CURRENT APPLICATION NUMBER: US/10/935,290  
; PRIOR FILING DATE: 2004-09-08  
; PRIOR APPLICATION NUMBER: PCT/US03/09625  
; PRIOR FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: 60/368,813  
; PRIOR FILING DATE: 2002-04-01  
; NUMBER OF SEQ ID NOS: 234  
; SEQ ID NO 55  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: scFv protein GMB619  
US-10-935-290-55

Query Match 98.2%; Score 162; DB 5; Length 244;  
Best Local Similarity 96.9%; Pred. No. 8e-14;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32  
Db 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 98

## RESULT 9

US-10-727-155-144  
; Sequence 144, Application US/10727155  
; Publication No. US20050049402A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. Babcock  
; APPLICANT: Jaspal S. Kang  
; APPLICANT: Orit Poord  
; APPLICANT: Larry Green  
; APPLICANT: Xiao Feng  
; APPLICANT: Scott Klakamp  
; APPLICANT: Mary Haak-Frendscho  
; APPLICANT: Palaniswami Rathanaswami  
; APPLICANT: Craig Pigott  
; APPLICANT: Meina Liang  
; APPLICANT: Rozanne Lee  
; APPLICANT: Kathy Manchulenko  
; APPLICANT: Raffaella Raggioni  
; APPLICANT: Giorgio Senaldi  
; APPLICANT: Qiaojuan Jane Su  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
; FILE REFERENCE: ABGENIX 073A  
; CURRENT APPLICATION NUMBER: US/10/727,155  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: 60/430729  
; PRIOR FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 320  
; SOFTWARE: PasteSeq for Windows Version 4.0  
; SEQ ID NO 144  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-727-155-144

Query Match 97.6%; Score 161; DB 5; Length 115;  
Best Local Similarity 96.9%; Pred. No. 4.8e-14;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32  
Db 66 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 97

## RESULT 10

US-10-727-155-198  
; Sequence 198, Application US/10727155  
; Publication No. US20050049402A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. Babcock  
; APPLICANT: Jaspal S. Kang  
; APPLICANT: Orit Poord  
; APPLICANT: Larry Green  
; APPLICANT: Xiao Feng  
; APPLICANT: Scott Klakamp  
; APPLICANT: Mary Haak-Frendscho  
; APPLICANT: Palaniswami Rathanaswami  
; APPLICANT: Craig Pigott  
; APPLICANT: Meina Liang  
; APPLICANT: Rozanne Lee  
; APPLICANT: Kathy Manchulenko  
; APPLICANT: Raffaella Raggioni  
; APPLICANT: Giorgio Senaldi  
; APPLICANT: Qiaojuan Jane Su  
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS  
; FILE REFERENCE: ABGENIX 073A  
; CURRENT APPLICATION NUMBER: US/10/727,155  
; PRIOR FILING DATE: 2003-12-02  
; PRIOR APPLICATION NUMBER: 60/430729  
; PRIOR FILING DATE: 2002-12-02  
; NUMBER OF SEQ ID NOS: 320

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/ SOFTWARE: PatSeq for Windows Version 4.0
/ SEQ ID NO 198
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-727-155-198
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Query Match          97.6%; Score 161; DB 5; Length 122;
Best Local Similarity 96.9%; Pred. No. 5,1e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 98
```

```
RESULT 11
US-10-727-155-214
/ Sequence 214, Application US/10727155
/ Publication No. US20050049402A1
/ GENERAL INFORMATION:
/ APPLICANT: John S. Babcock
/ APPLICANT: Jaspal S. Kang
/ APPLICANT: Orit Foord
/ APPLICANT: Larry Green
/ APPLICANT: Xiao Feng
/ APPLICANT: Scott Klakamp
/ APPLICANT: Mary Haak-Frendocho
/ APPLICANT: Palaniswami Rathnaswami
/ APPLICANT: Craig Pigott
/ APPLICANT: Meina Liang
/ APPLICANT: Rozanne Lee
/ APPLICANT: Kathy Manchlencho
/ APPLICANT: Raffaella Faggioni
/ APPLICANT: Giorgio Senaldi
/ APPLICANT: Qiaojuan Jane Su
/ TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
/ FILE REFERENCE: ABGENIX 073A
/ CURRENT APPLICATION NUMBER: US/10/727,155
/ PRIOR FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: 60/430729
/ NUMBER OF SEQ ID NOS: 320
/ SOFTWARE: PatSeq for Windows Version 4.0
/ SEQ ID NO 214
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-727-155-214
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Query Match          97.6%; Score 161; DB 5; Length 122;
Best Local Similarity 96.9%; Pred. No. 5,1e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 98
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```
RESULT 12
US-10-612-497-74
/ Sequence 74, Application US/10612497
/ Publication No. US20040228658A1
/ GENERAL INFORMATION:
/ APPLICANT: Douglas C. Hanson
/ APPLICANT: Mark J. Neveu
/ APPLICANT: Bileen E. Mueller
/ APPLICANT: Jeffrey H. Hanke
/ APPLICANT: Steven C. Gilman
/ APPLICANT: C. Geoffrey Davis
/ APPLICANT: Jose R. Corvalan
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
```

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/ FILE REFERENCE: ABX-PF1 DIV1
/ CURRENT APPLICATION NUMBER: US/10/612,497
/ CURRENT FILING DATE: 2003-07-01
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 60/113647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 74
/ LENGTH: 167
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-612-497-74
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Query Match          97.6%; Score 161; DB 5; Length 167;
Best Local Similarity 96.9%; Pred. No. 7,2e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
Db 58 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 89
```

```
RESULT 13
US-10-776-649-74
/ Sequence 74, Application US/10776649
/ Publication No. US20040228661A1
/ GENERAL INFORMATION:
/ APPLICANT: Douglas C. Hanson
/ APPLICANT: Mark J. Neveu
/ APPLICANT: Bileen E. Mueller
/ APPLICANT: Jeffrey H. Hanke
/ APPLICANT: Steven C. Gilman
/ APPLICANT: C. Geoffrey Davis
/ APPLICANT: Jose R. Corvalan
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1 DIV2
/ CURRENT APPLICATION NUMBER: US/10/776,649
/ CURRENT FILING DATE: 2004-02-10
/ PRIOR FILING DATE: 2003-07-01
/ PRIOR APPLICATION NUMBER: US 10/612497
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1998-12-23
/ PRIOR APPLICATION NUMBER: US 60/113647
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 74
/ LENGTH: 167
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-776-649-74
```

```
Query Match          97.6%; Score 161; DB 5; Length 167;
Best Local Similarity 96.9%; Pred. No. 7,2e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
Db 58 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 89
```

```
RESULT 14
US-10-153-382-3
/ Sequence 3, Application US/10153382
/ Publication No. US20030086930A1
/ GENERAL INFORMATION:
/ APPLICANT: PFIZER PRODUCTS INC.
/ TITLE OF INVENTION: USBS OF ANTI-CTLA-4 ANTIBODIES
/ FILE REFERENCE: PC23019A
/ CURRENT APPLICATION NUMBER: US/10/153,382
/ CURRENT FILING DATE: 2002-05-22
```

PRIOR APPLICATION NUMBER: 60/293042  
PRIOR FILING DATE: 2001-05-23  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 463  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-153-382-3

Query Match 97.6%; Score 161; DB 4; Length 463;  
Best Local Similarity 96.9%; Pred. No. 2.2e-13;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDN SKNTLFLQWNSLRADDTAVYYCAR 32  
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DB 86 RFTISRDN SKNTLFLQWNSLRADDTAVYYCAR 117

RESULT 15  
US-10-153-382-5  
Sequence 5, Application US/10153382  
Publication No. US20030086930A1  
GENERAL INFORMATION:  
APPLICANT: PFIZER PRODUCTS INC.  
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES  
FILE REFERENCE: PC23019A  
CURRENT APPLICATION NUMBER: US/10/153,382  
CURRENT FILING DATE: 2002-05-22  
PRIOR APPLICATION NUMBER: 60/293042  
PRIOR FILING DATE: 2001-05-23  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 463  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-153-382-5

Query Match 97.6%; Score 161; DB 4; Length 463;  
Best Local Similarity 96.9%; Pred. No. 2.2e-13;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDN SKNTLFLQWNSLRADDTAVYYCAR 32  
|||||  
DB 86 RFTISRDN SKNTLFLQWNSLRADDTAVYYCAR 117

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Job time : 39.619 secs

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OM protein - protein search, using BW model

Run on: November 21, 2005, 12:04:27 ; Search time 0.586081 Seconds  
(without alignments)

61.666 Million cell updates/sec

Title: US-10-632-706-196

Perfect score: 165

Sequence: 1 RFTISRDNKNTLFLQNNSLRADDTAVYYCAR 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	158	95.8	102	1	US-10-997-201A-6
2	155	93.9	98	1	US-10-789-273-10
3	155	93.9	98	7	US-11-144-248-32
4	155	93.9	122	7	US-11-144-248-24
5	155	93.9	125	7	US-11-144-248-16
6	155	93.9	139	1	US-10-721-763-33
7	155	93.9	470	7	US-11-144-248-46
8	154	93.3	138	1	US-10-789-273-12
9	151	91.5	98	7	US-11-144-248-30
10	151	91.5	444	7	US-11-172-320-6
11	151	91.5	473	7	US-11-144-248-50
12	147	89.1	174	7	US-11-144-248-4
13	147	89.1	470	7	US-11-144-248-49
14	146	88.5	124	7	US-11-144-248-8
15	146	88.5	470	7	US-11-144-248-45
16	145	87.3	121	1	US-10-789-273-9
17	144	87.3	138	1	US-10-789-273-8
18	138	83.4	120	7	US-11-077-978-7
19	136	82.4	121	7	US-11-077-978-2
20	133	80.6	138	1	US-10-789-273-4
21	128	77.6	118	1	US-10-648-816-9
22	128	77.6	118	1	US-10-648-816-10
23	128	77.6	118	1	US-10-648-816-11
24	128	77.6	118	1	US-10-648-816-12
25	128	77.6	118	1	US-10-648-816-13

26	128	77.6	118	1	US-10-648-816-14	Sequence 14, Appl
27	128	77.6	121	1	US-10-648-816-15	Sequence 15, Appl
28	128	77.6	121	1	US-10-648-816-16	Sequence 16, Appl
29	128	77.6	121	7	US-11-077-978-3	Sequence 3, Appl
30	127	77.0	543	1	US-10-495-664-3	Sequence 3, Appl
31	126	76.4	114	1	US-10-726-554-8	Sequence 8, Appl
32	119	72.1	119	7	US-11-010-954-5	Sequence 5, Appl
33	119	72.1	263	1	US-10-512-184-29	Sequence 29, Appl
34	118	71.5	250	1	US-10-512-184-27	Sequence 27, Appl
35	114	69.1	328	1	US-10-512-184-26	Sequence 26, Appl
36	114	69.1	327	1	US-10-512-184-62	Sequence 62, Appl
37	114	69.1	327	1	US-10-512-184-64	Sequence 64, Appl
38	114	69.1	328	1	US-10-512-184-63	Sequence 63, Appl
39	114	69.1	576	1	US-10-512-184-65	Sequence 65, Appl
40	114	69.1	625	1	US-10-512-184-47	Sequence 47, Appl
41	113	68.5	119	1	US-10-502-145-25	Sequence 25, Appl
42	111	67.3	118	7	US-11-012-393-71	Sequence 71, Appl
43	110	66.7	261	1	US-10-512-184-35	Sequence 35, Appl
44	110	66.7	313	1	US-10-512-184-72	Sequence 72, Appl
45	108	65.5	118	7	US-11-012-353-70	Sequence 70, Appl

#### ALIGNMENTS

RESULT 1  
US-10-997-201A-6  
Sequence 6, Application US/10997201A  
Publication No. US20050249739A1  
GENERAL INFORMATION:  
APPLICANT: Marasco, Wayne  
TITLE OF INVENTION: Anticodules Against SARS-COV and Methods of Use Thereof  
FILE REFERENCE: 20363-026  
CURRENT FILING DATE: 2004-11-24  
PRIOR APPLICATION NUMBER: US/10/997, 201A  
PRIOR FILING DATE: 2003-11-25  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 102  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-997-201A-6

Query Match 95.8% Score 158; DB 1; Length 102;  
Best Local Similarity 93.8% Pred. No. 4.2e-13;  
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNNSLRADDTAVYYCAR 32  
Db 57 RFTISRDNKNTLFLQNNSLRADDTAVYYCAR 86

RESULT 2  
US-10-789-273-10  
Sequence 10, Application US/10789273  
Publication No. US20050249725A1  
GENERAL INFORMATION:  
APPLICANT: Basi, Gurig  
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
FILE REFERENCE: EIM-002CP  
CURRENT FILING DATE: 2004-02-27  
PRIOR APPLICATION NUMBER: US/10/388, 389  
PRIOR FILING DATE: 2003-03-12  
PRIOR APPLICATION NUMBER: US 10/010, 942  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: US 60/251, 892

```
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-273-10
```

```
Query Match          93.9%; Score 155; DB 1; Length 98;
Best Local Similarity 90.6%; Pred. No. 1,9e-12;
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAK 98
```

## RESULT 3

```
US-11-144-248-32
; Sequence 32, Application US/11144248
; Publication NO. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-32
```

```
Query Match          93.9%; Score 155; DB 7; Length 98;
Best Local Similarity 90.6%; Pred. No. 1,9e-12;
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAK 98
```

## RESULT 4

```
US-11-144-248-24
; Sequence 24, Application US/11144248
; Publication NO. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
```

```
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-24
```

```
Query Match          93.9%; Score 155; DB 7; Length 122;
Best Local Similarity 90.6%; Pred. No. 2,4e-12;
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAK 98
```

## RESULT 5

```
US-11-144-248-16
; Sequence 16, Application US/11144248
; Publication NO. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-16
```

```
Query Match          93.9%; Score 155; DB 7; Length 125;
Best Local Similarity 90.6%; Pred. No. 2,4e-12;
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAK 98
```

## RESULT 6

```
US-10-721-763-33
; Sequence 33, Application US/10721763
; Publication NO. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCF
; CURRENT APPLICATION NUMBER: US/10/721,763
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 139
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;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-721-763-33

Query Match 93.9%; Score 155; DB 1; Length 139;  
Best Local Similarity 90.6%; Pred. No. 2.7e-12;  
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 32  
Db 86 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 117

RESULT 7  
US-11-144-248-46  
; Sequence 46, Application US/11144248  
; Publication No. US20050244408A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Bruce D.  
; APPLICANT: Beebe, Jean  
; APPLICANT: Miller, Penelope E.  
; APPLICANT: Moyer, James D.  
; APPLICANT: Corvalan, Jose R.  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
; FILE REFERENCE: ABX-PF2  
; CURRENT APPLICATION NUMBER: US/11/144,248  
; PRIOR FILING DATE: 2005-06-02  
; PRIOR APPLICATION NUMBER: US/10/038,591  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 60/259,927  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-144-248-46

Query Match 93.9%; Score 155; DB 7; Length 470;  
Best Local Similarity 90.6%; Pred. No. 8.3e-12;  
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 32  
Db 86 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 117

RESULT 8  
US-10-789-273-12  
; Sequence 12, Application US/10789273  
; Publication No. US20050249725A1  
; GENERAL INFORMATION:  
; APPLICANT: Basi, Gurliq  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDES  
; FILE REFERENCE: ELM-002CP  
; CURRENT APPLICATION NUMBER: US/10/789,273  
; PRIOR FILING DATE: 2004-02-27  
; PRIOR APPLICATION NUMBER: US/10/388,389  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 138  
; TYPE: PRT

;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Humanized 3D6 light chain variable region  
;; FEATURE:  
;; NAME/KEY: SIGNAL  
;; LOCATION: (1)...(19)  
US-10-789-273-12

Query Match 93.3%; Score 154; DB 1; Length 138;  
Best Local Similarity 90.6%; Pred. No. 3.4e-12;  
Matches 29; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 32  
Db 86 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 117

RESULT 9  
US-11-144-248-30  
; Sequence 30, Application US/11144248  
; Publication No. US20050244408A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Bruce D.  
; APPLICANT: Beebe, Jean  
; APPLICANT: Miller, Penelope E.  
; APPLICANT: Moyer, James D.  
; APPLICANT: Corvalan, Jose R.  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
; FILE REFERENCE: ABX-PF2  
; CURRENT APPLICATION NUMBER: US/11/144,248  
; PRIOR FILING DATE: 2005-06-02  
; PRIOR APPLICATION NUMBER: US/10/038,591  
; PRIOR FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 60/259,927  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-144-248-30

Query Match 91.5%; Score 151; DB 7; Length 98;  
Best Local Similarity 87.5%; Pred. No. 5.5e-12;  
Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 32  
Db 67 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 98

RESULT 10  
US-11-172-320-6  
; Sequence 6, Application US/11172320  
; Publication No. US20050244413A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, Guenther  
; APPLICANT: Baum, Anke  
; APPLICANT: Helder, Karl-Heinz  
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using  
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates and  
; TITLE OF INVENTION: Chemotherapeutic Agents  
; FILE REFERENCE: 1/1383  
; CURRENT APPLICATION NUMBER: US/11/172,320  
; PRIOR FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: US/10/645,215  
; PRIOR FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: EP 02 018 686.2  
; PRIOR FILING DATE: August 21, 2002  
; PRIOR APPLICATION NUMBER: US 60/405,956  
; PRIOR FILING DATE: August 26, 2002

NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 6  
LENGTH: 444  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Humanised Murine Antibody B1M4 4 Heavy Chain  
US-11-172-320-6

Query Match 91.5%; Score 151; DB 7; Length 444;  
Best Local Similarity 87.5%; Pred. No. 2.2e-11;  
Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32  
DB 67 RFTISRDNKNSLYLQNSLRADDTAVYYCAR 98

RESULT 11  
US-11-144-248-50

Sequence 50, Application US/11144248  
Publication No. US20050244408A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce D.  
APPLICANT: Beebe, Jean  
APPLICANT: Miller, Penelope E.  
APPLICANT: Moyer, James D.  
APPLICANT: Corvalan, Jose R.  
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
FILE REFERENCE: ABX-PF2  
CURRENT APPLICATION NUMBER: US/11/144,248  
CURRENT FILING DATE: 2005-06-02  
PRIOR APPLICATION NUMBER: US/10/038,591  
PRIOR FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: 60/259,927  
PRIOR FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 50  
LENGTH: 473  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-144-248-50

Query Match 91.5%; Score 151; DB 7; Length 473;  
Best Local Similarity 87.5%; Pred. No. 2.3e-11;  
Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32  
DB 86 RFTISRDNKNSLYLQNSLRADDTAVYYCAR 117

RESULT 12  
US-11-144-248-4

Sequence 4, Application US/11144248  
Publication No. US20050244408A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce D.  
APPLICANT: Beebe, Jean  
APPLICANT: Miller, Penelope E.  
APPLICANT: Moyer, James D.  
APPLICANT: Corvalan, Jose R.  
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
FILE REFERENCE: ABX-PF2  
CURRENT APPLICATION NUMBER: US/11/144,248  
CURRENT FILING DATE: 2005-06-02  
PRIOR APPLICATION NUMBER: US/10/038,591  
PRIOR FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: 60/259,927

PRIOR FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 4  
LENGTH: 174  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-144-248-4

Query Match 89.1%; Score 147; DB 7; Length 174;  
Best Local Similarity 84.4%; Pred. No. 2.6e-11;  
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32  
DB 59 RFTISRDNKNSLYLQNSLRADDTAVYYCAR 90

RESULT 13  
US-11-144-248-49

Sequence 49, Application US/11144248  
Publication No. US20050244408A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce D.  
APPLICANT: Beebe, Jean  
APPLICANT: Miller, Penelope E.  
APPLICANT: Moyer, James D.  
APPLICANT: Corvalan, Jose R.  
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
FILE REFERENCE: ABX-PF2  
CURRENT APPLICATION NUMBER: US/11/144,248  
CURRENT FILING DATE: 2005-06-02  
PRIOR APPLICATION NUMBER: US/10/038,591  
PRIOR FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: 60/259,927  
PRIOR FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 49  
LENGTH: 470  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-144-248-49

Query Match 89.1%; Score 147; DB 7; Length 470;  
Best Local Similarity 84.4%; Pred. No. 6.6e-11;  
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32  
DB 86 RFTISRDNKNSLYLQNSLRADDTAVYYCAR 117

RESULT 14  
US-11-144-248-8

Sequence 8, Application US/11144248  
Publication No. US20050244408A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Bruce D.  
APPLICANT: Beebe, Jean  
APPLICANT: Miller, Penelope E.  
APPLICANT: Moyer, James D.  
APPLICANT: Corvalan, Jose R.  
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
FILE REFERENCE: ABX-PF2  
CURRENT APPLICATION NUMBER: US/11/144,248  
CURRENT FILING DATE: 2005-06-02  
PRIOR APPLICATION NUMBER: US/10/038,591  
PRIOR FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: 60/259,927



; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 8  
 ; LENGTH: 124  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-144-248-8

Query Match 88.5%; Score 146; DB 7; Length 124;  
 Best Local Similarity 84.4%; Pred. No. 2.5e-11;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFTISRDN SKNTLFLQMSLRADDTAVYYCAR 32  
 |||||:|||||:|||||:|||||:|||||:  
 Db 66 RFTISRDN SKNTLFLQMSLRADDTAVYYCAR 97

RESULT 15  
 US-11-144-248-45  
 ; Sequence 45, Application US/11144248  
 ; Publication No. US20050244408A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cohen, Bruce D.  
 ; APPLICANT: Beebe, Jean  
 ; APPLICANT: Miller, Penelope E.  
 ; APPLICANT: Moyer, James D.  
 ; APPLICANT: Corvalan, Jose R.  
 ; APPLICANT: Gallo, Michael  
 ; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
 ; FILE REFERENCE: ABX-PF2  
 ; CURRENT APPLICATION NUMBER: US/11/144,248  
 ; CURRENT FILING DATE: 2005-06-02  
 ; PRIOR APPLICATION NUMBER: US/10/038,591  
 ; PRIOR FILING DATE: 2002-01-04  
 ; PRIOR APPLICATION NUMBER: 60/259,927  
 ; PRIOR FILING DATE: 2001-01-05  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 45  
 ; LENGTH: 470  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-144-248-45

Query Match 88.5%; Score 146; DB 7; Length 470;  
 Best Local Similarity 84.4%; Pred. No. 8.5e-11;  
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFTISRDN SKNTLFLQMSLRADDTAVYYCAR 32  
 |||||:|||||:|||||:|||||:|||||:  
 Db 66 RFTISRDN SKNTLFLQMSLRADDTAVYYCAR 117

Search completed: November 21, 2005, 12:33:52  
 Job time : 0.686081 secs

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